SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Harold Kleanthous et al.

(ii) TITLE OF THE INVENTION: Identification of Polynucleotides Encoding Novel Helicobacter Polypeptides in the Helicobacter Genome

(iii) NUMBER OF SEQUENCES: 370

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/833,457
(B) FILING DATE: 01-APR-97
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clark, Paul T.
(B) REGISTRATION NUMBER: 30,162
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...212
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
TTTTTTAGTT TGTTTTTGAG TATAATCCTA CGAAAATTTT AAGGAACGGC ATG GAG        56
                                                        Met Glu
                                                          1

TTT TTG GGA CTG ATT TTA AGT CTG GCC GCT ATT TTG ATA GCG TTT AAA      104
Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala Phe Lys
          5                  10                  15

AAG CCT GAA AAA GAA AAT TGG GCG TTT GGG ATT TTG ATG GTG GTG TGG      152
Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val Val Trp
     20                  25                  30

TTA GTG GAG CTT ATT ATT TTT ATA GCC CAC AGC TCT AGC GTT TTG CCT      200
Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val Leu Pro
35                   40                  45                  50

AAC ATG AAT CTA TAAGGGGGAT GCATGGATAA AGAAACCCGA TTTTACAACC TTTTT    257
Asn Met Asn Leu

TCTTTGGC                                                            265
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Glu Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala
 1               5                  10                  15
Phe Lys Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val
            20                  25                  30
Val Trp Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val
        35                  40                  45
Leu Pro Asn Met Asn Leu
    50
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 670 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...617
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CCCATAGACG ACAAAATCAA GCGGTTTTAT CAAAACCAAA AAACTTTAGA ATG AAA      56
                                                        Met Lys
                                                          1

AAA ATT GCT TTC ATT TTG GCT TTA TGG GTG GGC TTG TTA GGG GCG TTT     104
Lys Ile Ala Phe Ile Leu Ala Leu Trp Val Gly Leu Leu Gly Ala Phe
          5                  10                  15

GAG CCT AAA AAA AGT CAT ATT TAT TTT GGG GCT ATG GTG GGT TTA GCT     152
Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly Leu Ala
     20                  25                  30

CCT ATT AAA ATA ACC CCA AAA CCG GCT AGT GAT TCT TCT TAT ACG GCT     200
Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr Thr Ala
35                  40                  45                  50

TTT TTA TGG GGG GCT AAA GGA GGG TAT CAA TTC GCT TTT TTT AAA GCT     248
Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe Lys Ala
                55                  60                  65

CTA GCG TTA AGG GGT GAA TTT TCC TAC CTT ATG GCA ATC AAA CCC ACC     296
Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys Pro Thr
           70                  75                  80

GCA CTG CAC ACG ATT AAC ACT TCT TTA TTG AGC TTA AAT ATT GAT GTG     344
Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile Asp Val
      85                  90                  95

TTA AGC GAT TTT TAC ACT TAC AAA AAA TAC AGC TTT GGG GTG TAT GGG     392
Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val Tyr Gly
 100                 105                 110

GGG CTT GGG ATA GGG TAT TTT TAT CAA AGC AAC CAT TTA GGC ATG AAA     440
Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly Met Lys
115                 120                 125                 130

AAT AGT TCG TTT ATG GGT TAT AAC GGC TTG TTT AAT GTG GGG CTT GGC     488
Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly Leu Gly
                135                 140                 145

AGC ACG ATC GAT CGC CAC CAC CGC ATA GAG CTT GGG GCT AAA ATC CCT     536
Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys Ile Pro
           150                 155                 160

TTT TCA AAG ACT AGA AAT TCT TTT AAA AAT CCT TAT TTT TTA GAG AGC     584
Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu Glu Ser
      165                 170                 175

GTT TTT ATC CAT GCG ACT TAT AGC TAT ATG TTT TAAGAGAGAA TAGCCTATTA    637
Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe
 180                 185
```

GTGGTCGTTA TCAATAAGAT AAGATCCTTA ATG 670

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Lys Lys Ile Ala Phe Ile Leu Ala Leu Trp Val Gly Leu Leu Gly
 1               5                  10                  15
Ala Phe Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly
            20                  25                  30
Leu Ala Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr
        35                  40                  45
Thr Ala Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe
    50                  55                  60
Lys Ala Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys
65                  70                  75                  80
Pro Thr Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile
                85                  90                  95
Asp Val Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val
            100                 105                 110
Tyr Gly Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly
        115                 120                 125
Met Lys Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly
    130                 135                 140
Leu Gly Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys
145                 150                 155                 160
Ile Pro Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu
                165                 170                 175
Glu Ser Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...380
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
AGCGTGAAAA AAATTGAGTT GAATCAAAAC CTGCATTAAG GATTAAAAGA ATG CTC       56
                                                          Met Leu
                                                            1

AAA AAA AGT TTG TTA TTG CTT GTT TTT TTA GTC TTA CAG CTT AGC GGC      104
Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu Ser Gly
          5                  10                  15

GCT GAA GAA AAC AAT CAA GCC CCA AAA AAC ACG CCC CCT GAA TTA AAC      152
Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu Leu Asn
     20                  25                  30

CCC GCT AAC GCT AAG GGC GCG CCA AAC TCT AAC ACC CAG ATC ACC CCT      200
Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile Thr Pro
35                  40                  45                  50

AAA AAC GAT AAC TCT AAC CTG TTA GAC AAA TTA GGT TCG CCT GAA AAC      248
Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro Glu Asn
                55                  60                  65

GCT CAA ACC GAG CTT TCT GCC GGT ATT GAT TTG GCT AAA AAG GGC GAT      296
Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys Gly Asp
           70                  75                  80

TAT CAA GGG GCT TTC AAG CTT TTT TCC CAA TCG TGC GAT AAT GGT AAT      344
Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn Gly Asn
          85                  90                  95

GCG GCC GGG TGT TTT GCA AGT GGG GGC GAT GTA TGC TAATGGGGTA GGGATC    396
Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys
    100                 105                 110

CAAACCAACA GATTAAAAGC CGCTCGCTAT TATGAATG                            434
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Leu Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu
 1               5                  10                  15
Ser Gly Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu
            20                  25                  30
Leu Asn Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile
        35                  40                  45
Thr Pro Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro
    50                  55                  60
Glu Asn Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys
65                  70                  75                  80
Gly Asp Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn
```

```
                  85                  90                  95
Gly Asn Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 575 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 73...522
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
CCACAAAAGC TTAATGAATA TTAAATTAAA AACATGTTAA TCTTTAGTTA TTTTTAAAAT     60
TTAGGAAATC CC ATG CAT CAA AAC AAT AAA ACT TTT TTA CCC AGC CAA TCC    111
              Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser
               1               5                  10

GCT CAC CTC TCT AAA ATC ATT CTT TTT TTA AAC ACC GGC TTT TTA GCC      159
Ala His Leu Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala
    15                  20                  25

TAT CTG TTA AGC GCT TGT GGG GCG AAT GTG CCT ATA GAA GAA GTG TTG      207
Tyr Leu Leu Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu
30                  35                  40                  45

GTT AAA GAT CCT AAA GAG ACC AAA GCC CAA GAA GTC GCC AGA GAA GAA      255
Val Lys Asp Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu
                50                  55                  60

AAG GCT ATC CAG CAA GAA AAC GCC ACT ATT GAT GCG CGC ACC ACG CCT      303
Lys Ala Ile Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro
            65                  70                  75

TTA ATC AAT CGT TTC ACT AAT TAT AGC GCT TAT GGC TCT TTA AAC GGC      351
Leu Ile Asn Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly
        80                  85                  90

TTT TAC AAT TCA GTG GAT AAT CTC AAT TCG CCC ATG CAA AAC GGG ATG      399
Phe Tyr Asn Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met
    95                  100                 105

TAT GGA GGC TAT TAC ATG CCT TAT TAT TAC ATG CCC TAT GGT TTC ATG      447
Tyr Gly Gly Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met
110                 115                 120                 125

CCT TAT GGG TCA GGT CTT ATG CCT TAT GGG CCT TAT GGG TAT GGA GCG      495
Pro Tyr Gly Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala
```

```
                130                 135                 140

CCT GGA TAC TTC CCT TAC GCT TTT TAT TGATTGAGTG GCTTTAGAAA GCGTGGT   549
Pro Gly Tyr Phe Pro Tyr Ala Phe Tyr
            145                 150

GGTGTTGGTG TTTTTACTCA AACACG                                       575
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser Ala His Leu
 1               5                  10                  15
Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala Tyr Leu Leu
            20                  25                  30
Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu Val Lys Asp
        35                  40                  45
Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu Lys Ala Ile
    50                  55                  60
Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro Leu Ile Asn
65                  70                  75                  80
Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly Phe Tyr Asn
                85                  90                  95
Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met Tyr Gly Gly
            100                 105                 110
Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met Pro Tyr Gly
        115                 120                 125
Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala Pro Gly Tyr
    130                 135                 140
Phe Pro Tyr Ala Phe Tyr
145                 150
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...860
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
ATTATGTTAT TATTATACGA AATGTAGACT TTTAGAAGGA AAAATGTTGT ATG AAA      56
                                                        Met Lys
                                                          1

AAG TTT GTA GTG TTT AAA ACG CTC TGT TTA TCG GTA GTG TTA GGT AAT     104
Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu Gly Asn
      5                  10                  15

AGT CTT GTG GCA GCA GAA GGC AGC ACA GAA GTG CAA AAG CAA TTG GAA     152
Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln Leu Glu
  20                  25                  30

AAG CCA AAA GAG TAT AAA GCA GTG AAA GGC GAG AAA AAC GCT TGG TAT     200
Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala Trp Tyr
35                  40                  45                  50

TTG GGG ATT AGC TAT CAA GTC GGT CAG GCT TCG CAA AGC GTT AAA AAC     248
Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val Lys Asn
              55                  60                  65

CCC CCC AAA AGC AGT GAA TTT AAC TAC CCT AAG TTC CCT GTG GGT AAA     296
Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val Gly Lys
          70                  75                  80

ACC GAC TAT CTG GCC GTT ATG CAA GGC TTA GGG CTT ACT GTG GGT TAT     344
Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val Gly Tyr
      85                  90                  95

AAG CAG TTT TTC GGG GAA AAG AGA TGG TTT GGT GCA CGC TAT TAC GGC     392
Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr Tyr Gly
  100                 105                 110

TTC ATG GAT TAT GGG CAT GCC GTA TTT GGA GCG AAC GCT TTA ACA TCG     440
Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu Thr Ser
115                 120                 125                 130

GAT AAT GGT GGG GTG TGT GAG CTT CAC CAA CCA TGT GCG ACC AAA GTA     488
Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr Lys Val
              135                 140                 145

GGG ACA ATG GGC AAT CTG TCT GAC ATG TTC ACT TAT GGT GTG GGT ATT     536
Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val Gly Ile
          150                 155                 160

GAC ACT TTA TAC AAT GTC ATC AAT AAA GAA GAT GCG AGT TTT GGT TTC     584
Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe Gly Phe
      165                 170                 175

TTT TTT GGG GCT CAA ATC GCG GGT AAC TCT TGG GGT AAT ACG ACA GGG     632
Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr Thr Gly
  180                 185                 190

GCC TTT TTG GAA ACT AAA AGC CCT TAT AAG CAC ACT TCC TAT AGC CTT     680
Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr Ser Leu
195                 200                 205                 210
```

```
GAT CCG GCG ATT TTC CAG TTC CTT TTT AAT TTA GGG ATC CGC ACC CAT      728
Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg Thr His
                215                 220                 225

ATT GGC CGG CAT CAA GAA TTT GAC TTT GGC GTG AAG ATT CCC ACT ATC      776
Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro Thr Ile
            230                 235                 240

AAT GTT TAT TAT TTT AAC CAT GGG AAT TTG AGC TTC ACT TAC CGC CGT      824
Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr Arg Arg
        245                 250                 255

CAA TAC AGC CTT TAT GTG GGG TAT CGT TAC AAT TTC TGATTTAAAA CGCTTG    876
Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe
    260                 265                 270

TTTTTCTCTA ATTGAATTTT CAATTAGAGT TTTC                               910
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Lys Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu
 1               5                  10                  15
Gly Asn Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln
            20                  25                  30
Leu Glu Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala
        35                  40                  45
Trp Tyr Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val
    50                  55                  60
Lys Asn Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val
65                  70                  75                  80
Gly Lys Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val
                85                  90                  95
Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr
            100                 105                 110
Tyr Gly Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu
        115                 120                 125
Thr Ser Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr
    130                 135                 140
Lys Val Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val
145                 150                 155                 160
Gly Ile Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe
                165                 170                 175
Gly Phe Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr
            180                 185                 190
Thr Gly Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr
        195                 200                 205
Ser Leu Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg
```

```
    210                 215                 220
Thr His Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro
225                 230                 235                 240
Thr Ile Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr
                245                 250                 255
Arg Arg Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 58...1305
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
CGCAATTAAA AGGAATTTTA ACTAAAATAT TGAGTTTAAA TCCACGATGA GTTTTTA ATG     60
                                                               Met
                                                                1

CAA TAT AAG AAA AAT AAG AAA AGA TAT TAT TAT TTA GCG TTA GGG ATC      108
Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly Ile
            5                   10                  15

TTT TTT TTA AAT GGT CTG TCT TTG AAA GCT TTA GAA ATC GCC GTC AAA      156
Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val Lys
        20                  25                  30

CCT TTT GGC TAT CTG GGG CTA TTA TAT AAT CAA GGG GCG CAA AAA AAC      204
Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys Asn
    35                  40                  45

CCT CAC AGC TAT GTG GGG GCT TTA GCG CGT CTT GGG GTG GAT TTT TCT      252
Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe Ser
50                  55                  60                  65

TAT AGC AAC GGG TGG TCC TTT GGT ATT GGA GCG ATT GGG GCT TGG AAT      300
Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp Asn
                70                  75                  80

ATT TAT AAC AAA CAG CGT TTG GCT AAC CTT TAT ATC AGT CTA GGG AAT      348
Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly Asn
            85                  90                  95

TTT TTT GGT AGT TCT AAA AAT GTT AAA CCT TAT TTG AGC GCT GGC GAT      396
Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly Asp
        100                 105                 110
```

```
GTT TCT GAT GCG TAT GTT CAA TAC ACT AAC CAG CGT TTT AAA ATC GCT      444
Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile Ala
    115                 120                 125

TTA GGG CGT TTC AAT ACC GAT TTT GTG GAT TTT GAT TGG ATA GGG GGC      492
Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly Gly
130                 135                 140                 145

AAT ATT CAA GGG GTT TCT GTA GCT TTT AAG CAA AAT TCC ATG CGT TAT      540
Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg Tyr
                150                 155                 160

TTT GGG ATT TTT ATG GAT AGC ATG CTT TAT AAT GGG CAT CAA ATC AAC      588
Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile Asn
            165                 170                 175

AAA GAG CAA GGG AAT CGG ATC GCT ACT TCC CTA AAC GCT CTA GCG TCT      636
Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala Ser
        180                 185                 190

TAT GAC CCT GTG TCT AAA CGC TTG TAT GTG GGG GGG GAA GTG TTT GTT      684
Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe Val
    195                 200                 205

TTA GGT GCA GAA TAC AGG CAT GAA AAT CTT AAA GTG GTG CCT TTT ATT      732
Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe Ile
210                 215                 220                 225

TTA ACG GAC ACC CGC TTG CCT TTA TCC ACC CAA AAT GTT TTA GTG CAA      780
Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val Gln
                230                 235                 240

GTG GGG GGT AAG TTG GAG TAT GAC GCT TCT TTA GCT AAG GGT TTC ACT      828
Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe Thr
            245                 250                 255

TCG CAC ACT CTA GTG CAT GGC ATG TAT CAA TAC GGC AAC ACT GAT GCG      876
Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp Ala
        260                 265                 270

GCT ACA AGC GTT AAA AAT GCC GGC TTG TTT TTG ATC GAT CAA ACT TTT      924
Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr Phe
    275                 280                 285

AAA TAC AAA ATT TTT AAT TTT GGA ACG GGT TTT TAT ATC GTT CCG GCA      972
Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro Ala
290                 295                 300                 305

AGA AAC AAT AAG GGC TAT CTA TGG ACT TTT AAT GAC AGG ACT AAA TTC     1020
Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys Phe
                310                 315                 320

TAT GGC CGT GGG ATC AAT GCG CCC GGC GTG CCA GCG ATT TAT TTT GCA     1068
Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe Ala
            325                 330                 335

AAC TCT AGC ATT TCA GGC TAT GTT TTT TTA GGG CTT AAG ACT AAA AGG     1116
Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys Arg
```

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        340                 345                 350

GTG CGT TTA GAC GCG ATG GTG GCT TTT GGG GAT TAC CAA GAA TAT TCT    1164
Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr Ser
    355                 360                 365

TTA ATG AGC AGT TTT AGG GTT TGG ACT TAT AGG AGT TTG TCT TTT GAT    1212
Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe Asp
370                 375                 380                 385

ATG GGT GGG GGG TAT GTG TAT GCT TAC AAT TCT AAA GCC ACG AGA AAA    1260
Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg Lys
                390                 395                 400

AGT CTT GGA AAT AGT TCT TTT GTC TTT TTT GGG AAG TTT TTG TTT TAAAA  1310
Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe
            405                 410                 415

AATACCATTT CTACAATCAA TAGTGAAGAG TTTGCAATAA AGTAAGC                1357
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly
 1               5                  10                  15
Ile Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val
            20                  25                  30
Lys Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys
        35                  40                  45
Asn Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe
    50                  55                  60
Ser Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp
65                  70                  75                  80
Asn Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly
                85                  90                  95
Asn Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly
            100                 105                 110
Asp Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile
        115                 120                 125
Ala Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly
    130                 135                 140
Gly Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg
145                 150                 155                 160
Tyr Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile
                165                 170                 175
Asn Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala
            180                 185                 190
Ser Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe
```

```
        195                 200                 205
Val Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe
    210                 215                 220
Ile Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val
225                 230                 235                 240
Gln Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe
                245                 250                 255
Thr Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp
            260                 265                 270
Ala Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr
        275                 280                 285
Phe Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro
    290                 295                 300
Ala Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys
305                 310                 315                 320
Phe Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe
                325                 330                 335
Ala Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys
            340                 345                 350
Arg Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr
        355                 360                 365
Ser Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe
    370                 375                 380
Asp Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg
385                 390                 395                 400
Lys Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe
                405                 410                 415
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 73...1509
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
TTATGCTTCT TTGTTTTTAG ATCAGTTAAG AATTGTAGTC TTTAAGATGT ATTGGCTATT     60
AAAAGGAAAA AA ATG AAA AAT AGC ACG CCT TTA AAG AAT CAA GTT TTT TGT   111
              Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys
               1               5                  10

GGG TTA TAT GTT TTA AGT TTG AGC GCT TCT TTG CAA GCG TTT GAT TAT     159
Gly Leu Tyr Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr
    15                  20                  25

AAA ATT GAA GTT TCA GCG GAG TCC TTT TCT AAA GTT GGC TTT AAT AAA     207
Lys Ile Glu Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys
```

```
30                  35                  40                  45

AAA AAG ATT GAT ATA GCT AGG GGG ATT TAT CCT ACA GAG ACT TTT GTA      255
Lys Lys Ile Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val
                50                  55                  60

ACC GCT GTA GGG CAG GGC AAT ATC TAT GCG GAT TTT TTA CCC AAA GGC      303
Thr Ala Val Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Pro Lys Gly
            65                  70                  75

CTT AAA GAT CAA GGG CAT GTT TTA GAG GGA AAA ATC GGT GGC ACG CTA      351
Leu Lys Asp Gln Gly His Val Leu Glu Gly Lys Ile Gly Gly Thr Leu
        80                  85                  90

GGA GGG GTC GCT TAT GAT AGC ACG AAA TTC AAT CAA GGC GGA TCG GTT      399
Gly Gly Val Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val
    95                  100                 105

ATT TAT AAC TAC ATC GGT TAT TGG GAT GGC TAT TTA GGG GGT AAA AGA      447
Ile Tyr Asn Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg
110                 115                 120                 125

GCC TTG CTT GAT GGC ACG AGT ATC CAT GAG TGC GCG CTT GGA TCT GAT      495
Ala Leu Leu Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp
                130                 135                 140

GGC AAG GTG ATT GAT TCT ATA GCG TGC GGG AAC GCT AGG GCC AAT AAA      543
Gly Lys Val Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys
            145                 150                 155

ATC CGC CGT AAT TAC TTG ATG AAT AAC GCT TTT TTA GAA TAC CGC TAT      591
Ile Arg Arg Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr
        160                 165                 170

AAA GAT ATT TTT TTA GCT AAG GGA GGG CGT TAT CAA TCC AAT GCT CCT      639
Lys Asp Ile Phe Leu Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro
    175                 180                 185

TAT ATG AGC GGT TAC ACG CAA GGC TTT GAA ATC AGC GCT AAA GTC AAG      687
Tyr Met Ser Gly Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Val Lys
190                 195                 200                 205

GAT AAA AAT GAA GGA ATC CAC AAA TTA TGG TGG TTT AGC TCA TGG GGT      735
Asp Lys Asn Glu Gly Ile His Lys Leu Trp Trp Phe Ser Ser Trp Gly
                210                 215                 220

AGG GCG TTC GCT TAT GGG GAG TGG ATT TAT GAT TTT TAT TCT CCA AGA      783
Arg Ala Phe Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg
            225                 230                 235

ACC GTG GTT AAA AAC GGG CGC ACT TTG AAT TAT GGT ATC CAT TTA GTG      831
Thr Val Val Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val
        240                 245                 250

AAT TAT ACT TAT GAA AGA AAA GGG GTT AGC GTT AGC CCT TTT TTC CAA      879
Asn Tyr Thr Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln
    255                 260                 265
```

```
TTT TCG CCT GGG ACT TAT TAT AGC CCT GGG GTG GTT GTA GGC TAT GAT      927
Phe Ser Pro Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp
270                 275                 280                 285

AGT AAC CCT AAT TTT AAC GGC GTT GGC TTT AGA TCC GAA ACA AAA GCT      975
Ser Asn Pro Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala
                290                 295                 300

TAT ATT TTG CTC CCT GTC CAT GAC CCC TTA AGA AGG GAT ACT TAT CGT     1023
Tyr Ile Leu Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg
            305                 310                 315

TAC GCT ATA AAG GCT GGC ACT GCC GGG CAA AGC TTG CTC ATT AGG CAA     1071
Tyr Ala Ile Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln
        320                 325                 330

CGA TTT GAT TAC AAT GAA TTT AAT TTT GGG GGA GCG TTT TAT AAA GTA     1119
Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val
    335                 340                 345

TGG AAA AAC GCA AAC GCT TAC ATC GGC ACG ACA GGA AAC CCT TTA GGC     1167
Trp Lys Asn Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly
350                 355                 360                 365

ATT GAT TTT TGG ACC AAT AGC GTT TAT GAT ATA GGG CAA GCT TTA AGC     1215
Ile Asp Phe Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser
                370                 375                 380

CAT GTG GTA ACC GCT GAT GCC GTC TCT GGT TGG GTT TTT GGT GGG GGC     1263
His Val Val Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly
            385                 390                 395

GTG CAT AAA AAG TGG CTG TGG GGG ACT TTA TGG CGT TGG ACT AGC GGC     1311
Val His Lys Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly
        400                 405                 410

ACT TTA GCC AAT GAA GCG AGT GCG GCT GTT AAT GTG GGC TAT AAG ATC     1359
Thr Leu Ala Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile
    415                 420                 425

AGT AAG AGT TTG ACA GCG AGC GTG AAA TTA GAA TAT TTG GGC GTG ATG     1407
Ser Lys Ser Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met
430                 435                 440                 445

ACG CAT GCA GGC TTT ACG GTA GGG AGT TAC AGG CCC ACG CCC GGC TCT     1455
Thr His Ala Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser
                450                 455                 460

AAA GCG CTT TAT TCA GAC AGG AGT CAT TTG ATG ACA ACT CTT AGC GCT     1503
Lys Ala Leu Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala
            465                 470                 475

AAA TTC TAACCAATCG CTTTAAGCTG TTTATTAAAG CGTTAAAAAT CCCTTAATAA AA  1561
Lys Phe

A                                                                  1562
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 479 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys Gly Leu Tyr
 1               5                  10                  15
Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr Lys Ile Glu
            20                  25                  30
Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys Lys Lys Ile
        35                  40                  45
Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val Thr Ala Val
    50                  55                  60
Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Pro Lys Gly Leu Lys Asp
65                  70                  75                  80
Gln Gly His Val Leu Glu Gly Lys Ile Gly Gly Thr Leu Gly Gly Val
                85                  90                  95
Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val Ile Tyr Asn
            100                 105                 110
Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg Ala Leu Leu
        115                 120                 125
Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp Gly Lys Val
    130                 135                 140
Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys Ile Arg Arg
145                 150                 155                 160
Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr Lys Asp Ile
                165                 170                 175
Phe Leu Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro Tyr Met Ser
            180                 185                 190
Gly Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Val Lys Asp Lys Asn
        195                 200                 205
Glu Gly Ile His Lys Leu Trp Trp Phe Ser Ser Trp Gly Arg Ala Phe
    210                 215                 220
Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg Thr Val Val
225                 230                 235                 240
Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val Asn Tyr Thr
                245                 250                 255
Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln Phe Ser Pro
            260                 265                 270
Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp Ser Asn Pro
        275                 280                 285
Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala Tyr Ile Leu
    290                 295                 300
Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg Tyr Ala Ile
305                 310                 315                 320
Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln Arg Phe Asp
                325                 330                 335
Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val Trp Lys Asn
            340                 345                 350
Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly Ile Asp Phe
```

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        355                 360                 365
Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser His Val Val
    370                 375                 380
Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly Val His Lys
385                 390                 395                 400
Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly Thr Leu Ala
                405                 410                 415
Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile Ser Lys Ser
            420                 425                 430
Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met Thr His Ala
        435                 440                 445
Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser Lys Ala Leu
    450                 455                 460
Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala Lys Phe
465                 470                 475
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 98...757
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
CTAATATTTA TTTTAAACTT TGTTATTATT TAAGGTGTGA TTTGATTTTA GTCTGTATGG     60
GGCAAGTGTG GGGCAGGATA ACATAAGGAA TTGGGTT ATG AAT AAA ACA ACG GTT    115
                                          Met Asn Lys Thr Thr Val
                                           1               5

AAA ATA TTA ATG GGC ATG GCG TTA TTA TCA TCG CTT CAA GCC GCA GAG     163
Lys Ile Leu Met Gly Met Ala Leu Leu Ser Ser Leu Gln Ala Ala Glu
            10                  15                  20

GCA GAG CTT GAT GAA AAA TCA AAA AAA CCT AAA TTT GCG GAC AGG AAT     211
Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro Lys Phe Ala Asp Arg Asn
        25                  30                  35

ACA TTT TAT TTA GGG GTT GGG TAT CAA CTT AGT GCG ATC AAC ACA TCT     259
Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu Ser Ala Ile Asn Thr Ser
    40                  45                  50

TTT AGC ACC GAG TCT GTA GAT AAA TCG TAT TTT ATG ACC GGC AAT GGC     307
Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr Phe Met Thr Gly Asn Gly
55                  60                  65                  70

TTT GGT GTG GTG TTA GGG GGG AAA TTT GTG GCT AAA ACG CAA GCT GTA     355
Phe Gly Val Val Leu Gly Gly Lys Phe Val Ala Lys Thr Gln Ala Val
```

```
                75                  80                  85

GAG CAT GTG GGT TTC CGT TAC GGG TTG TTT TAT GAT CAG ACC TTT TCT     403
Glu His Val Gly Phe Arg Tyr Gly Leu Phe Tyr Asp Gln Thr Phe Ser
            90                  95                  100

TCT CAC AAA TCC TAT ATT TCT ACC TAT GGT TTA GAA TTT AGC GGT TTG     451
Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly Leu Glu Phe Ser Gly Leu
        105                 110                 115

TGG GAC GCT TTC AAT TCG CCA AAG ATG TTT TTA GGG TTA GAG TTT GGC     499
Trp Asp Ala Phe Asn Ser Pro Lys Met Phe Leu Gly Leu Glu Phe Gly
    120                 125                 130

TTA GGC ATC GCT GGG GCG ACT TAT ATG CCA GGA GGG GCT ATG CAT GGG     547
Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro Gly Gly Ala Met His Gly
135                 140                 145                 150

ATT ATC GCT CAA AAT TTA GGC AAA GAA AAT TCG CTT TTC CAA TTG CTT     595
Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn Ser Leu Phe Gln Leu Leu
                155                 160                 165

GTG AAA GTG GGT TTT CGT TTT GGC TTT TTG CAC AAT GAA ATC ACT TTC     643
Val Lys Val Gly Phe Arg Phe Gly Phe Leu His Asn Glu Ile Thr Phe
            170                 175                 180

GGG TTG AAA TTC CCT GTC ATT CCT AAC AAA AGA ACG GAA ATC ATT GAT     691
Gly Leu Lys Phe Pro Val Ile Pro Asn Lys Arg Thr Glu Ile Ile Asp
        185                 190                 195

GGC TTG AGC ACG ACT ACT TTA TGG CAC CGC TTA CCG GTA GCT TAT TTC     739
Gly Leu Ser Thr Thr Thr Leu Trp His Arg Leu Pro Val Ala Tyr Phe
    200                 205                 210

AAT TAT ATC TAT AAT TTT TAGATATGGT TATTTAGAGG TTTTAGATTT GACAAAAT   795
Asn Tyr Ile Tyr Asn Phe
215                 220

CAATCAACTC TCGTG                                                   810
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Asn Lys Thr Thr Val Lys Ile Leu Met Gly Met Ala Leu Leu Ser
 1               5                  10                  15
Ser Leu Gln Ala Ala Glu Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro
            20                  25                  30
Lys Phe Ala Asp Arg Asn Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu
```

```
        35                  40                  45
Ser Ala Ile Asn Thr Ser Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr
    50                  55                  60
Phe Met Thr Gly Asn Gly Phe Gly Val Val Leu Gly Gly Lys Phe Val
65                  70                  75                  80
Ala Lys Thr Gln Ala Val Glu His Val Gly Phe Arg Tyr Gly Leu Phe
                85                  90                  95
Tyr Asp Gln Thr Phe Ser Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly
            100                 105                 110
Leu Glu Phe Ser Gly Leu Trp Asp Ala Phe Asn Ser Pro Lys Met Phe
        115                 120                 125
Leu Gly Leu Glu Phe Gly Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro
    130                 135                 140
Gly Gly Ala Met His Gly Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn
145                 150                 155                 160
Ser Leu Phe Gln Leu Leu Val Lys Val Gly Phe Arg Phe Gly Phe Leu
                165                 170                 175
His Asn Glu Ile Thr Phe Gly Leu Lys Phe Pro Val Ile Pro Asn Lys
            180                 185                 190
Arg Thr Glu Ile Ile Asp Gly Leu Ser Thr Thr Thr Leu Trp His Arg
        195                 200                 205
Leu Pro Val Ala Tyr Phe Asn Tyr Ile Tyr Asn Phe
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1463
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
TTTATCTTTA AAAGTATTTG CATTTATCAA TCTCATTTTA GGAGGCATGC ATG AAA      56
                                                          Met Lys
                                                            1

AAG GCA AGT CAG GTT TTA TTC TTT GGG GCA TTT TTA AGC TCT TCT TTG     104
Lys Ala Ser Gln Val Leu Phe Phe Gly Ala Phe Leu Ser Ser Ser Leu
 5                  10                  15

CAA GGT TTT GAA GCT AAG CTC AAC GGC TTT GTG GAT CAA TCC AGC ACT     152
Gln Gly Phe Glu Ala Lys Leu Asn Gly Phe Val Asp Gln Ser Ser Thr
    20                  25                  30

ATC GGT TTT AAC CAG CAT AAA ATC AAT AAA GAA AGA GGT ATC TAC CCT     200
Ile Gly Phe Asn Gln His Lys Ile Asn Lys Glu Arg Gly Ile Tyr Pro
35                  40                  45                  50
```

```
ATG CAG CAA TTC GCA ACG ATT GCG GGC TAT TTA GGG CTT GGT TTT AGC      248
Met Gln Gln Phe Ala Thr Ile Ala Gly Tyr Leu Gly Leu Gly Phe Ser
                55                  60                  65

CTG TTA CCC AAA AAG GTT TCA GAC CAT GTT CTA AAA GGC AAA ATA GGA      296
Leu Leu Pro Lys Lys Val Ser Asp His Val Leu Lys Gly Lys Ile Gly
            70                  75                  80

GGC ATG GTG GGA TCT ATT TTC TAT GAT GGC ACG AAG AAG TTT GAA GAC      344
Gly Met Val Gly Ser Ile Phe Tyr Asp Gly Thr Lys Lys Phe Glu Asp
        85                  90                  95

AGC TCT GTA GCT TAC AAC CTC TTT GGT TAT TAT GAT GGG TTC ATG GGG      392
Ser Ser Val Ala Tyr Asn Leu Phe Gly Tyr Tyr Asp Gly Phe Met Gly
    100                 105                 110

GGT TAT ACA AAC ATC TTA CAA AGC GAT GAT TTA GCG ACA CAA AAC ATG      440
Gly Tyr Thr Asn Ile Leu Gln Ser Asp Asp Leu Ala Thr Gln Asn Met
115                 120                 125                 130

AAA TAC AAT AAA AAT GTC CGC AAC TAT GTC TTT AGC GAC GCG TAT TTA      488
Lys Tyr Asn Lys Asn Val Arg Asn Tyr Val Phe Ser Asp Ala Tyr Leu
                135                 140                 145

GAA TAC GCT TAT AAG AAT TAT TTT GAA ATA AAA GCC GGG CGC TAT TTA      536
Glu Tyr Ala Tyr Lys Asn Tyr Phe Glu Ile Lys Ala Gly Arg Tyr Leu
            150                 155                 160

TCC ACT ATG CCT TAT AAA AGC GGT CAA ACG CAA GGC TTT CAA ATT TCT      584
Ser Thr Met Pro Tyr Lys Ser Gly Gln Thr Gln Gly Phe Gln Ile Ser
        165                 170                 175

GGG CAA TAC AAG AAA GCG CGC TTG ACT TGG TTT AGC TCT TTT GGG AGG      632
Gly Gln Tyr Lys Lys Ala Arg Leu Thr Trp Phe Ser Ser Phe Gly Arg
    180                 185                 190

GCG TTC GCT TAC GGC TCG TTT TTG ATG GAT TGG TTT GCC GCT AGG ACC      680
Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala Arg Thr
195                 200                 205                 210

ACT TAT AGC GGA GGT TTT ACC AAA AAC GAT AAG GGA GGT TAT GAT AGC      728
Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr Asp Ser
                215                 220                 225

CAT GGG CGA AAG GTG CTT TAT GGC ACG CAT GCG GTG CAA CTC ACC TAT      776
His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu Thr Tyr
            230                 235                 240

AAA CCT CAT CGT TTC CTC ATA GAA GGC TTT TAT TAC CTT TCG CCT CAA      824
Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser Pro Gln
        245                 250                 255

ATC TTT AAC GCT CCG GGC GTT AAG ATT GGT TGG GAT TCT AAC CCT AAT      872
Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn Pro Asn
    260                 265                 270

TTT AGC GGC ACA GGC TTT CGC TCT GAT ACA GCT ATC ATA GGG TTT TTC      920
Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly Phe Phe
```

```
275                 280                 285                 290

CCC ATT TAC TAC CCT TGG ATG ATC GTT AAA TCC AAT GGA AGC CCG GTC     968
Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser Pro Val
                295                 300                 305

TAT AAA TAC GAC ACG CCT GCC ACT CAA AAT GGG CAA AAC CTC ATT ATC    1016
Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu Ile Ile
            310                 315                 320

CTC CAA CGC TTT GAC ATC AAC AAT TAC AAT GTT TCC ATC GCT TTT TAT    1064
Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala Phe Tyr
        325                 330                 335

AAA GTC TTT CAA AAC GCT AAT GGT TGG ATA GGC AAC ATG GGG AAT CCA    1112
Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly Asn Pro
    340                 345                 350

AGC GGT GTG ATC ATG GGG AGT AAC AGC GTC TAT GCG GGT TTT ACA GGC    1160
Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe Thr Gly
355                 360                 365                 370

ACA GCC CTT AAA AGA GAT GCC GCT ACC ATT TTC CTT TCT TGT GGC GGC    1208
Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys Gly Gly
                375                 380                 385

ACT CAT TTT GCC AAA AAA TTC ACA TGG AAA TTC GCC ACG CAA TAC TCC    1256
Thr His Phe Ala Lys Lys Phe Thr Trp Lys Phe Ala Thr Gln Tyr Ser
            390                 395                 400

AAT TCA GTG GTT TCT TGG GAA GCG AGA GCG ATG ATC TCT TTA GGT TAT    1304
Asn Ser Val Val Ser Trp Glu Ala Arg Ala Met Ile Ser Leu Gly Tyr
        405                 410                 415

AAA TTC ACT GAA TAC TTG AGC GGT AGC GTG GAT CTT GCA TAT TAT GGC    1352
Lys Phe Thr Glu Tyr Leu Ser Gly Ser Val Asp Leu Ala Tyr Tyr Gly
    420                 425                 430

GTG TAT ACT AAC AAA GGA TTT AAA CCG GGT GAA AAC GGG CCT GTG CCT    1400
Val Tyr Thr Asn Lys Gly Phe Lys Pro Gly Glu Asn Gly Pro Val Pro
435                 440                 445                 450

AAA GAC TTC CCC GCC CTT TAT TCT GAC AGG AGC GCG TTA TAC ACG GCT    1448
Lys Asp Phe Pro Ala Leu Tyr Ser Asp Arg Ser Ala Leu Tyr Thr Ala
                455                 460                 465

CTA GTA GCA TCT TTT TGATGCTACC CTATGATTAT GGTGGGCGTC TTTTGATGCT G  1504
Leu Val Ala Ser Phe
            470

TTTCTCTAGT CT                                                      1516
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Lys Lys Ala Ser Gln Val Leu Phe Phe Gly Ala Phe Leu Ser Ser
 1               5                  10                  15
Ser Leu Gln Gly Phe Glu Ala Lys Leu Asn Gly Phe Val Asp Gln Ser
            20                  25                  30
Ser Thr Ile Gly Phe Asn Gln His Lys Ile Asn Lys Glu Arg Gly Ile
        35                  40                  45
Tyr Pro Met Gln Gln Phe Ala Thr Ile Ala Gly Tyr Leu Gly Leu Gly
    50                  55                  60
Phe Ser Leu Leu Pro Lys Lys Val Ser Asp His Val Leu Lys Gly Lys
65                  70                  75                  80
Ile Gly Gly Met Val Gly Ser Ile Phe Tyr Asp Gly Thr Lys Lys Phe
                85                  90                  95
Glu Asp Ser Ser Val Ala Tyr Asn Leu Phe Gly Tyr Tyr Asp Gly Phe
            100                 105                 110
Met Gly Gly Tyr Thr Asn Ile Leu Gln Ser Asp Asp Leu Ala Thr Gln
        115                 120                 125
Asn Met Lys Tyr Asn Lys Asn Val Arg Asn Tyr Val Phe Ser Asp Ala
    130                 135                 140
Tyr Leu Glu Tyr Ala Tyr Lys Asn Tyr Phe Glu Ile Lys Ala Gly Arg
145                 150                 155                 160
Tyr Leu Ser Thr Met Pro Tyr Lys Ser Gly Gln Thr Gln Gly Phe Gln
                165                 170                 175
Ile Ser Gly Gln Tyr Lys Lys Ala Arg Leu Thr Trp Phe Ser Ser Phe
            180                 185                 190
Gly Arg Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala
        195                 200                 205
Arg Thr Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr
    210                 215                 220
Asp Ser His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu
225                 230                 235                 240
Thr Tyr Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser
                245                 250                 255
Pro Gln Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn
            260                 265                 270
Pro Asn Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly
        275                 280                 285
Phe Phe Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser
    290                 295                 300
Pro Val Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu
305                 310                 315                 320
Ile Ile Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala
                325                 330                 335
Phe Tyr Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly
            340                 345                 350
Asn Pro Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe
        355                 360                 365
Thr Gly Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys
    370                 375                 380
Gly Gly Thr His Phe Ala Lys Lys Phe Thr Trp Lys Phe Ala Thr Gln
385                 390                 395                 400
Tyr Ser Asn Ser Val Val Ser Trp Glu Ala Arg Ala Met Ile Ser Leu
```

```
                405                 410                 415
Gly Tyr Lys Phe Thr Glu Tyr Leu Ser Gly Ser Val Asp Leu Ala Tyr
            420                 425                 430
Tyr Gly Val Tyr Thr Asn Lys Gly Phe Lys Pro Gly Glu Asn Gly Pro
        435                 440                 445
Val Pro Lys Asp Phe Pro Ala Leu Tyr Ser Asp Arg Ser Ala Leu Tyr
    450                 455                 460
Thr Ala Leu Val Ala Ser Phe
465                 470
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 87...323
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
AAATTTATGT TATAATTAAA CGCATTGTAA ATAAATTCTC ATTTTGATAC ATTTTTACAA     60
TAAAACATTA CTTTAAGGAA CATCTT ATG AAA AAA ACG AAA AAA ACG ATT CTG    113
                             Met Lys Lys Thr Lys Lys Thr Ile Leu
                              1               5

CTT TCT CTA ACT CTC GCG GCG TCA TTG CTC CAT GCT GAA GAC AAC GGC     161
Leu Ser Leu Thr Leu Ala Ala Ser Leu Leu His Ala Glu Asp Asn Gly
10                  15                  20                  25

GTT TTT TTA AGC GTG GGT TAT CAA ATC GGT GAA GCG GTT CAA AAA GTG     209
Val Phe Leu Ser Val Gly Tyr Gln Ile Gly Glu Ala Val Gln Lys Val
                30                  35                  40

AAA AAC GCC GAC AAG GTG CAA AAA CTT TCA GAC ACT TAT GAA CAA TTA     257
Lys Asn Ala Asp Lys Val Gln Lys Leu Ser Asp Thr Tyr Glu Gln Leu
            45                  50                  55

AGC CGG CTT TTA ACC AAC GAT AAT GGC ACA AAC TCA AAG ACA AGC GCG     305
Ser Arg Leu Leu Thr Asn Asp Asn Gly Thr Asn Ser Lys Thr Ser Ala
        60                  65                  70

CAA NAT CAA CCA AGC GGT TAATAATTTG AACGAACGCG CAAAAACTTT AGCCGGTG   361
Gln Xaa Gln Pro Ser Gly
    75

GGACAACCAA TTCCCC                                                   377
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Met Lys Lys Thr Lys Lys Thr Ile Leu Leu Ser Leu Thr Leu Ala Ala
 1               5                  10                  15
Ser Leu Leu His Ala Glu Asp Asn Gly Val Phe Leu Ser Val Gly Tyr
            20                  25                  30
Gln Ile Gly Glu Ala Val Gln Lys Val Lys Asn Ala Asp Lys Val Gln
        35                  40                  45
Lys Leu Ser Asp Thr Tyr Glu Gln Leu Ser Arg Leu Leu Thr Asn Asp
    50                  55                  60
Asn Gly Thr Asn Ser Lys Thr Ser Ala Gln Xaa Gln Pro Ser Gly
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 60...2039
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
CCCTATCATA GGGCGTGGCA TGAAGAAAAA AGCAAAAGTC TTTTGGTATT GTTTTAATC      59

ATG ATT TAT TGG TTG TAT TTG GCG GTC TTT TTT TTG TTG AGC GCA TTA      107
Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
 1               5                  10                  15

GAC GCT AAA GAA ATC GCT ATG CAA CGA TTT GAC AAA CAA AAC CAT AAG      155
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
            20                  25                  30

ATT TTT GAA ATC CTT GCG GAT AAA GTG AGC GCT AAA GAC AAT GTG ATA      203
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
        35                  40                  45

ACC GCA TCA GGG AAT GCG ATC TTA TTG AAT TAT GAT GTG TAT ATT CTA      251
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
    50                  55                  60
```

```
GCG GAC AAG GTG CGT TAT GAC ACT AAA ACC AAA GAA GCG TTA TTA GAG      299
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
 65                  70                  75                  80

GGG AAT ATC AAG GTT TAT AGG GGC GAG GGT TTG CTC GTT AAA ACC GAT      347
Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp
                 85                  90                  95

TAC GTG AAA TTG AGT TTG AAT GAA AAA TAT GAA ATC ATT TTC CCC TTT      395
Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe
            100                 105                 110

TAT GTC CAA GAC AGC GTG AGC GGG ATT TGG GTG AGC GCG GAT ATT GCC      443
Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala
        115                 120                 125

AGC GGA AAG GAT CAA AAA TAT AAG GTT AAA AAC ATG AGC ACT TCA GGG      491
Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly
    130                 135                 140

TGC AGC ATT GAT AAC CCC ATT TGG CAT GTC AAT GCG ACT TCA GGC TCA      539
Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser
145                 150                 155                 160

TTC AAC ATG CAA AAA TCG CAT TTG TCT ATG TGG AAT CCT AAG ATC TAT      587
Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr
                165                 170                 175

GTC GGT GAT ATT CCT GTA TTG TAT TTG CCC TAT ATT TTC ATG TCC ACG      635
Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr
            180                 185                 190

AGC AAT AAA AGA ACT ACT GGG TTT TTA TAC CCT GAG TTT GGC ACT TCC      683
Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser
        195                 200                 205

AAC TTA GAC GGC TTT ATT TAT TTG CAA CCC TTT TAT TTA GCC CCC AAA      731
Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys
    210                 215                 220

AAC TCA TGG GAT ATG ACC TTT ACC CCA CAA ATC CGC TAT AAA AGG GGT      779
Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly
225                 230                 235                 240

TTT GGC TTG AAT TTT GAA GCG CGC TAC ATT AAC TCT AAA AAC GAC AGG      827
Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg
                245                 250                 255

TTT TTA TTC AAC GCG CGC TAT TTT AGG AAT TAC ACC CAA TAT GTC AAA      875
Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys
            260                 265                 270

CGC TAC GAT TTG AGG AAT CAA AAT ATC TAC GGG TTT GAA TTT TTA AGC      923
Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser
        275                 280                 285

TCT AGC AGG GAC ACT TTA CAA AAA TAC TTC CAC CTT AAG TCT AAT ATT      971
Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile
```

```
    290                 295                 300

GAC AAC GGG CAT TAC ATT GAC TTT TTA TAC ATG AAC GAT TTG GAC TAT      1019
Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr
305                 310                 315                 320

GTG CGT TTT GAA AAG GTT AAT AAG CGT ATC ACA GAC GCC ACG CAC ATG      1067
Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met
                325                 330                 335

TCT AGG GCG AAT TAC TAT TTG CAA ACA GAA AAC AAT TAT TAC GGC TTG      1115
Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu
            340                 345                 350

AAT ATC AAG TAT TTT TTA AAC CTG AAT AAA ATC AAC AAT AAC CGC ACT      1163
Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr
        355                 360                 365

TTC CAA TCT GTC CCT AAT TTG CAA TAC CAT AAA TAT TTA AAT TCT TTG      1211
Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu
    370                 375                 380

TAT TTT AGA AAT TTG TTG TAT TCG GTG GAT TAT CAG TTT AGA AAC ACC      1259
Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr
385                 390                 395                 400

GCA AGA GAG ATT GGT TAT GGC TAT GTG CAA AAC GCT TTG AAT GTG CCG      1307
Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro
                405                 410                 415

GTG GGC TTG CAA TTT TCT TTG TTT AAA AAG TAT TTG TCT TTA GGG CTT      1355
Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu
            420                 425                 430

TGG AAT GAT CTC CAA CTA TCT AAT GTG GCT TTA ATG CAA TCT AAA AAT      1403
Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn
        435                 440                 445

TCC TTC GTG CCT ACG ATC CCT AAT GAA TCA AGG GAA TTT GGG AAT TTT      1451
Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe
    450                 455                 460

GTG TCT TCA AAT TTT TCC ATG TAT GTC AAT ACG GAT TTG GCT AGA GAA      1499
Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu
465                 470                 475                 480

TAC AAC AAG CTT TTC CAC ACG ATC CAA CTA GAA GCG ATT TTC AAC ATC      1547
Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile
                485                 490                 495

CCT TAT TAC ACC TTT AAA AAC GGC TTA TTT TCT CAA AAC ATG TAT GCT      1595
Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala
            500                 505                 510

TTA AGC GCG CAA GCC TTA AAC AGC TAC ACT TCG CCT TTA TTG AGA GAT      1643
Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp
        515                 520                 525
```

```
TAT GAT TAT CAA GGG CGT TTG TAT GAC TCG GTG TGG AAT CCT AGC AGT    1691
Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser
    530                 535                 540

ATT TTA CCT AGC AAT GCG AGC AAC AAG ACG GTG GAT TTA ACC CTA ACG    1739
Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr
545                 550                 555                 560

CAA TAC CTT TAT GGC TTA GGG GGG CAA GAG TTA TTG TAT TTT AAA ATA    1787
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile
                565                 570                     575

TCG CAA CTC ATC AAT CTT GAC GAT AAA GTT TCG CCC TTT AGA ATG CCA    1835
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro
            580                 585                 590

CTA GAG AGC AAG ATC GGG TTT TCG CCC TTA ACG GGA TTG AAC ATC TTT    1883
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe
        595                 600                 605

GGG AAT GTC TTT TAT TCG TTT TAT CAA AAC CGC TTA GAA GAA ATC TCT    1931
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser
    610                 615                 620

GTG AAC GCC AAT TAC CAA CGC AAG TTT TTA AGC TTT AAC CTC TCT TAT    1979
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr
625                 630                 635                 640

TTT TTA AAA AAC AAT TTT AGC AGT GGG ATT AAT AGC ATT GTA GAA AAT    2027
Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn
                645                 650                 655

CTG CGG ATT ATT TAAAGGCGGG TTTTAGCAAC GACTTTGGCT ATTTTTCCAT GAGCGC  2085
Leu Arg Ile Ile
            660

GGATGTGGGT TATGATATTA GAAACAATGT GGTTTTAAAT TGGAATGTGG GGATTTATAA   2145
AAAAATCCGT TGTTTTGGGA TTGG                                          2169
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 660 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
 1               5                  10                  15
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
            20                  25                  30
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
        35                  40                  45
```

Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
50 55 60
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
65 70 75 80
Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp
85 90 95
Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe
100 105 110
Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala
115 120 125
Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly
130 135 140
Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser
145 150 155 160
Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr
165 170 175
Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr
180 185 190
Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser
195 200 205
Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys
210 215 220
Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly
225 230 235 240
Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg
245 250 255
Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys
260 265 270
Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser
275 280 285
Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile
290 295 300
Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr
305 310 315 320
Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met
325 330 335
Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu
340 345 350
Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr
355 360 365
Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu
370 375 380
Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr
385 390 395 400
Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro
405 410 415
Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu
420 425 430
Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn
435 440 445
Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe
450 455 460
Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu
465 470 475 480
Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile
485 490 495
Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala
500 505 510

```
Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp
        515                 520                 525
Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser
    530                 535                 540
Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr
545                 550                 555                 560
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile
                565                 570                 575
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro
            580                 585                 590
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe
        595                 600                 605
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser
    610                 615                 620
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr
625                 630                 635                 640
Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn
                645                 650                 655
Leu Arg Ile Ile
            660
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...401
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
TCAAGGTGTG CCAAACATGC CTTGAAACTC AATTTTTGAA TCTCAATTTT ATG AAA      56
                                                        Met Lys
                                                          1

GGA TTT GTT ATG AGT GGA TTA AAA GCA TTT AGT TGT GTA GTG GTT TTA     104
Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val Val Leu
  5                   10                  15

TGC GGT GCA ATG GCT AAT ACG GCT ATA GCT GGT CCT AAA ATA GAA GCA     152
Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile Glu Ala
    20                  25                  30

AGG GGT GAG TTT GGC AGA TTT TGG GGG GGA GCT GTT GGT GGT GCA ATT     200
Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly Ala Ile
35                  40                  45                  50

GGG GGT GGT GTT GGT GGT GCA GTG GGG GGA GCT GTT GGT GGT CCT GCG     248
Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly Pro Ala
```

```
                55                  60                  65

GGT GGT TGG GCT GGC AGA TTA GTT GGT GGT TCT GTG GGG AGA GAG TTT     296
Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg Glu Phe
            70                  75                  80

GGT CGG GAA ATA GGC GAT AGG GTA GAA GAT TAC ATC CGT GGC GTT GAT     344
Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly Val Asp
        85                  90                  95

AGA GAG CCA CAA GCC CCA AGA GAA CCC ACC TAT GAT CGT CAT TTC GTG     392
Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His Phe Val
    100                 105                 110

TAT GAC AGG TAGCTTTGGG CGAGAAAGGA GAGAGCATGA ATGTCAAAAA TCGTTTGAG   450
Tyr Asp Arg
115

CGAT                                                                454
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Met Lys Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val
 1               5                  10                  15
Val Leu Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile
            20                  25                  30
Glu Ala Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly
        35                  40                  45
Ala Ile Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly
    50                  55                  60
Pro Ala Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg
65                  70                  75                  80
Glu Phe Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly
                85                  90                  95
Val Asp Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His
            100                 105                 110
Phe Val Tyr Asp Arg
        115
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 856 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 59...802
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GCCATTTTAA GCTAATATAA TATAGAGCGA TTATCAAAAA ATAAAGGGAA AAGACTGA        58

ATG TTG AAA AGA ATG ATA TTA TTA GGG GCT TTG GGT GTT TTA GCG AGC       106
Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser
 1               5                  10                  15

GCT GAA GAG AGT GCG GCT TTT GTG GGA GTC AAT TAC CAG GTG AGC ATG       154
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met
            20                  25                  30

ATA CAA AAT CAG ACT AAA ATG GTG AAT GAC AAC GGC TTG CAA AAG CCT       202
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro
        35                  40                  45

TTG ATA AAG TTT CCG CCT TAC GCA GGA GCG GGT TTT GAA GTG GGC TAT       250
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr
    50                  55                  60

AAG CAA TTT TTT GGT AAG AAA AAA TGG TTT GGC ATG CGT TAT TAT GGG       298
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly
65                  70                  75                  80

TTT TTT GAC TAC GCG CAC AAC CGC TTT GGC GTG ATG AAA AAG GGC ATT       346
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile
                85                  90                  95

CCG GTG GGC GAT AGT GGG TTT ATT TAC AAT AGT TTT AGT TTT GGA GGG       394
Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly
            100                 105                 110

AAC ACT TTA ACG GAA AGG GAT TCC TAT CAG GGG CAA TAC TAT GTC AAT       442
Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn
        115                 120                 125

TTA TTC ACT TAT GGC GTG GGG TTA GAT ACG CTG TGG AAT TTT GTG AAT       490
Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn
    130                 135                 140

AAA GAA AAC ATG GTT TTT GGT TTT GTG GTG GGG ATC CAA TTA GCG GGG       538
Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly
145                 150                 155                 160

GAT AGT TGG GCA ACG AGC ATC AGT AAA GAA ATC GCT CAT TAT GCA AAA       586
Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys
                165                 170                 175

CAC CAC AGC AAT TCC AGT TAT AGC CCG GCC AAT TTC CAG TTT TTA TGG       634
```

```
His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp
            180                 185                 190

AAG TTT GGG GTC CGC ACC CAT ATC GCT AAA CAC AAT AGC CTA GAA TTA      682
Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu
        195                 200                 205

GGG ATT AAA GTG CCT ACG ATC ACA CAC CAG CTT TTC TCT CTT ACC AAC      730
Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn
    210                 215                 220

GAA AAG GGA TAC ACC TTA CAG GCT GAT GTG CGT AGA GTT TAT GCG TTT      778
Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe
225                 230                 235                 240

CAA ATC AGT TAC TTG AGG GAT TTT TAACCCCTTT TTAGATACAA TCACGCCTGA AA  834
Gln Ile Ser Tyr Leu Arg Asp Phe
                245

CTATCCATTT AAAGGTGTGA AA                                            856
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser
 1               5                  10                  15
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met
            20                  25                  30
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro
        35                  40                  45
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr
    50                  55                  60
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly
65                  70                  75                  80
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile
                85                  90                  95
Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly
            100                 105                 110
Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn
        115                 120                 125
Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn
    130                 135                 140
Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly
145                 150                 155                 160
Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys
                165                 170                 175
His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp
```

```
            180                 185                 190
Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu
        195                 200                 205
Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn
    210                 215                 220
Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe
225                 230                 235                 240
Gln Ile Ser Tyr Leu Arg Asp Phe
                245
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 69...2699
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
TAATAATAAC CTTAGGTTTA AAACTTGACT AAATTTTTAG AAAAAAGTAA ATAAAAAGGC     60
TAAAAGAA ATG CTT AGA AAT CAA TTT CGT ATC GTG TTT GTC TCT TGT ATT    110
         Met Leu Arg Asn Gln Phe Arg Ile Val Phe Val Ser Cys Ile
           1               5                  10

GTC GCT AGC AAT TTG CAA GCT CAA GAA ACA ACC CAC ACT TTG GGT AAG     158
Val Ala Ser Asn Leu Gln Ala Gln Glu Thr Thr His Thr Leu Gly Lys
 15                  20                  25                  30

GTA ACC ACT AAG GGT GAA AGG ACT TTT GAA TAC AAC AAT AAA ATG TAT     206
Val Thr Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn Asn Lys Met Tyr
                 35                  40                  45

ATT GAC AGA AAA GAG CTC CAA CAA CGC CAA AGT AAC CAA ATC CGT GAT     254
Ile Asp Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp
             50                  55                  60

ATT TTT AGG ACT AGA GCG GAT GTG AAT GTG GCC AGT GGG GGC TTG ATG     302
Ile Phe Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met
         65                  70                  75

GCG CAA AAG ATC TAT GTT AGG GGG ATT GAG AGC CGT CTC TTA AGG GTA     350
Ala Gln Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val
     80                  85                  90

ACA ATA GAT GGC GTC GCC CAA AAT GGT AAC ATT TTC CAC CAT GAC GCT     398
Thr Ile Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala
95                  100                 105                 110
```

```
AAC ACC GTG ATC GAT CCT AAC ATG ATT AAA GAA GTG GAA GTG ATC AAG      446
Asn Thr Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys
                115                 120                 125

GGG GCG GCG AAC GCT TCA GCA GGC CCA GGT GCG GTG GCG GGT AAA TTG      494
Gly Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu
            130                 135                 140

TCT TTC ACC ACG ATT GAC GCT AAC GAC TTC TTA AGA AAG AAT CAA ACT      542
Ser Phe Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr
        145                 150                 155

TAT GGC GCT AAA GCG GAA GCG GCC TTT TAT ACC AAC TTC GGG TAT CGC      590
Tyr Gly Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg
    160                 165                 170

ATG AAC GCC ACT GCG GCT TAC CGG GGG AAA AAC TGG GAC ATC CTA GCC      638
Met Asn Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala
175                 180                 185                 190

TAT TAC AAC CAT CAA AAT ATT TTT TAC TAC AGA GAC GGG AAC AAC GCT      686
Tyr Tyr Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala
                195                 200                 205

TTT AGG AAT GTC TTC CAC CCT AAC TAC GAT TTA CAA GAT CCA AGC AAT      734
Phe Arg Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn
            210                 215                 220

AGC GAT ATG AGC GTA GGG ACT CCC AGT GAA GTC AAT AGC GTT TTA GCT      782
Ser Asp Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala
        225                 230                 235

AAA ATT AAT GGC TAT ATC AAC GAA ACA GAC AGC ATT AGC GTG AGC TAC      830
Lys Ile Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr
    240                 245                 250

AAC CTC ACA CGA GAC AAT TCT ACA AGG CTT TTA CGC CCT AAC ACC ACT      878
Asn Leu Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr
255                 260                 265                 270

TCA GCC CTC TCT AAA GCC AAT GAC CCA GGA AGC CAG CCA GCC CCC TTT      926
Ser Ala Leu Ser Lys Ala Asn Asp Pro Gly Ser Gln Pro Ala Pro Phe
                275                 280                 285

GTG ATT GAC TTT GGG AAA GAA TTA GCC CAT ACG ATC AAC TTC AAC CAC      974
Val Ile Asp Phe Gly Lys Glu Leu Ala His Thr Ile Asn Phe Asn His
            290                 295                 300

AAT TTG AGC TTG AAA TAC AAG CAT GAA GGC GGC CCT AAT TTT AAC CAG     1022
Asn Leu Ser Leu Lys Tyr Lys His Glu Gly Gly Pro Asn Phe Asn Gln
        305                 310                 315

CCG CGC GTT GAA TCC ACC GCC TTT TTA GGG GTA AGG GGG GGC AAT TAT     1070
Pro Arg Val Glu Ser Thr Ala Phe Leu Gly Val Arg Gly Gly Asn Tyr
    320                 325                 330

AAC CCT GTG GTG AAT CCT TTC GCT TAC AAT TCT AAC GAG CCG GCT AAC     1118
Asn Pro Val Val Asn Pro Phe Ala Tyr Asn Ser Asn Glu Pro Ala Asn
```

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335                 340                 345                 350

CCA GAT TAT ATC CCT GAA GTG AAA GAG TGG TGT AAT AAC CCA GAT AAT    1166
Pro Asp Tyr Ile Pro Glu Val Lys Glu Trp Cys Asn Asn Pro Asp Asn
                355                 360                 365

ATC AGC CAG TGC ACG CAA GGG GCT ATC AGG CCT TCT AAT GGA GGC TAT    1214
Ile Ser Gln Cys Thr Gln Gly Ala Ile Arg Pro Ser Asn Gly Gly Tyr
            370                 375                 380

CAA ATA GGC TAT GGC ACG CCT AAT TCT ATT AAT TGG CAA GGG ACT AGC    1262
Gln Ile Gly Tyr Gly Thr Pro Asn Ser Ile Asn Trp Gln Gly Thr Ser
        385                 390                 395

GAT TCT AGT GGA GGG GCG CAA GCA GGG TAT GGG CAG CTT AAC GCT ATT    1310
Asp Ser Ser Gly Gly Ala Gln Ala Gly Tyr Gly Gln Leu Asn Ala Ile
    400                 405                 410

TCT ACA AGC GCG AAC GTT TAT CAT GGG CTT GTC CCT AAA AAT CCT GAT    1358
Ser Thr Ser Ala Asn Val Tyr His Gly Leu Val Pro Lys Asn Pro Asp
415                 420                 425                 430

TAT GAC ATG ACC CCC CCT AAC GCT CAA AAC CCT AGC GCA AAC GAT TGG    1406
Tyr Asp Met Thr Pro Pro Asn Ala Gln Asn Pro Ser Ala Asn Asp Trp
                435                 440                 445

ACT TTA GGG AAT GCG GAC GCT GAG GGG ACT TTA GCC AGA AGG ATT TTT    1454
Thr Leu Gly Asn Ala Asp Ala Glu Gly Thr Leu Ala Arg Arg Ile Phe
            450                 455                 460

TTA ATC AAC TCG GGC GTT AAT TTT AAA GTA ACC CAC CCC ATT AGC GAA    1502
Leu Ile Asn Ser Gly Val Asn Phe Lys Val Thr His Pro Ile Ser Glu
        465                 470                 475

GAT TAT GGG AAT GTG TTT GAA TAC GGC ATG ATT TAT CAA AAC CTG AGC    1550
Asp Tyr Gly Asn Val Phe Glu Tyr Gly Met Ile Tyr Gln Asn Leu Ser
    480                 485                 490

GTT TTC TCT GGA TTG GAT AAA GGC AAA AAC GGC TAT TAT AAA AAC AAC    1598
Val Phe Ser Gly Leu Asp Lys Gly Lys Asn Gly Tyr Tyr Lys Asn Asn
495                 500                 505                 510

ATT GAT CCT AAC GAC CCT AAC GGG CCG GGC TTG CCT TAC CGC CAT TAC    1646
Ile Asp Pro Asn Asp Pro Asn Gly Pro Gly Leu Pro Tyr Arg His Tyr
                515                 520                 525

TAC ACC GAT CAA AGC TCC CAA TAC CCC CAA AAT CTC AAC ACC CCT AAC    1694
Tyr Thr Asp Gln Ser Ser Gln Tyr Pro Gln Asn Leu Asn Thr Pro Asn
            530                 535                 540

CCG CTC TAT CGT AAC ATG CCC CAA AAT TCG CAT GCG ATC GGC AAT ATC    1742
Pro Leu Tyr Arg Asn Met Pro Gln Asn Ser His Ala Ile Gly Asn Ile
        545                 550                 555

ATC GGA GGG TTT ATG CAA GCA AAC TAC AAC ATT TTA AGC AAT GTG ATC    1790
Ile Gly Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile
    560                 565                 570
```

```
GTG GGT GCG GGA ACT CGT TAT GAT ATT TAC ACC TTG CTA GAC AAA AAC    1838
Val Gly Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn
575                 580                 585                 590

GGC CGC ACG CAT GTA ACT TCT GGT TTC TCG CCT TCT GCA ACC GTG CTT    1886
Gly Arg Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu
                595                 600                 605

TAT AAC CCC ATT GAA AGC ATT GGC TTG AAA GTG AGT TAT GCG TAT GTA    1934
Tyr Asn Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val
            610                 615                 620

ACT AAG GGG GCT TTG CCT GGC GAT GGC GTT TTG ATG CGC GAT CCT ACG    1982
Thr Lys Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr
        625                 630                 635

GTG ATT TAT CAA AGG AAT TTG CGC CCT GCG ATC GGT CAA AAT GTG GAA    2030
Val Ile Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu
    640                 645                 650

TTT AAT GTG GAT TTC AAC AGC AAG TAT TTC AAT GTG CGC GGG GCA GCG    2078
Phe Asn Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala
655                 660                 665                 670

TTC TAT CAA GTC ATC AAT AAT TTC ATC AAC AGC TAC GGG CAA GAC ACT    2126
Phe Tyr Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr
                675                 680                 685

TCT AAA AAT GGA GGG GGT AAC GCA ACC GCA AAA AAC ATG TCA GGG AAT    2174
Ser Lys Asn Gly Gly Gly Asn Ala Thr Ala Lys Asn Met Ser Gly Asn
            690                 695                 700

TTA CCC GAA ACC ATT AAC ATT TAT GGT TAT GAA GTT TCA GGG AAT GTG    2222
Leu Pro Glu Thr Ile Asn Ile Tyr Gly Tyr Glu Val Ser Gly Asn Val
        705                 710                 715

AGG TAT AAG AAT TTC TTA GGG ACT TTC TCA GTG GCT CGC TCT TGG CCA    2270
Arg Tyr Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro
    720                 725                 730

ACG GCT AGG GGG CAT TTA TTA GCG GAC ACT TAC GCT CTA GCT GCA ACG    2318
Thr Ala Arg Gly His Leu Leu Ala Asp Thr Tyr Ala Leu Ala Ala Thr
735                 740                 745                 750

ACT GGG AAT GTG TTT ATT TTA AAA GCC GAT TAT GAT GTT CGC AGG TGG    2366
Thr Gly Asn Val Phe Ile Leu Lys Ala Asp Tyr Asp Val Arg Arg Trp
                755                 760                 765

GGG CTT ACT TTA ACC TGG CTC TCG CGC TTT GTA ACT AAC ATG TAT TAT    2414
Gly Leu Thr Leu Thr Trp Leu Ser Arg Phe Val Thr Asn Met Tyr Tyr
            770                 775                 780

GAG GGC TAT TCT ATC TAT TAC CCG CAA TAC GGC TTG ATC AAA ATC CAT    2462
Glu Gly Tyr Ser Ile Tyr Tyr Pro Gln Tyr Gly Leu Ile Lys Ile His
        785                 790                 795

AAA CCC GGG TAT GGC GTG CAT AAT GTC TTT ATC AAC TGG ACT CCG CCT    2510
Lys Pro Gly Tyr Gly Val His Asn Val Phe Ile Asn Trp Thr Pro Pro
```

```
    800                 805                 810

TCT AAA AAA TGG CAG GGT TTA AGG ATT TCA GCC GTG TTT AAT AAT ATC     2558
Ser Lys Lys Trp Gln Gly Leu Arg Ile Ser Ala Val Phe Asn Asn Ile
815                 820                 825                 830

TTA AAC AAG CAA TAT GTG GAT CAA ACT TCT GTG TTT CAA GCG AGC GCG     2606
Leu Asn Lys Gln Tyr Val Asp Gln Thr Ser Val Phe Gln Ala Ser Ala
                835                 840                 845

GAC GCT CCA GCG AGC GAT ATG ATC CCT AAA GGT AAG CGC ATG GCG CTC     2654
Asp Ala Pro Ala Ser Asp Met Ile Pro Lys Gly Lys Arg Met Ala Leu
            850                 855                 860

CCG GCT CCT GGA TTT AAC GCG CGT TTT GAG GTA TCC TAT CAG TTC TAAAA   2704
Pro Ala Pro Gly Phe Asn Ala Arg Phe Glu Val Ser Tyr Gln Phe
        865                 870                 875

TGAAAGGAAT CTTAGGATTT CTTTTTGAAT TTTGAACATG GAAACA                  2750
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 877 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Leu Arg Asn Gln Phe Arg Ile Val Phe Val Ser Cys Ile Val Ala
  1               5                  10                  15
Ser Asn Leu Gln Ala Gln Glu Thr Thr His Thr Leu Gly Lys Val Thr
            20                  25                  30
Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn Asn Lys Met Tyr Ile Asp
        35                  40                  45
Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp Ile Phe
    50                  55                  60
Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met Ala Gln
65                  70                  75                  80
Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val Thr Ile
                85                  90                  95
Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala Asn Thr
            100                 105                 110
Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys Gly Ala
        115                 120                 125
Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu Ser Phe
    130                 135                 140
Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr Tyr Gly
145                 150                 155                 160
Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg Met Asn
                165                 170                 175
Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala Tyr Tyr
            180                 185                 190
Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala Phe Arg
```

```
        195                 200                 205
Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn Ser Asp
    210                 215                 220
Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala Lys Ile
225                 230                 235                 240
Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr Asn Leu
                245                 250                 255
Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr Ser Ala
            260                 265                 270
Leu Ser Lys Ala Asn Asp Pro Gly Ser Gln Pro Ala Pro Phe Val Ile
        275                 280                 285
Asp Phe Gly Lys Glu Leu Ala His Thr Ile Asn Phe Asn His Asn Leu
    290                 295                 300
Ser Leu Lys Tyr Lys His Glu Gly Gly Pro Asn Phe Asn Gln Pro Arg
305                 310                 315                 320
Val Glu Ser Thr Ala Phe Leu Gly Val Arg Gly Gly Asn Tyr Asn Pro
                325                 330                 335
Val Val Asn Pro Phe Ala Tyr Asn Ser Asn Glu Pro Ala Asn Pro Asp
            340                 345                 350
Tyr Ile Pro Glu Val Lys Glu Trp Cys Asn Asn Pro Asp Asn Ile Ser
        355                 360                 365
Gln Cys Thr Gln Gly Ala Ile Arg Pro Ser Asn Gly Gly Tyr Gln Ile
    370                 375                 380
Gly Tyr Gly Thr Pro Asn Ser Ile Asn Trp Gln Gly Thr Ser Asp Ser
385                 390                 395                 400
Ser Gly Gly Ala Gln Ala Gly Tyr Gly Gln Leu Asn Ala Ile Ser Thr
                405                 410                 415
Ser Ala Asn Val Tyr His Gly Leu Val Pro Lys Asn Pro Asp Tyr Asp
            420                 425                 430
Met Thr Pro Pro Asn Ala Gln Asn Pro Ser Ala Asn Asp Trp Thr Leu
        435                 440                 445
Gly Asn Ala Asp Ala Glu Gly Thr Leu Ala Arg Arg Ile Phe Leu Ile
    450                 455                 460
Asn Ser Gly Val Asn Phe Lys Val Thr His Pro Ile Ser Glu Asp Tyr
465                 470                 475                 480
Gly Asn Val Phe Glu Tyr Gly Met Ile Tyr Gln Asn Leu Ser Val Phe
                485                 490                 495
Ser Gly Leu Asp Lys Gly Lys Asn Gly Tyr Tyr Lys Asn Asn Ile Asp
            500                 505                 510
Pro Asn Asp Pro Asn Gly Pro Gly Leu Pro Tyr Arg His Tyr Tyr Thr
        515                 520                 525
Asp Gln Ser Ser Gln Tyr Pro Gln Asn Leu Asn Thr Pro Asn Pro Leu
    530                 535                 540
Tyr Arg Asn Met Pro Gln Asn Ser His Ala Ile Gly Asn Ile Ile Gly
545                 550                 555                 560
Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile Val Gly
                565                 570                 575
Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn Gly Arg
            580                 585                 590
Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu Tyr Asn
        595                 600                 605
Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val Thr Lys
    610                 615                 620
Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr Val Ile
625                 630                 635                 640
Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu Phe Asn
                645                 650                 655
Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala Phe Tyr
```

```
            660                 665                 670
Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr Ser Lys
        675                 680                 685
Asn Gly Gly Gly Asn Ala Thr Ala Lys Asn Met Ser Gly Asn Leu Pro
    690                 695                 700
Glu Thr Ile Asn Ile Tyr Gly Tyr Glu Val Ser Gly Asn Val Arg Tyr
705                 710                 715                 720
Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro Thr Ala
                725                 730                 735
Arg Gly His Leu Leu Ala Asp Thr Tyr Ala Leu Ala Ala Thr Thr Gly
            740                 745                 750
Asn Val Phe Ile Leu Lys Ala Asp Tyr Asp Val Arg Arg Trp Gly Leu
        755                 760                 765
Thr Leu Thr Trp Leu Ser Arg Phe Val Thr Asn Met Tyr Tyr Glu Gly
    770                 775                 780
Tyr Ser Ile Tyr Tyr Pro Gln Tyr Gly Leu Ile Lys Ile His Lys Pro
785                 790                 795                 800
Gly Tyr Gly Val His Asn Val Phe Ile Asn Trp Thr Pro Pro Ser Lys
                805                 810                 815
Lys Trp Gln Gly Leu Arg Ile Ser Ala Val Phe Asn Asn Ile Leu Asn
            820                 825                 830
Lys Gln Tyr Val Asp Gln Thr Ser Val Phe Gln Ala Ser Ala Asp Ala
        835                 840                 845
Pro Ala Ser Asp Met Ile Pro Lys Gly Lys Arg Met Ala Leu Pro Ala
    850                 855                 860
Pro Gly Phe Asn Ala Arg Phe Glu Val Ser Tyr Gln Phe
865                 870                 875
```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...317
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
TTTAAAATCA CCCGTTACAG CATCACTGAA ATCACTAATA GGGGTGATTG ATG CGT      56
                                                        Met Arg
                                                          1

AAG GTT TTA TAC GCT CTT GTG GGC TTT TTG TTG GCT TTT AGC GCT TTA     104
Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser Ala Leu
          5                  10                  15

AAA GCC GAT GAT TTT TTA GAA GAA GCG AAC GAA ACA GCC CCG GCG CAT     152
Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro Ala His
     20                  25                  30
```

```
TTA AAC CAC CCT ATG CAG GAT TTA AAC GCC ATT CAA GGG AGC TTT TTT      200
Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser Phe Phe
 35                  40                  45                  50

GAC AAA AAC CGC TCA AAA ATG TCC AAC ACT TTG AAC ATT GAT TAC TTT      248
Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp Tyr Phe
                 55                  60                  65

CAA GGG CAA ACT TAT AAA ATC CCG CTT GCG TTA TGC GAT GGC GMC CTT      296
Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly Xaa Leu
            70                  75                  80

ATT GTT TTT TTC AAA ACC CAT TAGCGATTTT GTTTTAGGGG ATAAGGTGGG TTTT    351
Ile Val Phe Phe Lys Thr His
         85

GATGCGAAAA TTTTAGAAA                                                 370
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Met Arg Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser
  1               5                  10                  15
Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro
            20                  25                  30
Ala His Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser
        35                  40                  45
Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp
    50                  55                  60
Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly
65                  70                  75                  80
Xaa Leu Ile Val Phe Phe Lys Thr His
                85
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...305
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
ATGCAATAAA AAAAGAAATT CTTAGGATTT CTCACATTAA GGAGTTTTAA ATG AAA      56
                                                          Met Lys
                                                            1

AAG GTT TTT TTA GGT ATG GCA TTA GCC TTT AGT GTG TCC ATG GCA GAA     104
Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met Ala Glu
          5                  10                  15

AAA AGT GGC GCG TTT TTA GGA GGG GGG TTT CAA TAT TCT AAT TTA GAA     152
Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn Leu Glu
     20                  25                  30

AAC CAA AAC ACC ACC CGC ACC CCA GGC GCT AAC AAT AAC ACC CCG ATA     200
Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr Pro Ile
35                   40                  45                  50

GAC ACT TCA ATG TTT GGC AGC AAC AAA ACA GCT CCA GCC CAA GAA ACG     248
Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln Glu Thr
                55                  60                  65

CAA AGC GCT TCC AAA CCG GAC ACT AAA GTC AAT CCA AGC GCA AGT TGG     296
Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala Ser Trp
           70                  75                  80

ATG AAA AAA TAAGAAGGAA GTTATGAAAA AGTCATTCAA AAAATTAGGC TTTGTCTCT   354
Met Lys Lys
        85

TTA                                                                 357
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Met Lys Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met
 1               5                  10                  15
Ala Glu Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn
            20                  25                  30
Leu Glu Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr
        35                  40                  45
Pro Ile Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln
    50                  55                  60
Glu Thr Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala
65                  70                  75                  80
Ser Trp Met Lys Lys
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...908
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
GAATGTAGCA TTTAGAACTC AAGTAGAGAA AATGTAGAAG GAAGGAATAC ATG AAG      56
                                                          Met Lys
                                                           1

AAA TCT GTT ATA GTA GGT GCT ATC TCT CTA GCA ATG ACA AGC TTA TTG     104
Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser Leu Leu
          5                  10                  15

TCA GCA GAG ACC CCT AAG CAA GAA AAA GCT ATT AAG ACT AGC CCT ACC     152
Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser Pro Thr
     20                  25                  30

AAA AAA GGT GAA AGA AAT GCT GCT TTT ATA GGG ATT GAT TAC CAG TTG     200
Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr Gln Leu
35                  40                  45                  50

GGT ATG CTC AGC ACT ACC GCT CAA AAT TGT TCC CAT GGG AAT TGC AAT     248
Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn Cys Asn
                55                  60                  65

GGT AAT CAA AGT GGG GCT TAC GGC TCT AAT ACG CCT AAC ATG CCT ACA     296
Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met Pro Thr
            70                  75                  80

GCG TCA AAC CCA ACA GGA GGG TTT ACT CAT GGC GCT CTA GGG ACT CGT     344
Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly Thr Arg
        85                  90                  95

GGG TAT AAA GGC TTA AGC AAC CAA CAA TAC GCT ATC AAT GGT TTT GGT     392
Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly Phe Gly
    100                 105                 110

TTT GTT GTA GGG TAT AAG CAT TTT TTC AAG AAA TCC CCG CAA TTT GGA     440
Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln Phe Gly
115                 120                 125                 130

ATG CGT TAT TAC GGA TTC TTT GAT TTT GCA AGC TCT TAT TAT AAG TAT     488
```

```
Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr Lys Tyr
                135                 140                 145

TAC ACT TAT AAT GAT TAT GGC ATG AGA GAC GCT CGC AAG GGT TCT CAA      536
Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly Ser Gln
            150                 155                 160

AGT TTC ATG TTT GGC TAT GGG GCT GGC ACA GAT GTG TTG TTT AAC CCG      584
Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe Asn Pro
        165                 170                 175

GCT ATT TTC AAT CGT GAG AAC TTG CAT TTT GGG TTT TTC TTG GGC GTT      632
Ala Ile Phe Asn Arg Glu Asn Leu His Phe Gly Phe Phe Leu Gly Val
    180                 185                 190

GCG ATC GGT GGC ACC TCT TGG GGT CCA ACA AAC TAT TAT TTT AAG GAC      680
Ala Ile Gly Gly Thr Ser Trp Gly Pro Thr Asn Tyr Tyr Phe Lys Asp
195                 200                 205                 210

TTG GCT GAT GAG TAT AGA GGG AGT TTC CAC CCA TCA AAT TTC CAG GTC      728
Leu Ala Asp Glu Tyr Arg Gly Ser Phe His Pro Ser Asn Phe Gln Val
                215                 220                 225

TTA GTT AAT GGT GGG ATT CGC TTA GGC ACT AAA CAC CAA GGT TTT GAA      776
Leu Val Asn Gly Gly Ile Arg Leu Gly Thr Lys His Gln Gly Phe Glu
            230                 235                 240

ATT GGC TTG AAA ATC CAA ACC ATC CGC AAC AAT TAC TAC ACC GCT AGT      824
Ile Gly Leu Lys Ile Gln Thr Ile Arg Asn Asn Tyr Tyr Thr Ala Ser
        245                 250                 255

GCG GAT AAT GTG CCT GAA GGG ACT ACT TAT AGA TTC ACT TTC CAC CGC      872
Ala Asp Asn Val Pro Glu Gly Thr Thr Tyr Arg Phe Thr Phe His Arg
    260                 265                 270

CCC TAT GCC TTT TAT TGG CGT TAC ATT GTA AGC TTT TAAGGTGTTT TAGGGC    924
Pro Tyr Ala Phe Tyr Trp Arg Tyr Ile Val Ser Phe
275                 280                 285

TAATCTTATG GGGGCATAGA AAAGGGCTTT TGCTCTT                            961
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Lys Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser
 1               5                  10                  15
Leu Leu Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser
            20                  25                  30
```

```
Pro Thr Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr
        35                  40                  45
Gln Leu Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn
    50                  55                  60
Cys Asn Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met
65                  70                  75                  80
Pro Thr Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly
                85                  90                  95
Thr Arg Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly
            100                 105                 110
Phe Gly Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln
        115                 120                 125
Phe Gly Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr
    130                 135                 140
Lys Tyr Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly
145                 150                 155                 160
Ser Gln Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe
                165                 170                 175
Asn Pro Ala Ile Phe Asn Arg Glu Asn Leu His Phe Gly Phe Phe Leu
            180                 185                 190
Gly Val Ala Ile Gly Gly Thr Ser Trp Gly Pro Thr Asn Tyr Tyr Phe
        195                 200                 205
Lys Asp Leu Ala Asp Glu Tyr Arg Gly Ser Phe His Pro Ser Asn Phe
    210                 215                 220
Gln Val Leu Val Asn Gly Gly Ile Arg Leu Gly Thr Lys His Gln Gly
225                 230                 235                 240
Phe Glu Ile Gly Leu Lys Ile Gln Thr Ile Arg Asn Asn Tyr Tyr Thr
                245                 250                 255
Ala Ser Ala Asp Asn Val Pro Glu Gly Thr Thr Tyr Arg Phe Thr Phe
            260                 265                 270
His Arg Pro Tyr Ala Phe Tyr Trp Arg Tyr Ile Val Ser Phe
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...236
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
GGGATTTTAT TTCTTATAGC AGAAATTATT TTTAAAGTAA AAGACAAATC ATG TTT      56
                                                        Met Phe
                                                          1

AGA GAT ATA GTA GAT ATT TTA ATA TCT GTT GTT ATT ATT GGA TTA GTA     104
Arg Asp Ile Val Asp Ile Leu Ile Ser Val Val Ile Ile Gly Leu Val
```

```
          5                   10                  15

TTA ACA GCT ATT AGA GCT ACT ATA ATG GCG TTT AAA GGC GAT ACT GAT      152
Leu Thr Ala Ile Arg Ala Thr Ile Met Ala Phe Lys Gly Asp Thr Asp
    20                  25                  30

GAT GAT GAA GTT GAG AGT GAT GGG TTT TTT AGT AGA ATA TGG GAT AAA      200
Asp Asp Glu Val Glu Ser Asp Gly Phe Phe Ser Arg Ile Trp Asp Lys
35                  40                  45                  50

TTC GTT GAA TAT TTC GGC TAT ACT CTA GTT ACT ATA TAATGTTTTT TCCTTA    252
Phe Val Glu Tyr Phe Gly Tyr Thr Leu Val Thr Ile
                55                  60

TATAATTGGA CCAGTTATCG CTTTAATTTT TATATTT                            289
```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Met Phe Arg Asp Ile Val Asp Ile Leu Ile Ser Val Val Ile Ile Gly
 1               5                  10                  15
Leu Val Leu Thr Ala Ile Arg Ala Thr Ile Met Ala Phe Lys Gly Asp
            20                  25                  30
Thr Asp Asp Asp Glu Val Glu Ser Asp Gly Phe Phe Ser Arg Ile Trp
        35                  40                  45
Asp Lys Phe Val Glu Tyr Phe Gly Tyr Thr Leu Val Thr Ile
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...1491
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
GACACACATT AGTTATAGTT TCTAAGAGAG TTCTCCCCCT ATCTCTTAGA T ATG CCT     57
```

```
                                                                  Met Pro
                                                                   1

TTT TGT ATT TTT ATT TTA ATA TCT TTG GGA GTT AGG GTT TTG GAA ATT      105
Phe Cys Ile Phe Ile Leu Ile Ser Leu Gly Val Arg Val Leu Glu Ile
         5                  10                  15

AAG AAA TAT TTT TCT TAC TCT CTA TTT TTT TTG CTT TTT TCT AGT CTC      153
Lys Lys Tyr Phe Ser Tyr Ser Leu Phe Phe Leu Leu Phe Ser Ser Leu
    20                  25                  30

TTT TTA TCC AAA CTT CAA GCT TAT AAA TTC AAC ATG AGC ATT GTT GGA      201
Phe Leu Ser Lys Leu Gln Ala Tyr Lys Phe Asn Met Ser Ile Val Gly
35                  40                  45                  50

AAG GTG AGC AGC TAT ACC AAG TTT GGC TTT AAC AAC CAA AGA TAC CAG      249
Lys Val Ser Ser Tyr Thr Lys Phe Gly Phe Asn Asn Gln Arg Tyr Gln
                55                  60                  65

CCT TCT AAA GAC ATT TAT CCT ACA GGT AGC TAC ACT TCT TTA CTC GGC      297
Pro Ser Lys Asp Ile Tyr Pro Thr Gly Ser Tyr Thr Ser Leu Leu Gly
            70                  75                  80

GAA TTG AAT TTG AGC ATG GGT TTA TAC AAG GGT TTG AGA GCG GAA GTG      345
Glu Leu Asn Leu Ser Met Gly Leu Tyr Lys Gly Leu Arg Ala Glu Val
        85                  90                  95

GGG GCT ATG ATG GCA GCG CTC CCC TAT GAC TCT ACC GCC TAT CAA GGC      393
Gly Ala Met Met Ala Ala Leu Pro Tyr Asp Ser Thr Ala Tyr Gln Gly
    100                 105                 110

AAC AAT ATC CCT AAC GGC CAG CCC GGC TCT AGG ACC GAT CCT TTT GGG      441
Asn Asn Ile Pro Asn Gly Gln Pro Gly Ser Arg Thr Asp Pro Phe Gly
115                 120                 125                 130

GCG GGT ATC TTT TGG CAA TAT ATT GGT TGG TAT GCG GGG CAT AGT GGT      489
Ala Gly Ile Phe Trp Gln Tyr Ile Gly Trp Tyr Ala Gly His Ser Gly
                135                 140                 145

TTG CAA GTG CAA AAA CCT CGT TTA GCC ATG GTG CAT AAC GCT TTT TTG      537
Leu Gln Val Gln Lys Pro Arg Leu Ala Met Val His Asn Ala Phe Leu
            150                 155                 160

AGC TAC AAC TAC AAA AAA GAC AAA TTC AGT TTT GGC GTG AAA GGG GGG      585
Ser Tyr Asn Tyr Lys Lys Asp Lys Phe Ser Phe Gly Val Lys Gly Gly
        165                 170                 175

CGC TAT GAC GCT GAA GAG TAT GAT TGG TTC ACT TCT TAC ACT CAA GGG      633
Arg Tyr Asp Ala Glu Glu Tyr Asp Trp Phe Thr Ser Tyr Thr Gln Gly
    180                 185                 190

GTT GAA GGC TTT GTC AAA TAT AAA GAC ACC AGA TTC AGG GTG ATG TAT      681
Val Glu Gly Phe Val Lys Tyr Lys Asp Thr Arg Phe Arg Val Met Tyr
195                 200                 205                 210

TCA GAC GCT AGG GCT TCA GCG TCA AGC GAC TGG TTT TGG TAT TTT GGG      729
Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr Phe Gly
                215                 220                 225
```

```
CGT TAC TAT ACA AGC GGT AAG GCT CTA ATG GTA GCT GAT TTG AAA TAT      777
Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu Lys Tyr
            230                 235                 240

GAA AAA GAC AAC CTA AAA ATC AAC CCT TAT TTT TAT GCG ATC TTT CAA      825
Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile Phe Gln
        245                 250                 255

AGA ATG TAT GCG CCA GGC ATT AAT ATC ACT TAT GAC ACC AAC CCT AAT      873
Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn Pro Asn
    260                 265                 270

TTC AAC AAT AAG GGT TTT CGT TTT GTA GGC ACT TTC GTA GGG TTT TTC      921
Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly Phe Phe
275                 280                 285                 290

CCC ATT TTT GCC ACT CCG GCT AAT CAA AAT GAT ATT ATC CTC TTC CAA      969
Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu Phe Gln
                295                 300                 305

CAA GTG CCA TTA GGC AAG AGT GGG CAA ACT TAT TTC TTC CGC ACT CGT     1017
Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg Thr Arg
            310                 315                 320

TTT TAC TAT AAT AAG TGG CAA TTT GGG GGC AGC GTC TAT AAA AAC ATC     1065
Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys Asn Ile
        325                 330                 335

GGT AAC GCT AAT GGT GAT ATA GGT ATT TAT GGC GAC CCT TTG GGG TAT     1113
Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu Gly Tyr
    340                 345                 350

AAC ATT TGG ACG AAT AGT ATT TAT GAC GCA GAA ATT AAC AAT ATT GTT     1161
Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn Ile Val
355                 360                 365                 370

GGC GCT GAT GTT ATT AAC GGG TTT TTG TAT GTA GGC TCA CAA TAT AGA     1209
Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln Tyr Arg
                375                 380                 385

GGG TTT AGT TGG AAA ATT TTA GGC CGT TGG ACG GAT AGC CCA AGG GCT     1257
Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro Arg Ala
            390                 395                 400

GAT GAA AGG AGT CTC GCG CTC TTT TTG AGT TAT TTT TCT AAT AAG TAT     1305
Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn Lys Tyr
        405                 410                 415

AAT ATT AGA ATG GAT TTA AAA CTA GAA TAT TAT GGC AAT ATC ACC AAA     1353
Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile Thr Lys
    420                 425                 430

AAA GGC TAT TGT ATT GGG TAT TGT GGC ATG TAT GTT CCA GTC GAT CCT     1401
Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val Asp Pro
435                 440                 445                 450

AAC GGG CCT GGG ACA CAG CCT TTA ACG CAC AAT GTG TAT TCT GAC AGG     1449
Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser Asp Arg
```

```
                455                 460                 465

AGC CAT ATA ATG TTT AAC ATT GCT TAC GGT TTT AGG ATT TAC TAGCATTTT  1500
Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr
            470                 475                 480

ATCCTTAATG GATATTTTTG ATTAGCCTTT TTAAAATATT GAAA                  1544
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Pro Phe Cys Ile Phe Ile Leu Ile Ser Leu Gly Val Arg Val Leu
 1               5                  10                  15
Glu Ile Lys Lys Tyr Phe Ser Tyr Ser Leu Phe Phe Leu Leu Phe Ser
            20                  25                  30
Ser Leu Phe Leu Ser Lys Leu Gln Ala Tyr Lys Phe Asn Met Ser Ile
        35                  40                  45
Val Gly Lys Val Ser Ser Tyr Thr Lys Phe Gly Phe Asn Asn Gln Arg
    50                  55                  60
Tyr Gln Pro Ser Lys Asp Ile Tyr Pro Thr Gly Ser Tyr Thr Ser Leu
65                  70                  75                  80
Leu Gly Glu Leu Asn Leu Ser Met Gly Leu Tyr Lys Gly Leu Arg Ala
                85                  90                  95
Glu Val Gly Ala Met Met Ala Ala Leu Pro Tyr Asp Ser Thr Ala Tyr
            100                 105                 110
Gln Gly Asn Asn Ile Pro Asn Gly Gln Pro Gly Ser Arg Thr Asp Pro
        115                 120                 125
Phe Gly Ala Gly Ile Phe Trp Gln Tyr Ile Gly Trp Tyr Ala Gly His
    130                 135                 140
Ser Gly Leu Gln Val Gln Lys Pro Arg Leu Ala Met Val His Asn Ala
145                 150                 155                 160
Phe Leu Ser Tyr Asn Tyr Lys Lys Asp Lys Phe Ser Phe Gly Val Lys
                165                 170                 175
Gly Gly Arg Tyr Asp Ala Glu Glu Tyr Asp Trp Phe Thr Ser Tyr Thr
            180                 185                 190
Gln Gly Val Glu Gly Phe Val Lys Tyr Lys Asp Thr Arg Phe Arg Val
        195                 200                 205
Met Tyr Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr
    210                 215                 220
Phe Gly Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu
225                 230                 235                 240
Lys Tyr Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile
                245                 250                 255
Phe Gln Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn
            260                 265                 270
Pro Asn Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly
        275                 280                 285
Phe Phe Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu
```

```
    290                 295                 300
Phe Gln Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg
305                 310                 315                 320
Thr Arg Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys
                325                 330                 335
Asn Ile Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu
            340                 345                 350
Gly Tyr Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn
        355                 360                 365
Ile Val Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln
    370                 375                 380
Tyr Arg Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro
385                 390                 395                 400
Arg Ala Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn
                405                 410                 415
Lys Tyr Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile
            420                 425                 430
Thr Lys Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val
        435                 440                 445
Asp Pro Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser
    450                 455                 460
Asp Arg Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr
465                 470                 475                 480
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...605
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
AATTTTAGGT TATTAGTTAC CATTTTATTA TTCTTAAGGA TGTGTTTATA ATG AGA      56
                                                        Met Arg
                                                          1

ATT AAG GCT TAT TTT TTG CGT TTT ATC GCG CTG GTT TTG ATT GTT TTG     104
Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile Val Leu
          5                  10                  15

TTA GGT TTT AGT GCT TGT AAA AAT TCT CAA AAA TCT CAA GAT TCT CAA     152
Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp Ser Gln
     20                  25                  30

AAC AAT ACC CCC CAA CAA GAT AGC CCT AAA ACC TAC ACC GCT ATG GAT     200
Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala Met Asp
35                  40                  45                  50
```

```
TTG AAT AAC CAA GAA TAC ACC ATC ACA GGC GAT TTA GAT TCT CTC AAT      248
Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser Leu Asn
                55                  60                  65

ATC AGC CCG GAT TCC AAC ACC CCT ACC CTA TTA GTT TTA AGC GCT TTA      296
Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser Ala Leu
            70                  75                  80

GAT AAT TCT TTA AAA GAT TAC GCC CCC AGC TTT AAC ATC TTA AAA AAA      344
Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu Lys Lys
        85                  90                  95

ACT TTT AAA GAT CGT TTG AGG GTG CTT ATT TTA CTC AAT AAA CCC TAT      392
Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys Pro Tyr
    100                 105                 110

TCA AGC GAT GCA ATC AAA GAC TTT AGC GCG CAT TTT CAA GCT GAT TTG      440
Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala Asp Leu
115                 120                 125                 130

ATG ATT TTA AAC CCT AAA GAT ACC GCT CTT TTT GAT CAT TTA AAG TAT      488
Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu Lys Tyr
                135                 140                 145

GAC GCT TTA AAC CAT TCT TTT AAC ATG CTC TTA TAC CAC AAA CAC CAA      536
Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys His Gln
            150                 155                 160

TTG ATC AAA ATG TAT CAA GGG ATC GTG CCA ATA GAA ATG CTC CAA TTT      584
Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu Gln Phe
        165                 170                 175

GAT ATT TCC AAT TTA AAG GAT TAAAAAAAAC CATGTTTAAT TTTTTCAAAA AAAT    639
Asp Ile Ser Asn Leu Lys Asp
    180                 185

TGTCAATAAA ATTAAGGGT                                                 658
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
Met Arg Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile
 1               5                  10                  15
Val Leu Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp
            20                  25                  30
Ser Gln Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala
        35                  40                  45
Met Asp Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser
```

```
    50                  55                  60
Leu Asn Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser
65                  70                  75                  80
Ala Leu Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu
                85                  90                  95
Lys Lys Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys
            100                 105                 110
Pro Tyr Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala
        115                 120                 125
Asp Leu Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu
    130                 135                 140
Lys Tyr Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys
145                 150                 155                 160
His Gln Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu
                165                 170                 175
Gln Phe Asp Ile Ser Asn Leu Lys Asp
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...407
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
AATCCCTTCA AAAATGATAT AATAGACTTG ATGAACTCAT TTTAAGGAAA ATG CCC      56
                                                          Met Pro
                                                            1

ATG CGT TTG CAC ACT GCC TTT TTT GGT ATT AAT TCA TTG CTT GTT GCC      104
Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu Val Ala
          5                  10                  15

TCT CTT TTG ATA AGC GGT TGC AGT CTC TTT AAA AAG CGT AAC ACT AAC      152
Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn Thr Asn
     20                  25                  30

GCC CAG CTA ATC CCC CCT TCA GCT AAT GGC TTG CAA GCC CCC ATT TAT      200
Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro Ile Tyr
35                  40                  45                  50

CCC CCA ACC AAT TTC ACC CCT AGA AAG AGC ATT CAG CCT CTC CCA AGC      248
Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu Pro Ser
                55                  60                  65

CCT CGC CTT GAG AAT AAC GAT CAG CCC GTC ATT AGT TCT AAC CCC ACT      296
```

```
Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn Pro Thr
            70                  75                  80

AAC GCT ATC CCT AAC ACC CCC ATT CTC ACG CCT AAT AAT GTC ATT GAA     344
Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val Ile Glu
        85                  90                  95

TTG AAC GCA TGG GCA TGG GCG TGG CTC CAG AAT CCA CCA TTT CAC CCT     392
Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe His Pro
    100                 105                 110

CTC AAG CCC TGG CTC TAGCCAAGCG GGCGGCTATC GTTGATGGCT ACCGCCAGTT G   448
Leu Lys Pro Trp Leu
115

GGTGAAAAAA TG                                                       460
```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Met Pro Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu
 1               5                  10                  15
Val Ala Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn
            20                  25                  30
Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro
        35                  40                  45
Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu
    50                  55                  60
Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn
65                  70                  75                  80
Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val
                85                  90                  95
Ile Glu Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe
            100                 105                 110
His Pro Leu Lys Pro Trp Leu
        115
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1232
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
GTTGTGATTT TATTGTGTTT TCATATCAAT TTTCATATCA AGGAGTTTAA ATG AAA      56
                                                        Met Lys
                                                          1

GAA ACA AGA CTT TTA AAA TTG AGA GCG TTG AGC TTA GCA TGT TTA ATG     104
Glu Thr Arg Leu Leu Lys Leu Arg Ala Leu Ser Leu Ala Cys Leu Met
          5                  10                  15

GGA TTA GGC GTG AGT GGG TGC GCG TTT TTA GAT AAG CAA ATC TTA AAC     152
Gly Leu Gly Val Ser Gly Cys Ala Phe Leu Asp Lys Gln Ile Leu Asn
     20                  25                  30

GAC CAT TTG ACT AAA GCT AAA AAT AAC CCA AAA TAC GAT TGC CAA AAA     200
Asp His Leu Thr Lys Ala Lys Asn Asn Pro Lys Tyr Asp Cys Gln Lys
35                   40                  45                  50

GAA ATG TGG TCT TTC CCT AAA AAA TAC GAT GGG ATA AAT CAG TGT TTA     248
Glu Met Trp Ser Phe Pro Lys Lys Tyr Asp Gly Ile Asn Gln Cys Leu
                55                  60                  65

AAG GCT CAA GAA GAG CTT ATT GAA CCA ATC ATC ACT AAA AAG ATC GAT     296
Lys Ala Gln Glu Glu Leu Ile Glu Pro Ile Ile Thr Lys Lys Ile Asp
           70                  75                  80

CAG TAT CAA TGC GAT GAT TTC ACT AAT GAA GGC TTA AAA GAT AAG TGT     344
Gln Tyr Gln Cys Asp Asp Phe Thr Asn Glu Gly Leu Lys Asp Lys Cys
      85                  90                  95

TTC AAA AGA AAC GAT GCC TAC TTA AAC ACC CTT TTA ACG CCC ATC ATT     392
Phe Lys Arg Asn Asp Ala Tyr Leu Asn Thr Leu Leu Thr Pro Ile Ile
 100                 105                 110

CAA AAA CAA GAG CGT CGT TTT AGC TGC TCT GAT TTC CAT AAC CCA GAG     440
Gln Lys Gln Glu Arg Arg Phe Ser Cys Ser Asp Phe His Asn Pro Glu
115                 120                 125                 130

CTA AAA GAA CAA TGC ATG GAT AAA ACT AAC GCT TAT GAA AAG CAA AAA     488
Leu Lys Glu Gln Cys Met Asp Lys Thr Asn Ala Tyr Glu Lys Gln Lys
                135                 140                 145

GAC CGA CAA AAA AGA CTA ATT AAT CTC GTG CAA TTA GAA GCG TTT GAA     536
Asp Arg Gln Lys Arg Leu Ile Asn Leu Val Gln Leu Glu Ala Phe Glu
           150                 155                 160

AAA GAA TAC GCG CAA TAT AAA CCA TAC ATT ATC CCT TAC TTC ACC AAA     584
Lys Glu Tyr Ala Gln Tyr Lys Pro Tyr Ile Ile Pro Tyr Phe Thr Lys
      165                 170                 175

GAA TGC GTT AAA AAT GCG CCC CAT TTA GCC AAC AAG GAA AGA CTA TGC     632
Glu Cys Val Lys Asn Ala Pro His Leu Ala Asn Lys Glu Arg Leu Cys
```

```
    180                 185                 190

CAA AAA GAA GTG CAT GAA AAA TTT GAC GAC CCT TAT TCT AGC TCT AAA      680
Gln Lys Glu Val His Glu Lys Phe Asp Asp Pro Tyr Ser Ser Ser Lys
195                 200                 205                 210

GAA TTG AGC GTT CAA TCG GCT ATT TCT TTT TGC ATT AAA AAA GTT GAT      728
Glu Leu Ser Val Gln Ser Ala Ile Ser Phe Cys Ile Lys Lys Val Asp
                215                 220                 225

GCT AAA TTA GAA AAA GCC GCT CTT ATG AAT GGC GTT TAT ATA AGC CCT      776
Ala Lys Leu Glu Lys Ala Ala Leu Met Asn Gly Val Tyr Ile Ser Pro
            230                 235                 240

TAT AAA AAA TCC ACC CAT TGC CAA AGA ACG CAT TTG GAA AAT AAG AGC      824
Tyr Lys Lys Ser Thr His Cys Gln Arg Thr His Leu Glu Asn Lys Ser
        245                 250                 255

TTG AAA GAA ATC GCT TTA AAT ATG AAC CCT AAA TTA GAA AAG CAA AGC      872
Leu Lys Glu Ile Ala Leu Asn Met Asn Pro Lys Leu Glu Lys Gln Ser
    260                 265                 270

CCT TTT ATT GAT GCG GAT AAA ATG GCT ATG CAA TCT GCG GGG TTA TTG      920
Pro Phe Ile Asp Ala Asp Lys Met Ala Met Gln Ser Ala Gly Leu Leu
275                 280                 285                 290

AGA AAG AAT AAA GGT GTC TTG ATT GCT TTT GCT ACA GAT ATT TGC ATG      968
Arg Lys Asn Lys Gly Val Leu Ile Ala Phe Ala Thr Asp Ile Cys Met
                295                 300                 305

GAG CGT AAC GAA CAT AAA AAA GAA GAG TTT ATC AGC CTT AAA GAT AGT     1016
Glu Arg Asn Glu His Lys Lys Glu Glu Phe Ile Ser Leu Lys Asp Ser
            310                 315                 320

TGC ACC CAA TCG CAA GCC AAA ATC TAT AAC AAC AAG GAG CGC TTT GAC     1064
Cys Thr Gln Ser Gln Ala Lys Ile Tyr Asn Asn Lys Glu Arg Phe Asp
        325                 330                 335

AAA TTC ATA CAA GAT TAC CAA AAA GAC TTA AAA ACT TGT CTT TTA GAC     1112
Lys Phe Ile Gln Asp Tyr Gln Lys Asp Leu Lys Thr Cys Leu Leu Asp
    340                 345                 350

ACT TCT AAC ACT AAA GAA GAA GTG GAG CAA AAT TTT TCA CAA TGC CAA     1160
Thr Ser Asn Thr Lys Glu Glu Val Glu Gln Asn Phe Ser Gln Cys Gln
355                 360                 365                 370

AAA GAG CAA TTG AGA GAT GAT AAC AAA GGC TTG GGT TTC ACT TTA GAA     1208
Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr Leu Glu
                375                 380                 385

GAA TTG GTT AAA AAA TAC GCT AAG TAAAGTTATT TAATTTTATG GATGGTTTTA    1262
Glu Leu Val Lys Lys Tyr Ala Lys
            390

AAAATCCATT CCATAGTTAT TGT                                          1285
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Met Lys Glu Thr Arg Leu Leu Lys Leu Arg Ala Leu Ser Leu Ala Cys
 1               5                  10                  15
Leu Met Gly Leu Gly Val Ser Gly Cys Ala Phe Leu Asp Lys Gln Ile
            20                  25                  30
Leu Asn Asp His Leu Thr Lys Ala Lys Asn Asn Pro Lys Tyr Asp Cys
        35                  40                  45
Gln Lys Glu Met Trp Ser Phe Pro Lys Lys Tyr Asp Gly Ile Asn Gln
    50                  55                  60
Cys Leu Lys Ala Gln Glu Glu Leu Ile Glu Pro Ile Ile Thr Lys Lys
65                  70                  75                  80
Ile Asp Gln Tyr Gln Cys Asp Asp Phe Thr Asn Glu Gly Leu Lys Asp
                85                  90                  95
Lys Cys Phe Lys Arg Asn Asp Ala Tyr Leu Asn Thr Leu Leu Thr Pro
            100                 105                 110
Ile Ile Gln Lys Gln Glu Arg Arg Phe Ser Cys Ser Asp Phe His Asn
        115                 120                 125
Pro Glu Leu Lys Glu Gln Cys Met Asp Lys Thr Asn Ala Tyr Glu Lys
    130                 135                 140
Gln Lys Asp Arg Gln Lys Arg Leu Ile Asn Leu Val Gln Leu Glu Ala
145                 150                 155                 160
Phe Glu Lys Glu Tyr Ala Gln Tyr Lys Pro Tyr Ile Ile Pro Tyr Phe
                165                 170                 175
Thr Lys Glu Cys Val Lys Asn Ala Pro His Leu Ala Asn Lys Glu Arg
            180                 185                 190
Leu Cys Gln Lys Glu Val His Glu Lys Phe Asp Asp Pro Tyr Ser Ser
        195                 200                 205
Ser Lys Glu Leu Ser Val Gln Ser Ala Ile Ser Phe Cys Ile Lys Lys
    210                 215                 220
Val Asp Ala Lys Leu Glu Lys Ala Ala Leu Met Asn Gly Val Tyr Ile
225                 230                 235                 240
Ser Pro Tyr Lys Lys Ser Thr His Cys Gln Arg Thr His Leu Glu Asn
                245                 250                 255
Lys Ser Leu Lys Glu Ile Ala Leu Asn Met Asn Pro Lys Leu Glu Lys
            260                 265                 270
Gln Ser Pro Phe Ile Asp Ala Asp Lys Met Ala Met Gln Ser Ala Gly
        275                 280                 285
Leu Leu Arg Lys Asn Lys Gly Val Leu Ile Ala Phe Ala Thr Asp Ile
    290                 295                 300
Cys Met Glu Arg Asn Glu His Lys Lys Glu Glu Phe Ile Ser Leu Lys
305                 310                 315                 320
Asp Ser Cys Thr Gln Ser Gln Ala Lys Ile Tyr Asn Asn Lys Glu Arg
                325                 330                 335
Phe Asp Lys Phe Ile Gln Asp Tyr Gln Lys Asp Leu Lys Thr Cys Leu
            340                 345                 350
Leu Asp Thr Ser Asn Thr Lys Glu Glu Val Glu Gln Asn Phe Ser Gln
        355                 360                 365
Cys Gln Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr
```

```
    370                 375                 380
Leu Glu Glu Leu Val Lys Lys Tyr Ala Lys
385                 390
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 84...704
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
TTGATCATTC TTATTTCGCA CAACCCAAGC ACGCTAAAAT TAGCCACTAA GCATGTGAAA     60
TTAGAGCATG GGCGTTTGAC AGA ATG CTA AGG GTT TTA AGC GTT GGT GTT GCT    113
                          Met Leu Arg Val Leu Ser Val Gly Val Ala
                           1               5                  10

TTT ATT TTA CTA GGG TGT CAG TTT TTC AAC AAA ACG ACG CTG CAT TTA     161
Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys Thr Thr Leu His Leu
                15                  20                  25

AAA TAT AAA GAT TAC CCC AAA AAT AGC GCT TTA AAA ACC GCT TTC ACT     209
Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr
            30                  35                  40

TTA ACC CCC CCT AAA ATC TTT TTT AAC GCC CGT TTT GTG CCG CCC TTT     257
Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala Arg Phe Val Pro Pro Phe
        45                  50                  55

TAC CAA AAA GAA TTT AAA AAA GCG ATC ACC CAA CAA ATC GCT TAT TTT     305
Tyr Gln Lys Glu Phe Lys Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe
    60                  65                  70

TTA AAA GAT AAA AGT GCT TTT ATT CTC AAT GTT TCA GGC AAT GTT TTT     353
Leu Lys Asp Lys Ser Ala Phe Ile Leu Asn Val Ser Gly Asn Val Phe
75                  80                  85                  90

TTT TCT TTT GAA GAG AAT CCT AAA GAT TTA AAA GCC ATT AAA GAA AGG     401
Phe Ser Phe Glu Glu Asn Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg
                95                  100                 105

CTT AAA AAG ACG ATT GAG CCT AAC GCT GAC CCA AAA GCC GTC ATG CGT     449
Leu Lys Lys Thr Ile Glu Pro Asn Ala Asp Pro Lys Ala Val Met Arg
            110                 115                 120

TTT TTA AAC CTT CAA GCG AGC TTG ATT TTA GAA TGC GTC CCG CAA ACC     497
Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu Cys Val Pro Gln Thr
```

```
        125                 130                 135

ACT TGC CCG TTT GAC ACC CTT TTA ATC CCC ACC GCT TTC AGC GTG CCT     545
Thr Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr Ala Phe Ser Val Pro
    140                 145                 150

GTT TAT TAC GCT AAT CGT TTG GGC GAT AAC CCC TCT CTT TTT TCC CAA     593
Val Tyr Tyr Ala Asn Arg Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln
155                 160                 165                 170

GAG GAT AAA ACC TAT CAT AAC GCT TTG ATC AAA GCC CTT AAT AAG GCT     641
Glu Asp Lys Thr Tyr His Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala
                175                 180                 185

TAC TAT TCT CTT ATG GAG GGT TTA GAA AAG CGT TTG AAC GCT ATA AAA     689
Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys
            190                 195                 200

AAT GCA GAG TGG CTT TAAGGCATGA AAAAGATTGC ATTTTTTATT TTTGTCATTT T   745
Asn Ala Glu Trp Leu
        205

GTTTTCGGTA GGGATTTATT TAATTTGGCA TGTTTTATTG GAAAAAGCCC TAGAATTGAA   805
ATTAGCAACC TCAGCTAATG ATTTGCTTTT                                    835
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Met Leu Arg Val Leu Ser Val Gly Val Ala Phe Ile Leu Leu Gly Cys
 1               5                  10                  15
Gln Phe Phe Asn Lys Thr Thr Leu His Leu Lys Tyr Lys Asp Tyr Pro
            20                  25                  30
Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr Leu Thr Pro Pro Lys Ile
        35                  40                  45
Phe Phe Asn Ala Arg Phe Val Pro Pro Phe Tyr Gln Lys Glu Phe Lys
    50                  55                  60
Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe Leu Lys Asp Lys Ser Ala
65                  70                  75                  80
Phe Ile Leu Asn Val Ser Gly Asn Val Phe Phe Ser Phe Glu Glu Asn
                85                  90                  95
Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg Leu Lys Lys Thr Ile Glu
            100                 105                 110
Pro Asn Ala Asp Pro Lys Ala Val Met Arg Phe Leu Asn Leu Gln Ala
        115                 120                 125
Ser Leu Ile Leu Glu Cys Val Pro Gln Thr Thr Cys Pro Phe Asp Thr
    130                 135                 140
Leu Leu Ile Pro Thr Ala Phe Ser Val Pro Val Tyr Tyr Ala Asn Arg
145                 150                 155                 160
```

```
Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln Glu Asp Lys Thr Tyr His
                  165                 170                 175
Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala Tyr Tyr Ser Leu Met Glu
              180                 185                 190
Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys Asn Ala Glu Trp Leu
          195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 763 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...710
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
AAAAAATAAC CATGAGTTAT TCAAAAATTT AACTTTATAA GACAGGTGGC ATG CGT      56
                                                        Met Arg
                                                          1

TTA AAA CAT TTT AAA ACT TTC CTT TTT ATC ACA ATG GCA ATC ATT GTA     104
Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile Ile Val
          5                  10                  15

ATA GGT ACC GGT TGC GCG AAC AAA AAG AAA AAA AAA GAC GAA TAC AAC     152
Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn
     20                  25                  30

AAA CCG GCG ATC TTT TGG TAT CAA GGG ATT TTG AGA GAA ATC CTT TTT     200
Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe
35                  40                  45                  50

GCT AAT TTA GAA ACA GCG GAC AAT TAC TAT TCT TCT TTA CAA AGC GAA     248
Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu
                  55                  60                  65

CAC ATC AAT TCC CCC CTT GTC CCA GAA GCG ATG CTA GCT TTA GGG CAA     296
His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln
              70                  75                  80

GCG CAC ATG AAA AAG AAA GAG TAT GTT TTA GCG TCT TTT TAC TTT GAT     344
Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp
          85                  90                  95

GAA TAC ATC AAG CGC TTT GGG ACT AAG GAC AAT GTG GAT TAT TTG ACT     392
Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr
     100                 105                 110
```

```
TTT TTA AAA TTG CAA TCG CAT TAT TAC GCT TTC AAA AAC CAT TCT AAA      440
Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys
115                 120                 125                 130

GAC CAG GAA TTT ATC TCT AAT TCT ATT GTG AGT TTA GGC GAA TTT ATA      488
Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile
                135                 140                 145

GAA AAA TAC CCT AAC AGC CGT TAC CGC CCC TAT GTA GAA TAC ATG CAA      536
Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln
            150                 155                 160

ATC AAA TTC ATT TTA GGG CAA AAT GAG CTC AAT CGC GCG ATC GCG AAT      584
Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn
        165                 170                 175

GTC TAT AAA AAA CGC CAC AAG CCT GAG GGC GTG AAA CGC TAT TTA GAA      632
Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu
    180                 185                 190

AGG ATA GAT GAG ACT TTA GAA AAA GAG ACT AAA CCC AAA CCA TCG CAC      680
Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His
195                 200                 205                 210

ATG CCT TGG TAT GTG TTA ATT TTT GAT TGG TAGGATATTT CAAAACCATA CAC    733
Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
                215                 220

ATTATAACAG AGAGATGAAA AATGACTGAA                                    763
```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Met Arg Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile
 1               5                  10                  15
Ile Val Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu
            20                  25                  30
Tyr Asn Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile
        35                  40                  45
Leu Phe Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln
    50                  55                  60
Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu
65                  70                  75                  80
Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr
                85                  90                  95
Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr
            100                 105                 110
Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His
```

```
        115                 120                 125
Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu
    130                 135                 140
Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr
145                 150                 155                 160
Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile
                165                 170                 175
Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr
            180                 185                 190
Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro
        195                 200                 205
Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 75...749
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
GAAAAAGGCT CTGCTTTGAT AGATAAATTT GACGCTAACC CCTATAAAAC GATTTTTGGA     60
GAAAGGAAAT AATC ATG AGA GCT ACG GCG ATA AAA ATC TTT TCA CTC TCA      110
                Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser
                 1               5                  10

TCA GCA TTA GCC CTA TTG CTT CAT GGT TGC TTG AGC ATC AAT TTA AAA      158
Ser Ala Leu Ala Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys
        15                  20                  25

CAA ATG CTA CCA GAG ATC AGA ACT TAC GAT TTG AAT GCG AGT TCT TTT      206
Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe
    30                  35                  40

GAA ATC ACG CAA TGC GCT AAA CCT TTG ACT GAA GTG AGG CTC ATT AGT      254
Glu Ile Thr Gln Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser
45                  50                  55                  60

ATT TTG AGC GCG GAT TTA TTC AAC ACT AAA GAG ATC GTT TTT AAA GCC      302
Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala
                65                  70                  75

AAA GAC GGG CAG ATC ACG CAT GGG AAG CAC CAA AAA TGG ATA GAC TTG      350
Lys Asp Gly Gln Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu
            80                  85                  90
```

```
CCT CGC AAC ATG CTA AAA ACC ATG TTC ATG CAA GAA GCG CAA AAA GCA      398
Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala
        95                  100                 105

TGC TTA GGC GTG GCT TTG CCT CCT TAT GGC GCG GGT GCA CCC ACT TAT      446
Cys Leu Gly Val Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr
    110                 115                 120

GCG GTT CGT TTT ACG ATT TTA TCG TTT TCT CTT TTA GAA AAA GAA AAT      494
Ala Val Arg Phe Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn
125                 130                 135                 140

TCT ACC TAT AGG GCG GAA TTT GCA CTA GGC TAT GAC ATT AGC GTG AAA      542
Ser Thr Tyr Arg Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys
                145                 150                 155

GGC GAT TCG CAT TCT GGG GTG ATC ATT AAG CAT GAA AAT ATT TCT AGC      590
Gly Asp Ser His Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser
            160                 165                 170

TTG GAA AAT AAA ACG ACC AAA ACG AGT AAA AAT GGC AAT CAA GAT TTT      638
Leu Glu Asn Lys Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe
        175                 180                 185

CAA GAA AGC GCG ATA CAA TCT CTC CAA CAT GTA AGC GTG CAA GCG ATT      686
Gln Glu Ser Ala Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile
    190                 195                 200

CAA GAA GCG GTT TCT TTG ATT AAA AAA GCC ATT GAA GCG CAA AGC GTA      734
Gln Glu Ala Val Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val
205                 210                 215                 220

AGC CCG TTA AAA AAA TAAAAAATAA GGAGGAATTG TTTGATTTTA CGATTGGCTG G   790
Ser Pro Leu Lys Lys
                225

AGCAAGCGTT T                                                        801
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser Ser Ala Leu Ala
 1               5                  10                  15
Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys Gln Met Leu Pro
            20                  25                  30
Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe Glu Ile Thr Gln
        35                  40                  45
Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser Ile Leu Ser Ala
```

```
    50                  55                  60
Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala Lys Asp Gly Gln
65                  70                  75                  80
Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu Pro Arg Asn Met
                85                  90                  95
Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala Cys Leu Gly Val
            100                 105                 110
Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr Ala Val Arg Phe
        115                 120                 125
Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn Ser Thr Tyr Arg
    130                 135                 140
Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys Gly Asp Ser His
145                 150                 155                 160
Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser Leu Glu Asn Lys
                165                 170                 175
Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe Gln Glu Ser Ala
            180                 185                 190
Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile Gln Glu Ala Val
        195                 200                 205
Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val Ser Pro Leu Lys
    210                 215                 220
Lys
225
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...395
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
TTTTATGATA AGATAGTCAA ATTATACATT GACTTAAGGA AATTTAATTG ATG AAA      56
                                                        Met Lys
                                                          1

TCT AAA ATC ACT CAT TTT ATC GCT ATC TCT TTT GTT TTA AGC CTG TTT     104
Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser Leu Phe
          5                  10                  15

AGC GCA TGC AAA GAC GAG CCT AAA AAA TCG TCT CAA TCG CAC CAA AAC     152
Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His Gln Asn
     20                  25                  30

AAC ACT AAA ATC ACT AAA AAC AAT CCA ATC AAT CAA GCG AAT AAT GAT     200
Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn Asn Asp
35                  40                  45                  50
```

```
ATA AGA AAA ATT GAG CAT GAA GAA GAA GAT GAA AAA GCC ACC AAA GAA      248
Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr Lys Glu
                 55                  60                  65

GTG AAC GAT TTG ATC AAT AAC GAA AAT AAA ATT GAT GAA ATC AAT AAT      296
Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile Asn Asn
            70                  75                  80

GAA GAA AAC GCT GAT CCT TCG CAA AAA AGA ACG AAC AAC GTT TTG CAA      344
Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val Leu Gln
        85                  90                  95

CGA GCC ACT AAC CAC CAA GAC AAT CTC AAT TCC CCA CTC AAC AGG AAG      392
Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn Arg Lys
    100                 105                 110

TAT TAAAGTGTGA AACTTTTTTC AAAGGATTTA TTTAAAAAAG TAACCCCTTT ATT       448
Tyr
115
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Met Lys Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser
 1               5                  10                  15
Leu Phe Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His
            20                  25                  30
Gln Asn Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn
        35                  40                  45
Asn Asp Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr
    50                  55                  60
Lys Glu Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile
65                  70                  75                  80
Asn Asn Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val
                85                  90                  95
Leu Gln Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn
            100                 105                 110
Arg Lys Tyr
        115
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 121...1065
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
CTATCAAGTC AGTATTTCCA ATATCCAATT AGCCAATGAT CTCAAAGATT CTAATATTTT     60
TATCCACCAG CGTTTAATCA TCCCCACCAA CAAAAAATTA CTCGCTACAA GGGAATTTTA    120
  ATG GGT TTG GCG TTG GAA AAA GTT TGT TTT TTA GGC GTT ATT TTT TTG    168
  Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu
  1               5                  10                  15

ATT AGC GCT TGC ACG GTT AAA AAA GAG GGG GTA AAG AAT TTG TCT TAC     216
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr
            20                  25                  30

AAG CAT GAA AGC TTG CGC GCT TAT GAA AAC GCT AAA GAT TAT GAT CCG     264
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
        35                  40                  45

ACA ACC AAA AAA GCC GCC TAT AAA CGC AAT TTT TTT GAA CGC CAT TTC     312
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
    50                  55                  60

AAA CGC TAC TCC GAT TCG CAA GAT AGC AAC ACA AAA GAT CAG CCA CTA     360
Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
65                  70                  75                  80

GAT AAC GGC ATG CGC GAT TCT AGC TCG ATC CAA AGA GCC ACC ATG CGC     408
Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
                85                  90                  95

CCT TAT CAA GTG GGG GGC AAG TGG TAT TAC CCC ACT AAA GTG GAT TTA     456
Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
            100                 105                 110

GGC GAA AAA TTT GAT GGC GTT GCG AGT TGG TAT GGC CCT AAC TTC CAT     504
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
        115                 120                 125

GCC AAA AAA ACC AGT AAT GGG GAA ATT TAT AAC ATG TAT GCC CAC ACC     552
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
    130                 135                 140

GCC GCG CAC AAA ACT TTA CCC ATG AAC ACC GTG GTG AAA GTC ATC AAT     600
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn
145                 150                 155                 160

GTT GAT AAT AAC TTA AGC ACC ATT GTG CGC ATC AAC GAT AGA GGG CCT     648
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro
                165                 170                 175

TTT GTG AGC GAT CGC ATC ATT GAT TTG TCT AAT GCG GCC GCT AGG GAT     696
```

```
Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp
            180                 185                 190

ATT GAC ATG GTT AAA AAA GGC ACA GCC AGC GTG CGT CTC ATT GTT TTG      744
Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu
        195                 200                 205

GGC TTT GGT GGG GTT ATC TCC ACG CAA TAC GAA CAA TCC TTT AAC GCC      792
Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala
    210                 215                 220

AGC TCT TCA AAG ATC TTG CAC AAG GAA TTT AAA GTC GGC GAG AGC GAA      840
Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu
225                 230                 235                 240

AAA AGC GTG AGC GGA GGG AAA TTT TCT TTG CAA ATG GGG GCT TTT AGA      888
Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg
                245                 250                 255

AAC CAA ATA GGT GCT CAA ACT TTA GCG GAT AAA TTG CAA GCA GAA AAT      936
Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn
            260                 265                 270

CCA AAT TAC AGC GTC AAG GTT GCT TTT AAA GAC GAT TTG TAT AAA GTT      984
Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val
        275                 280                 285

TTA GTT CAA GGG TTT CAA AGC GAA GAA GAG GCT AGG GAT TTT ATG AAA     1032
Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys
    290                 295                 300

AAA TAC AAC CAG AAT GCG GTT TTA ACG AGA GAA TGATTAAGTT ATTGCTTTTA   1085
Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu
305                 310                 315

GATGTGGATG GCACGCTCAC AGACGGATCG TTGTAT                             1121
```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu
 1               5                  10                  15
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr
            20                  25                  30
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
        35                  40                  45
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
    50                  55                  60
```

```
Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
65                  70                  75                  80
Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
                85                  90                  95
Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
            100                 105                 110
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
        115                 120                 125
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
    130                 135                 140
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn
145                 150                 155                 160
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro
                165                 170                 175
Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp
            180                 185                 190
Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu
        195                 200                 205
Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala
    210                 215                 220
Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu
225                 230                 235                 240
Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg
                245                 250                 255
Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn
            260                 265                 270
Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val
        275                 280                 285
Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys
    290                 295                 300
Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 811 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...761
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
TATAATAAGG AAATTCTAAA CGAAAATTAA ACTGAATGAA AGGAGTTTGA ATG AAA      56
                                                          Met Lys
                                                            1

AAA ATC GTT TTA GTA GCG ATA GCC TTA TTG ATG AGC GCT TGC GCG AGC      104
Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys Ala Ser
```

```
          5                   10                  15

TAT AAG ATC ACG CCT GAA CAT GTT ACT TCC TAT AAT AAT GGG ATT CAA      152
Tyr Lys Ile Thr Pro Glu His Val Thr Ser Tyr Asn Asn Gly Ile Gln
    20                  25                  30

GTG ATG ACT TCC ACG CAA GCC AAA TCT AAA GTC CAG CTA GAA ATC GCT      200
Val Met Thr Ser Thr Gln Ala Lys Ser Lys Val Gln Leu Glu Ile Ala
35                  40                  45                  50

CAA AGC AAG TTG AAA GGC TTG AAC GAG TCC CCC TTA GTG CTG TAT GTA      248
Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu Tyr Val
                55                  60                  65

GCG GCG CAA GTT ATA GAG GGA AGT CCT GTG GTG TTT AGC CGT AAA GCC      296
Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg Lys Ala
            70                  75                  80

ATT TCA GTG TCT ATC AAC CAA ACG AAT TTA CCG GTC TTA AGC CTG AGA      344
Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser Leu Arg
        85                  90                  95

CAG GTG ATG AAA TCC AGT TTT GAT TTT GAG GGT ATT TTA CAA AGT TTT      392
Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln Ser Phe
    100                 105                 110

AAT ATC GCC GTG CCG ACC ACC CCT ATT GAT AAT GTC AAT ATG ATC ACC      440
Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met Ile Thr
115                 120                 125                 130

CCG CCT ATG TTT TAT TAC GGG CAA GGG GGA TTT TTA GCT TAT AAC GGC      488
Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr Asn Gly
                135                 140                 145

ATG ATG TAT GGG GGA ATG GGC ATG TAT GGG CCA GGC TTT GGC ATG ATG      536
Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly Met Met
            150                 155                 160

ATG ATG GAT GAT GTA GAA GAG CAA GAA GTC ATG CAA GAA AGC CGC CAA      584
Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser Arg Gln
        165                 170                 175

GCT TTA AAA ATC CTA GCG ATC AAT TAC CTT AAA AAC AAC ACC CTT AAT      632
Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr Leu Asn
    180                 185                 190

GTT GAG AGT AAG GCT AAG GGA GGG TTT GTG GTG GTG GAT ACC AAA AAC      680
Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr Lys Asn
195                 200                 205                 210

CTT AAA ACC CCG GGT GTG GTG GTG GTT AAA GTC TTT TTA GAA GAT GAA      728
Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu Asp Glu
                215                 220                 225

ATC CAC ACC TTT AAA ATT GAT ATT TCT AAG ATG TAATCGCCCC CTTTAATAAA    781
Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met
            230                 235
```

AGCCTTTGGG CCATCCACCT AAAGGTTTTT 811

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Lys Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys
 1               5                  10                  15
Ala Ser Tyr Lys Ile Thr Pro Glu His Val Thr Ser Tyr Asn Asn Gly
            20                  25                  30
Ile Gln Val Met Thr Ser Thr Gln Ala Lys Ser Lys Val Gln Leu Glu
        35                  40                  45
Ile Ala Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu
    50                  55                  60
Tyr Val Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg
65                  70                  75                  80
Lys Ala Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser
                85                  90                  95
Leu Arg Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln
            100                 105                 110
Ser Phe Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met
        115                 120                 125
Ile Thr Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr
    130                 135                 140
Asn Gly Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly
145                 150                 155                 160
Met Met Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser
                165                 170                 175
Arg Gln Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr
            180                 185                 190
Leu Asn Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr
        195                 200                 205
Lys Asn Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu
    210                 215                 220
Asp Glu Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 97...1371
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
TAAAAAAAAC TACCCTTAAA AAAATCAATC TAAAATTCTT AAATTAAAAT ATAGCTATAA      60
TACACTAAAA CAATCTCAAG GTTTCAAAAT TTAGCC ATG CGT CTT CTT CTG TTC       114
                                        Met Arg Leu Leu Leu Phe
                                         1               5

AAT CAA AAC GCT TTT TTA TTA GCG TGC ATG TTT GTT TCA AGC GTG TAT       162
Asn Gln Asn Ala Phe Leu Leu Ala Cys Met Phe Val Ser Ser Val Tyr
            10                  15                  20

GTG AAC GCT GTC TTA GAC GCT TAT GCA ATT GAA AAC CCC TAT ATT TCT       210
Val Asn Ala Val Leu Asp Ala Tyr Ala Ile Glu Asn Pro Tyr Ile Ser
        25                  30                  35

ATC ACA CTC ACA AGC CTA TTA GCC CCT TTA AGC ATG CTA GCG TTT TTA       258
Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu Ser Met Leu Ala Phe Leu
    40                  45                  50

AAA ACC CCT AGA AAT AGT GCT TTT GCT TTG GGG TTT TTT GTG GGG GCG       306
Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly Phe Phe Val Gly Ala
55                  60                  65                  70

TTA TTG TTT TAT TGG TGC GCT TTA AGC TTT CGC TAC TCG GAT TTC ACT       354
Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe Arg Tyr Ser Asp Phe Thr
                75                  80                  85

TAT TTA TTG CCC TTA ATC ATT GTT TTA ATA GCG TTA GTT TAT GGG GTT       402
Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile Ala Leu Val Tyr Gly Val
            90                  95                  100

TTA TTT TAT TTG TTG CTC TAT TTT GAA AAC CCC TAT TTC AGG CTT TTG       450
Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn Pro Tyr Phe Arg Leu Leu
        105                 110                 115

AGT TTT TTA GGC TCT AGT TTT ATC CAC CCC TTT GGA TTT GAT TGG TTA       498
Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe Gly Phe Asp Trp Leu
    120                 125                 130

GTC CCA GAT AGC TTT TTT TCT TAT AGC GTG TTT AGA GTG GAT AAA TTA       546
Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe Arg Val Asp Lys Leu
135                 140                 145                 150

TCG CTA GGG CTT GTT TTT TTG GCT TGC ATT TTT TTG AGC ACT AAA CCA       594
Ser Leu Gly Leu Val Phe Leu Ala Cys Ile Phe Leu Ser Thr Lys Pro
                155                 160                 165

TTG AAA AAA TAT AGG ATC ATA GGG GTT TTA TTG TTA CTT GGC GCG TTG       642
Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu Leu Leu Leu Gly Ala Leu
            170                 175                 180

GAT TTT AAT GGT TTC AAA ACA AGC GAT TTA AAA AAG GTT GGA AAT ATT       690
Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu Lys Lys Val Gly Asn Ile
```

```
        185                 190                 195

GAA TTA GTC TCT ACA AAA ACG CCC CAA GAT TTG AAA TTT GAC TCA AGT      738
Glu Leu Val Ser Thr Lys Thr Pro Gln Asp Leu Lys Phe Asp Ser Ser
    200                 205                 210

TAC CTT AAT GAT ATT GAA AAC AAC ATT CTT AAA GAA ATC AAG CTC GCT      786
Tyr Leu Asn Asp Ile Glu Asn Asn Ile Leu Lys Glu Ile Lys Leu Ala
215                 220                 225                 230

CAA AGC AAG CAA AAA ACC TTG ATT GTT TTT CCA GAA ACC GCC TAC CCC      834
Gln Ser Lys Gln Lys Thr Leu Ile Val Phe Pro Glu Thr Ala Tyr Pro
                235                 240                 245

ATC GCT TTA GAA AAC TCC CCC TTT AAA GCG AAG CTA GAA GAT TTA AGC      882
Ile Ala Leu Glu Asn Ser Pro Phe Lys Ala Lys Leu Glu Asp Leu Ser
            250                 255                 260

GAT AAT ATT GCT ATT TTA ATA GGG ACA TTA CGG ACT CAA GGC TAT AAT      930
Asp Asn Ile Ala Ile Leu Ile Gly Thr Leu Arg Thr Gln Gly Tyr Asn
        265                 270                 275

CTT TAT AAC AGC TCG TTT TTA TTT TCT AAA GAA AGC GTT CAG ATC GCT      978
Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Glu Ser Val Gln Ile Ala
    280                 285                 290

GAT AAA GTA ATT TTA GCC CCC TTT GGC GAG ACC ATG CCT TTA CCG GAA     1026
Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Thr Met Pro Leu Pro Glu
295                 300                 305                 310

TTT CTT CAA AAA CCC CTT GAA AAG CTC TTT TTT GGC GAG AGC ACT TAT     1074
Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe Gly Glu Ser Thr Tyr
                315                 320                 325

TTA TAC CGC AAT GCT CCT CAT TTC AGC GAT TTT ACA TTA GAC GAT TTT     1122
Leu Tyr Arg Asn Ala Pro His Phe Ser Asp Phe Thr Leu Asp Asp Phe
            330                 335                 340

ACT TTT CGC CCC CTG ATT TGC TAT GAA GGC ACT TCC AAA CCC GCT TAT     1170
Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly Thr Ser Lys Pro Ala Tyr
        345                 350                 355

TCA AAC AGC CCT TCA AAA ATT TTT ATC GTG ATG AGC AAT AAC GCA TGG     1218
Ser Asn Ser Pro Ser Lys Ile Phe Ile Val Met Ser Asn Asn Ala Trp
    360                 365                 370

TTT AGC CCA AGC ATT GAA CCC ACC TTA CAA AGA ACG CTT TTA AAA TAC     1266
Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln Arg Thr Leu Leu Lys Tyr
375                 380                 385                 390

TAC GCA AGG CGT TAT GAT AAG ATC ATC TTG CAC AGC GCG AAC TTT TCA     1314
Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu His Ser Ala Asn Phe Ser
                395                 400                 405

ACT TCT TAC ATC TTA AGC CCT AGT TTA TTA GGC GAT ATT CTT TTT AGG     1362
Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu Gly Asp Ile Leu Phe Arg
            410                 415                 420
```

AAA CGA TCA TGATTAAAGC GATTAATATT TCTCATGCTT TTGAAAAGCC TCTTTATAA 1420
Lys Arg Ser
425

TGGCG 1425

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Leu Leu Leu Phe Asn Gln Asn Ala Phe Leu Leu Ala Cys Met
1 5 10 15
Phe Val Ser Ser Val Tyr Val Asn Ala Val Leu Asp Ala Tyr Ala Ile
20 25 30
Glu Asn Pro Tyr Ile Ser Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu
35 40 45
Ser Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu
50 55 60
Gly Phe Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe
65 70 75 80
Arg Tyr Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile
85 90 95
Ala Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn
100 105 110
Pro Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile His Pro
115 120 125
Phe Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr Ser Val
130 135 140
Phe Arg Val Asp Lys Leu Ser Leu Gly Leu Val Phe Leu Ala Cys Ile
145 150 155 160
Phe Leu Ser Thr Lys Pro Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu
165 170 175
Leu Leu Leu Gly Ala Leu Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu
180 185 190
Lys Lys Val Gly Asn Ile Glu Leu Val Ser Thr Lys Thr Pro Gln Asp
195 200 205
Leu Lys Phe Asp Ser Ser Tyr Leu Asn Asp Ile Glu Asn Asn Ile Leu
210 215 220
Lys Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile Val Phe
225 230 235 240
Pro Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe Lys Ala
245 250 255
Lys Leu Glu Asp Leu Ser Asp Asn Ile Ala Ile Leu Ile Gly Thr Leu
260 265 270
Arg Thr Gln Gly Tyr Asn Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys
275 280 285
Glu Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu
290 295 300
Thr Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe

```
305                 310                 315                 320
Phe Gly Glu Ser Thr Tyr Leu Tyr Arg Asn Ala Pro His Phe Ser Asp
                325                 330                 335
Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly
            340                 345                 350
Thr Ser Lys Pro Ala Tyr Ser Asn Ser Pro Ser Lys Ile Phe Ile Val
        355                 360                 365
Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln
    370                 375                 380
Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu
385                 390                 395                 400
His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu
                405                 410                 415
Gly Asp Ile Leu Phe Arg Lys Arg Ser
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...713
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
TGTAGTAAGA TACCTAGTTT TCAAATCTAT TAAAAGATAA AGGTTATTAC ATG TTT      56
                                                          Met Phe
                                                            1

TCA CTT TCT TAT GTT TCC AAG AAA TTT TTA AGC GTT TTA TTA TTG ATT     104
Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu Leu Ile
          5                  10                  15

TCG CTG TTT TTA AGC GCT TGC AAA TCC AAC AAT AAA GAC AAG TTA GAC     152
Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys Leu Asp
    20                  25                  30

GAA AAT CTT TTA AGC TCT GGC TCT CAA AGC TCC AAA GAA TTA AAC GAT     200
Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu Asn Asp
35                  40                  45                  50

GAG CGA GAC AAT ATA GAC AAA AAG AGT TAC GCT GGT TTA GAA GAT GTT     248
Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu Asp Val
                55                  60                  65

TTT TCA GAC AAT AAG TCC ATT AGT CCT AAC GAT AAA TAC ATG CTT TTA     296
Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met Leu Leu
            70                  75                  80
```

```
GTT TTT GGC CGT AAT GGT TGC TCC TAT TGC GAA AGG TTT AAA AAA GAT      344
Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys Lys Asp
        85                  90                  95

CTC AAA AAT GTC AAA GAA TTG CGC GAC TAC ATT AAA GAG CAT TTT AGC      392
Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His Phe Ser
    100                 105                 110

GCT TAC TAT GTC AAT ATC AGC TAC TCC AAA GAG CAT GAT TTT AAA GTC      440
Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe Lys Val
115                 120                 125                 130

GGC GAT AAA AAT AAT GAA AAA GAA ATC AAA ATG TCC ACA GAA GAA TTA      488
Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu Glu Leu
                135                 140                 145

GCG CAA ATT TAT GCC GTC CAA TCC ACC CCT ACG ATT GTT TTA TCC GAT      536
Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu Ser Asp
            150                 155                 160

AAA ACC GGC AAA ACC ATC TAT GAA TTG CCC GGC TAT ATG CCC TCT ACG      584
Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro Ser Thr
        165                 170                 175

CAA TTT TTA GCC GTG TTA GAA TTT ATC GGC GAT GGG AAG TAT CAA GAC      632
Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr Gln Asp
    180                 185                 190

ACA AAA GAC GAT GAG GAT CTC ACT AAA AAA TTA AAG GCT TAC ATC AAG      680
Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr Ile Lys
195                 200                 205                 210

TAT AAA ACC AAC CTT TCT AAA AGC AAG TCT AAC TAGGAAAGCC TAATGAAGAA    733
Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn
                215                 220

TCTCAAAAGC CTGCTTTCTT TTTTGCTGGC TTC                                 766
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Met Phe Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu
 1               5                  10                  15
Leu Ile Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys
            20                  25                  30
Leu Asp Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu
        35                  40                  45
Asn Asp Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu
```

```
    50                  55                  60
Asp Val Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met
65                  70                  75                  80
Leu Leu Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys
                85                  90                  95
Lys Asp Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His
            100                 105                 110
Phe Ser Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe
        115                 120                 125
Lys Val Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu
    130                 135                 140
Glu Leu Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu
145                 150                 155                 160
Ser Asp Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro
                165                 170                 175
Ser Thr Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr
            180                 185                 190
Gln Asp Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr
        195                 200                 205
Ile Lys Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 980 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 53...931
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
TGAATGAAAT CCTAGATTCT AACGCCATTG TATATTATCT CGCTAAAAAT TC ATG AGA     58
                                                          Met Arg
                                                           1

TTG TTA TTC TTG TTA TTG AGT GCT GCT TTT ATG TTA CTG GCT GAA GAA     106
Leu Leu Phe Leu Leu Leu Ser Ala Ala Phe Met Leu Leu Ala Glu Glu
          5                  10                  15

AAA ATA TCT TTA AAC GAT GAC GCC CCC ATT AAA CTA GTG CAT TGG CAA     154
Lys Ile Ser Leu Asn Asp Asp Ala Pro Ile Lys Leu Val His Trp Gln
    20                  25                  30

AAT GCA TTA AAA GAA GTC CAA CCT GAT TCA AAC GCT CCA GCA ACA CCA     202
Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala Thr Pro
35                  40                  45                  50

CCT ATA AAA GCC GTG CAA ACC ACG CTC ACT TTT GAA ACG CCT TTT AAC     250
Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro Phe Asn
```

```
                    55                  60                  65

AAA ACG CCT AAA ATC ATG GAA GTT GAA GGG CAA AAG GTG ATC GTC TTA      298
Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile Val Leu
            70                  75                  80

AAA AAC GCT AAA CTG GAT TCT AAA AAA ACC ATG GAT TTT AAA GAA GCC      346
Lys Asn Ala Lys Leu Asp Ser Lys Lys Thr Met Asp Phe Lys Glu Ala
        85                  90                  95

TCT TTG AAT GCT TTA GAA ATG TTT TCC TAC CAA AAT GAC ATC TAC CTC      394
Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile Tyr Leu
    100                 105                 110

TTG TCT AAA AAA GCT AAA GTG GAA TTA GAA ATC CAA GCT TCA AAC AGC      442
Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser Asn Ser
115                 120                 125                 130

AAG GAT AAA AAA CGG CTC CGC TTT CTC TTT TTA CCC AAA GGT TTT CAT      490
Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly Phe His
                135                 140                 145

TTA GCC CCA CCG CCT AAC CTG AAA GAA AAA TCT CAG CAA ACT AAC CTT      538
Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr Asn Leu
            150                 155                 160

GCA CAA AAA GAC ACC AAC GAG CAA CCC CAA AGC CCT TTA AAC ACT CTA      586
Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn Thr Leu
        165                 170                 175

GAG TTA AAA CCC CCA CTA AAT TTA AGC CAT GCT TAT AAG GCG CTA GCG      634
Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala Leu Ala
    180                 185                 190

GTT ATT GCT GCC TTA CTC TTA ATA TTG TAT GTC ATC AAA AAA AAA ATT      682
Val Ile Ala Ala Leu Leu Leu Ile Leu Tyr Val Ile Lys Lys Lys Ile
195                 200                 205                 210

GTT CCC ACA CAA GGG TCT TTT TCT GCA AAA GAT TTT AAG TTA GAA ATT      730
Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu Glu Ile
                215                 220                 225

AGC GTT TTG GGT CGT GTT GAT GCG AAC CAT AAA ATC ATT TCA ATA GAA      778
Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser Ile Glu
            230                 235                 240

ACC AAT AAG GAG CGT TAC TTG GTC TTA CTA AGC GAT AAA TAC GGC CTG      826
Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr Gly Leu
        245                 250                 255

CTT TTA GAC AAA ATA AGC CCA AAA ACA TCT AAA GAA GAA CTG ATT AAA      874
Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu Ile Lys
    260                 265                 270

GAA GCT GAA AAT AAT ATA AAG AAT TCA AAA TTA GGA AAT TTA TAT GCC      922
Glu Ala Glu Asn Asn Ile Lys Asn Ser Lys Leu Gly Asn Leu Tyr Ala
275                 280                 285                 290
```

GGA AAA TTC TAAACTACAA CCTGCTAAGT TAGGGAAAAA TTTTGACCCT GTGGATCAT 980
Gly Lys Phe

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Met Arg Leu Leu Phe Leu Leu Leu Ser Ala Ala Phe Met Leu Leu Ala
 1               5                  10                  15
Glu Glu Lys Ile Ser Leu Asn Asp Asp Ala Pro Ile Lys Leu Val His
            20                  25                  30
Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala
        35                  40                  45
Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro
    50                  55                  60
Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile
65                  70                  75                  80
Val Leu Lys Asn Ala Lys Leu Asp Ser Lys Lys Thr Met Asp Phe Lys
                85                  90                  95
Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile
            100                 105                 110
Tyr Leu Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser
        115                 120                 125
Asn Ser Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly
    130                 135                 140
Phe His Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr
145                 150                 155                 160
Asn Leu Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn
                165                 170                 175
Thr Leu Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala
            180                 185                 190
Leu Ala Val Ile Ala Ala Leu Leu Leu Ile Leu Tyr Val Ile Lys Lys
        195                 200                 205
Lys Ile Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu
    210                 215                 220
Glu Ile Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser
225                 230                 235                 240
Ile Glu Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr
                245                 250                 255
Gly Leu Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu
            260                 265                 270
Ile Lys Glu Ala Glu Asn Asn Ile Lys Asn Ser Lys Leu Gly Asn Leu
        275                 280                 285
Tyr Ala Gly Lys Phe
    290
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 70...567
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
CTAGCGCGAT CTTTGGTCTC ACACAAGCTA TAACAAGCTT GAGAATCGCA TAATATATTC      60
TTGTTCTAC ATG CTA TCA CCA GCA ACT TTC AAA CAA ATA ACT CTA GCA TTA      111
          Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu
           1               5                  10

ATC GCT TCA AGA CTA ATC GTT GTA ATC CTA TAT GCT TTT ATC TTT ATT      159
Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile
15                  20                  25                  30

GTT CTC TCT TTT TAT ATG CTC AAT ATC ATC ACT ATT CTT AAT TTT AAA      207
Val Leu Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys
                35                  40                  45

GCG CTT ATT TTG GGG TTT GTT AGT GTT TTT TCA AGC GCA TTG TTT TGT      255
Ala Leu Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys
            50                  55                  60

TTT TGC TTG GCA ATT TTT GTA GCT AGA ATT TTT CAA AAC GAA CAA AGC      303
Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser
        65                  70                  75

ATC TTA GGA TTT TGT AAT ATC ATC AAT CTC TAT GCG CTA ATG TCT TGT      351
Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys
    80                  85                  90

AAT GTT TTT GTT CCT TTA GAA TAC CTA CCT AGT ATT GGT CAA TTA TTT      399
Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe
95                  100                 105                 110

ATC AAA ACA TCT ATT TTT TAC TAC CTT AAT CAA CTT CTA ATC AAA GCT      447
Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala
                115                 120                 125

TTT CAA GGG ATT GAT ACT ATA CTG GTT TTA GCA ACT TCA ACA TTT TTC      495
Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe
            130                 135                 140

ATT ATT GGT GGC ATT ATT TTA TTT TTA CTA AGC GCT AAT CGC ATG TTA      543
Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu
        145                 150                 155

CTA ACA CCA AAA GAA CGC ATG CGT TAAAGGCTTA GTCCCACCAT TGATTTATTT      597
```

Leu Thr Pro Lys Glu Arg Met Arg
160 165

AATGGCTCAA AAAAGGGGTA AGC 620

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu Ile Ala
1 5 10 15
Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile Val Leu
20 25 30
Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys Ala Leu
35 40 45
Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys Phe Cys
50 55 60
Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser Ile Leu
65 70 75 80
Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys Asn Val
85 90 95
Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe Ile Lys
100 105 110
Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala Phe Gln
115 120 125
Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe Ile Ile
130 135 140
Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu Leu Thr
145 150 155 160
Pro Lys Glu Arg Met Arg
165

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...1366
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
ATTGATTTCT TTTGGGAAGT GGATTTGAAA AACTTAAAAA GCCATTAAC ATG CAA GTT     58
                                                        Met Gln Val
                                                         1

AAA GAA AAC AAA CAA CTC TGC TTA ATT TCA TTA GGT TGC TCT AAA AAT      106
Lys Glu Asn Lys Gln Leu Cys Leu Ile Ser Leu Gly Cys Ser Lys Asn
     5                  10                  15

TTG GTG GAT TCA GAG GTG ATG TTA GGC AAG CTT TAT AAT TAC ACG CTC      154
Leu Val Asp Ser Glu Val Met Leu Gly Lys Leu Tyr Asn Tyr Thr Leu
20                  25                  30                  35

ACT AAT GAC GCT AAG AGC GCT GAT GTG ATT TTG ATC AAC ACT TGC GGG      202
Thr Asn Asp Ala Lys Ser Ala Asp Val Ile Leu Ile Asn Thr Cys Gly
                40                  45                  50

TTT ATT GAA AGC GCT AAA CAA GAG AGT ATC CAA ACC ATT CTC AAC GCC      250
Phe Ile Glu Ser Ala Lys Gln Glu Ser Ile Gln Thr Ile Leu Asn Ala
            55                  60                  65

GCC AAA GAC AAA AAA GAG GGA GCG ATT TTG ATT GCG AGC GGG TGC TTG      298
Ala Lys Asp Lys Lys Glu Gly Ala Ile Leu Ile Ala Ser Gly Cys Leu
        70                  75                  80

AGC GAA CGC TAT AAA GAT GAA ATC AAA GAA TTG ATC CCT GAA GTG GAT      346
Ser Glu Arg Tyr Lys Asp Glu Ile Lys Glu Leu Ile Pro Glu Val Asp
    85                  90                  95

ATT TTT ACC GGC GTG GGG GAT TAT GAC AAG ATC GAT ATA ATG ATT GCT      394
Ile Phe Thr Gly Val Gly Asp Tyr Asp Lys Ile Asp Ile Met Ile Ala
100                 105                 110                 115

AAA AAA CAA AAC CAG TTC AGC GAG CAA GTG TTT TTA AGC GAG CAT TAC      442
Lys Lys Gln Asn Gln Phe Ser Glu Gln Val Phe Leu Ser Glu His Tyr
                120                 125                 130

AAC GCA CGC ATC ATC ACG GGA TCG AGC GTG CAT GCG TAT GTG AAA ATT      490
Asn Ala Arg Ile Ile Thr Gly Ser Ser Val His Ala Tyr Val Lys Ile
            135                 140                 145

TCT GAG GGT TGC AAT CAA AAA TGT TCT TTT TGC GCT ATC CCT AGC TTT      538
Ser Glu Gly Cys Asn Gln Lys Cys Ser Phe Cys Ala Ile Pro Ser Phe
        150                 155                 160

AAG GGG AAA TTG CAA AGC AGG GAA TTG GAC TCC ATT TTA AAA GAA GTG      586
Lys Gly Lys Leu Gln Ser Arg Glu Leu Asp Ser Ile Leu Lys Glu Val
    165                 170                 175

GAA AAT CTC GCG CTT AAA GGC TAT ACG GAT ATG ACT TTT ATC GCT CAA      634
Glu Asn Leu Ala Leu Lys Gly Tyr Thr Asp Met Thr Phe Ile Ala Gln
180                 185                 190                 195

GAC TCT AGC TCC TTT TTA TAC GAT AAG GGG CAA AAA GAC GGC TTG ATC      682
Asp Ser Ser Ser Phe Leu Tyr Asp Lys Gly Gln Lys Asp Gly Leu Ile
                200                 205                 210

CAG CTC ATT AGA GCG ATT GAT AAA CAG CAA GCC TTA AAG AGC GCG CGT      730
Gln Leu Ile Arg Ala Ile Asp Lys Gln Gln Ala Leu Lys Ser Ala Arg
```

```
            215                 220                 225

ATT TTA TAT CTC TAC CCC TCT AGC ACC ACG CTA GAG CTT ATT GGC GCG      778
Ile Leu Tyr Leu Tyr Pro Ser Ser Thr Thr Leu Glu Leu Ile Gly Ala
        230                 235                 240

ATT GAA AGT TCG CCC ATT TTT CAA AAT TAT TTT GAC ATG CCC ATC CAG      826
Ile Glu Ser Ser Pro Ile Phe Gln Asn Tyr Phe Asp Met Pro Ile Gln
    245                 250                 255

CAC ATC AGC GAC TCC ATG CTC AAA AAG ATG CGG CGC AAC TCT AGC CAA      874
His Ile Ser Asp Ser Met Leu Lys Lys Met Arg Arg Asn Ser Ser Gln
260                 265                 270                 275

GCG CAC CAT TTA AAG CTT TTA GAT GCC ATG AAG CAG GTT AAA GAA AGC      922
Ala His His Leu Lys Leu Leu Asp Ala Met Lys Gln Val Lys Glu Ser
                280                 285                 290

TTT ATC AGA AGC ACG ATC ATT GTA GGG CAT CCG GAA GAA AAT GAG AGC      970
Phe Ile Arg Ser Thr Ile Ile Val Gly His Pro Glu Glu Asn Glu Ser
            295                 300                 305

GAA TTT GAA GAA TTG AGC GCG TTT TTA GAC GAG TTC CAG TTT GAT AGA     1018
Glu Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Gln Phe Asp Arg
        310                 315                 320

TTG AAT ATT TTT GCT TTC AGC GCT GAA GAA AAC ACG CAT GCC TAT TCT     1066
Leu Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His Ala Tyr Ser
    325                 330                 335

TTA GAA AAA GTG CCT AAA AAA ACC ATC AAC GCT CGC ATC AAA GCC TTG     1114
Leu Glu Lys Val Pro Lys Lys Thr Ile Asn Ala Arg Ile Lys Ala Leu
340                 345                 350                 355

AAT AAA ATC GCT TTA AAG CAC CAA AAC CAT TCC TTT AAG GCT TTG TTG     1162
Asn Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys Ala Leu Leu
                360                 365                 370

AAT AAG CCC ATT AAG GCG TTA GTG GAA AAT AAA GAG GGC GAG TAT TTT     1210
Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly Glu Tyr Phe
            375                 380                 385

TAC AAA GCA AGG GAT CTC AGA TGG GCG CCT GAA GTG GAT GGG GAA ATC     1258
Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp Gly Glu Ile
        390                 395                 400

TTG ATC AAT GAT AGC GAA CTA ACC ACC CCC TTA AAA CCC GGG CAT TAT     1306
Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro Gly His Tyr
    405                 410                 415

ACG ATT GCA CCT AGC GAA TTT AAA GAT AAT ATC CTA CTC GCT AAG GTT     1354
Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu Ala Lys Val
420                 425                 430                 435

TTA AGC CCT TTT TAAAAGTTAG CCATAAGGCT AAAAGCACGG CTAAAGCGT          1405
Leu Ser Pro Phe
```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
Met Gln Val Lys Glu Asn Lys Gln Leu Cys Leu Ile Ser Leu Gly Cys
 1               5                  10                  15
Ser Lys Asn Leu Val Asp Ser Glu Val Met Leu Gly Lys Leu Tyr Asn
            20                  25                  30
Tyr Thr Leu Thr Asn Asp Ala Lys Ser Ala Asp Val Ile Leu Ile Asn
        35                  40                  45
Thr Cys Gly Phe Ile Glu Ser Ala Lys Gln Glu Ser Ile Gln Thr Ile
    50                  55                  60
Leu Asn Ala Ala Lys Asp Lys Lys Glu Gly Ala Ile Leu Ile Ala Ser
65                  70                  75                  80
Gly Cys Leu Ser Glu Arg Tyr Lys Asp Glu Ile Lys Glu Leu Ile Pro
                85                  90                  95
Glu Val Asp Ile Phe Thr Gly Val Gly Asp Tyr Asp Lys Ile Asp Ile
            100                 105                 110
Met Ile Ala Lys Lys Gln Asn Gln Phe Ser Glu Gln Val Phe Leu Ser
        115                 120                 125
Glu His Tyr Asn Ala Arg Ile Ile Thr Gly Ser Ser Val His Ala Tyr
    130                 135                 140
Val Lys Ile Ser Glu Gly Cys Asn Gln Lys Cys Ser Phe Cys Ala Ile
145                 150                 155                 160
Pro Ser Phe Lys Gly Lys Leu Gln Ser Arg Glu Leu Asp Ser Ile Leu
                165                 170                 175
Lys Glu Val Glu Asn Leu Ala Leu Lys Gly Tyr Thr Asp Met Thr Phe
            180                 185                 190
Ile Ala Gln Asp Ser Ser Ser Phe Leu Tyr Asp Lys Gly Gln Lys Asp
        195                 200                 205
Gly Leu Ile Gln Leu Ile Arg Ala Ile Asp Lys Gln Gln Ala Leu Lys
    210                 215                 220
Ser Ala Arg Ile Leu Tyr Leu Tyr Pro Ser Ser Thr Thr Leu Glu Leu
225                 230                 235                 240
Ile Gly Ala Ile Glu Ser Ser Pro Ile Phe Gln Asn Tyr Phe Asp Met
                245                 250                 255
Pro Ile Gln His Ile Ser Asp Ser Met Leu Lys Lys Met Arg Arg Asn
            260                 265                 270
Ser Ser Gln Ala His His Leu Lys Leu Leu Asp Ala Met Lys Gln Val
        275                 280                 285
Lys Glu Ser Phe Ile Arg Ser Thr Ile Ile Val Gly His Pro Glu Glu
    290                 295                 300
Asn Glu Ser Glu Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Gln
305                 310                 315                 320
Phe Asp Arg Leu Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His
                325                 330                 335
Ala Tyr Ser Leu Glu Lys Val Pro Lys Lys Thr Ile Asn Ala Arg Ile
            340                 345                 350
Lys Ala Leu Asn Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys
```

```
        355                 360                 365
Ala Leu Leu Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly
    370                 375                 380
Glu Tyr Phe Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp
385                 390                 395                 400
Gly Glu Ile Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro
                405                 410                 415
Gly His Tyr Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu
            420                 425                 430
Ala Lys Val Leu Ser Pro Phe
        435
```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 200...1366
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
TGCGCGTTAT RTGGTTTTGA TTGAAAAGTT AGGCATTAAA GACAGATAAT TTTTATCGGT     60
TTTAGGGTGT GGCGAGTTTG TGTTGAAAGA GCGTTTGAAG GCCTTTTTTA GTGCGGACTC    120
TGTTTTCACT TTAATTTTTG CCCTTTTCTT TCTCACTTCG TTTAAAAAAC CTTTAACTCA    180
AGTCTTGTTG ATTGTTTTA ATG GTT TTT TTG TTT TTT AGG TGT TAT TTC CAA     232
                      Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln
                       1               5                  10

GCG TCT TTG AAA GAA ACT TTC GCA ATT AAT CAT TTA AAA ACA ATG TCT      280
Ala Ser Leu Lys Glu Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser
            15                  20                  25

TTT AAA TGG CTC ACT CTG GCT TTT TTG GGC GTG TTT TTA AGC ATC TTC      328
Phe Lys Trp Leu Thr Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe
        30                  35                  40

CCT AAC ATG TTT AAC ATG CAT GAT AGC CAA ACT TTC CGC TAC AAT TTA      376
Pro Asn Met Phe Asn Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu
    45                  50                  55

TTC GCT CTA AAC ATG TCC TTA ACT TAT GCT TGC GGG GCG TTA TGC TTG      424
Phe Ala Leu Asn Met Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu
60                  65                  70                  75

CTT TTT GCC AGT TGC TTA AGA ATC AAA TTG AAT CAA AAA ATC CTT TTT      472
Leu Phe Ala Ser Cys Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe
                80                  85                  90
```

```
TAC AGC ATG GCT GTT GCA AAT TTC ATC AAC GGC TTG CTC TCA TTG GTG      520
Tyr Ser Met Ala Val Ala Asn Phe Ile Asn Gly Leu Leu Ser Leu Val
            95                  100                 105

CAA AAA ATT TAT TTT AAC ATG CCC AGA GCG CAA GGG TTT AGC ACG GTT      568
Gln Lys Ile Tyr Phe Asn Met Pro Arg Ala Gln Gly Phe Ser Thr Val
        110                 115                 120

AAG GAG TAT GTG GTT TTA GTG AGC GTG TCC ATT TTA GGC TGT TAT ATT      616
Lys Glu Tyr Val Val Leu Val Ser Val Ser Ile Leu Gly Cys Tyr Ile
    125                 130                 135

TAT GCG CTT TAT TCG CAC AAT CAA AAA GAA AAA CTT TTT TTC ACG CTT      664
Tyr Ala Leu Tyr Ser His Asn Gln Lys Glu Lys Leu Phe Phe Thr Leu
140                 145                 150                 155

TCT GTT TTT GTG GGG TTT TTA GTC GTT ATT TTA AGC GCC ACA AGG AGC      712
Ser Val Phe Val Gly Phe Leu Val Val Ile Leu Ser Ala Thr Arg Ser
                160                 165                 170

GCG ACA ATC GCT TTT GTT ATT ACT TTT TTA ATC CTT TCT TGC TTT ATT      760
Ala Thr Ile Ala Phe Val Ile Thr Phe Leu Ile Leu Ser Cys Phe Ile
            175                 180                 185

TTA TAC GCC AAA AAA TCG CTC AAA CCA TTG GGT TAT ATG GTG GTC GTG      808
Leu Tyr Ala Lys Lys Ser Leu Lys Pro Leu Gly Tyr Met Val Val Val
        190                 195                 200

AGT CTT ATT TTG AGC GCT TTG TAT GTG GGG AGT AAC GCT TTA GAA AAA      856
Ser Leu Ile Leu Ser Ala Leu Tyr Val Gly Ser Asn Ala Leu Glu Lys
    205                 210                 215

AAG GGG GCA ATA GAG CAA TCT AGA GTT CAA AAT CAA AGC TTT GAA GAA      904
Lys Gly Ala Ile Glu Gln Ser Arg Val Gln Asn Gln Ser Phe Glu Glu
220                 225                 230                 235

GAT CTG AAA CGC TAC GCT AAA AAG GAC GCT GAT AGC AGT ATC GGA TGG      952
Asp Leu Lys Arg Tyr Ala Lys Lys Asp Ala Asp Ser Ser Ile Gly Trp
                240                 245                 250

CGT TTG GAG CGT TGG AAA GAA GCC CTA ACG GTT TTG CGT TTA AGG CCC     1000
Arg Leu Glu Arg Trp Lys Glu Ala Leu Thr Val Leu Arg Leu Arg Pro
            255                 260                 265

TTT TTT GGT ATG GCC GCT AGC GAG AAA TGC CAG AGG TTA GAA GAG ATT     1048
Phe Phe Gly Met Ala Ala Ser Glu Lys Cys Gln Arg Leu Glu Glu Ile
        270                 275                 280

TTA TCC TTA TCA AAG TCT TAT AGG GCC AAA GAT TTG ATT CTC TGT TAT     1096
Leu Ser Leu Ser Lys Ser Tyr Arg Ala Lys Asp Leu Ile Leu Cys Tyr
    285                 290                 295

GAA AGA TAC GAC AAT CAA ATC ATT CAC ATT TTA GCC ACT AGG GGG ATC     1144
Glu Arg Tyr Asp Asn Gln Ile Ile His Ile Leu Ala Thr Arg Gly Ile
300                 305                 310                 315

ATA GGC TTT TTG ATC TGG CTC TTT TTT TTA TTA GTT ATT GTA AAG ATT     1192
Ile Gly Phe Leu Ile Trp Leu Phe Phe Leu Leu Val Ile Val Lys Ile
```

```
                320                 325                 330

TTT TGG AGC GGG ATA AAG CAA AAC TCT TTA ATA TCG TTT TTT ATA CTA    1240
Phe Trp Ser Gly Ile Lys Gln Asn Ser Leu Ile Ser Phe Phe Ile Leu
            335                 340                 345

ATG ACA CTC GCC TTT TAC CTC ATT TTT GGC ATT GGG TTT GAC CCC TTT    1288
Met Thr Leu Ala Phe Tyr Leu Ile Phe Gly Ile Gly Phe Asp Pro Phe
        350                 355                 360

GAT TTC TTC ATT ACG GGA AGT TTT TTT GTA GGA ATG ATC ATG ATG GCT    1336
Asp Phe Phe Ile Thr Gly Ser Phe Phe Val Gly Met Ile Met Met Ala
    365                 370                 375

GTT TTT TTA AAA AAA GAT AAA AGT GCT TTT TAGCATCAAG GGGTTTGACA TTA  1389
Val Phe Leu Lys Lys Asp Lys Ser Ala Phe
380                 385

GTCAAGCGGT AGTTTCTTGT GATTCGTTCT T                                 1420
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln Ala Ser Leu Lys Glu
 1               5                  10                  15
Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser Phe Lys Trp Leu Thr
            20                  25                  30
Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe Pro Asn Met Phe Asn
        35                  40                  45
Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu Phe Ala Leu Asn Met
    50                  55                  60
Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu Leu Phe Ala Ser Cys
65                  70                  75                  80
Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe Tyr Ser Met Ala Val
                85                  90                  95
Ala Asn Phe Ile Asn Gly Leu Leu Ser Leu Val Gln Lys Ile Tyr Phe
            100                 105                 110
Asn Met Pro Arg Ala Gln Gly Phe Ser Thr Val Lys Glu Tyr Val Val
        115                 120                 125
Leu Val Ser Val Ser Ile Leu Gly Cys Tyr Ile Tyr Ala Leu Tyr Ser
    130                 135                 140
His Asn Gln Lys Glu Lys Leu Phe Phe Thr Leu Ser Val Phe Val Gly
145                 150                 155                 160
Phe Leu Val Val Ile Leu Ser Ala Thr Arg Ser Ala Thr Ile Ala Phe
                165                 170                 175
Val Ile Thr Phe Leu Ile Leu Ser Cys Phe Ile Leu Tyr Ala Lys Lys
            180                 185                 190
Ser Leu Lys Pro Leu Gly Tyr Met Val Val Val Ser Leu Ile Leu Ser
```

```
        195                 200                 205
Ala Leu Tyr Val Gly Ser Asn Ala Leu Glu Lys Lys Gly Ala Ile Glu
    210                 215                 220
Gln Ser Arg Val Gln Asn Gln Ser Phe Glu Glu Asp Leu Lys Arg Tyr
225                 230                 235                 240
Ala Lys Lys Asp Ala Asp Ser Ser Ile Gly Trp Arg Leu Glu Arg Trp
                245                 250                 255
Lys Glu Ala Leu Thr Val Leu Arg Leu Arg Pro Phe Phe Gly Met Ala
            260                 265                 270
Ala Ser Glu Lys Cys Gln Arg Leu Glu Glu Ile Leu Ser Leu Ser Lys
        275                 280                 285
Ser Tyr Arg Ala Lys Asp Leu Ile Leu Cys Tyr Glu Arg Tyr Asp Asn
    290                 295                 300
Gln Ile Ile His Ile Leu Ala Thr Arg Gly Ile Ile Gly Phe Leu Ile
305                 310                 315                 320
Trp Leu Phe Phe Leu Leu Val Ile Val Lys Ile Phe Trp Ser Gly Ile
                325                 330                 335
Lys Gln Asn Ser Leu Ile Ser Phe Phe Ile Leu Met Thr Leu Ala Phe
            340                 345                 350
Tyr Leu Ile Phe Gly Ile Gly Phe Asp Pro Phe Asp Phe Phe Ile Thr
        355                 360                 365
Gly Ser Phe Phe Val Gly Met Ile Met Met Ala Val Phe Leu Lys Lys
    370                 375                 380
Asp Lys Ser Ala Phe
385
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 89...1198
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
AAAAAGGAAA TAGCACGATG AAACCTAAAG GGGATATTAG CGTTAATATG CTAATATAGT     60
AGAACATTAT GACTACAAAA AGGGTGAT ATG CTG ATC TCC ATA GCG TTT TTA      112
                               Met Leu Ile Ser Ile Ala Phe Leu
                                1               5

TTG GTT TTA TAT CTT TTG AAT TAT AGT TCT TTC AGG ATG TTG AAA TCG     160
Leu Val Leu Tyr Leu Leu Asn Tyr Ser Ser Phe Arg Met Leu Lys Ser
    10                  15                  20

TTT TTA ACC TTA AAG AAA ATC TCT CAA TAC GCT TAT TTA TGG TTT TTT     208
Phe Leu Thr Leu Lys Lys Ile Ser Gln Tyr Ala Tyr Leu Trp Phe Phe
25                  30                  35                  40

ATC CTT TTG AGC ATA GGC GAG GCG GCT TTT GTT TTT TAT AGA AAT ATT     256
```

```
Ile Leu Leu Ser Ile Gly Glu Ala Ala Phe Val Phe Tyr Arg Asn Ile
                45                  50                  55

ATG CCT AGC CAT TTG TTT GTT TTG ACT TCA GCG TGT TCG TTT GTG TCT      304
Met Pro Ser His Leu Phe Val Leu Thr Ser Ala Cys Ser Phe Val Ser
            60                  65                  70

TTT ATT ATT TTT ATC CTT TCT TTA AGT TTT TAC GGG TTT TCC TAT TCC      352
Phe Ile Ile Phe Ile Leu Ser Leu Ser Phe Tyr Gly Phe Ser Tyr Ser
        75                  80                  85

ATA GAA AAA ATA GAT TTT TTG CAT TCA AGG CGT AAA AGT TTA AAA AAC      400
Ile Glu Lys Ile Asp Phe Leu His Ser Arg Arg Lys Ser Leu Lys Asn
    90                  95                  100

TTT TTA AAA TTG GGG TTT TAT CTG GCG TTA TTA GGG TAT TTT TGG CGT      448
Phe Leu Lys Leu Gly Phe Tyr Leu Ala Leu Leu Gly Tyr Phe Trp Arg
105                 110                 115                 120

GGG TTT TAT GAA GGG TTG GCC CGC CCT AAA ATC AAA GAA ACC CCT ATT      496
Gly Phe Tyr Glu Gly Leu Ala Arg Pro Lys Ile Lys Glu Thr Pro Ile
                125                 130                 135

TAT TTG GAT AAG CTG GAT AAA GAA TTA AAG ATT ATT TTA CTC ACA GAC      544
Tyr Leu Asp Lys Leu Asp Lys Glu Leu Lys Ile Ile Leu Leu Thr Asp
            140                 145                 150

ATG CAT GTG GGG AGT TTG TTG CAA AAA GAT TTT GTT GAT TAC ATT GTA      592
Met His Val Gly Ser Leu Leu Gln Lys Asp Phe Val Asp Tyr Ile Val
        155                 160                 165

GAA GAA GTC AAT CAA AAA GAA GTG GAT ATG GTG CTG ATT GGG GGG GAT      640
Glu Glu Val Asn Gln Lys Glu Val Asp Met Val Leu Ile Gly Gly Asp
    170                 175                 180

TTA GTG GAT GAA AGC ATT GAA AAA GTC AAA TCT TTT TTA CTG CCT TTA      688
Leu Val Asp Glu Ser Ile Glu Lys Val Lys Ser Phe Leu Leu Pro Leu
185                 190                 195                 200

AAC AAC CTT AAA AGC ACG CAT GGC ACT TTT TAT GTG CCA GGA AAT CAT      736
Asn Asn Leu Lys Ser Thr His Gly Thr Phe Tyr Val Pro Gly Asn His
                205                 210                 215

GAG TAT TAT CAT GGC ATA GAG CCG ATT TTA TCG TTT CTT GAC ACG CTT      784
Glu Tyr Tyr His Gly Ile Glu Pro Ile Leu Ser Phe Leu Asp Thr Leu
            220                 225                 230

AAT TTG ACG ATT TTA GGG AAT GAG TGC GTG CAT TTA GGG GGG ATC AAT      832
Asn Leu Thr Ile Leu Gly Asn Glu Cys Val His Leu Gly Gly Ile Asn
        235                 240                 245

TTG TGC GGC GTG TAT GAT TAT TTC GCA AGG AAG CGT CAA AAT TTT GCC      880
Leu Cys Gly Val Tyr Asp Tyr Phe Ala Arg Lys Arg Gln Asn Phe Ala
    250                 255                 260

CCT GAT ATT GAC AAA GCT TTA AAA AAG CGC AAT GAG AGT AAG CCC ACG      928
Pro Asp Ile Asp Lys Ala Leu Lys Lys Arg Asn Glu Ser Lys Pro Thr
265                 270                 275                 280
```

```
ATC CTT TTG GCC CAC CAA CCT AAA CAA ATT AGA AGC CTC AAA GAA AGC      976
Ile Leu Leu Ala His Gln Pro Lys Gln Ile Arg Ser Leu Lys Glu Ser
                285                 290                 295

CAC TCT GTA GAT TTA GTC CTT TCA GGG CAT ACC CAT GCA GGG CAA ATC     1024
His Ser Val Asp Leu Val Leu Ser Gly His Thr His Ala Gly Gln Ile
            300                 305                 310

TTT CCC TTT AGC CTT TTA GTC AAG TTG GCG CAA ACC TAT TTA CAT GGT     1072
Phe Pro Phe Ser Leu Leu Val Lys Leu Ala Gln Thr Tyr Leu His Gly
        315                 320                 325

TTA TAC AAG CAC AGC CCC ACC ACT CAA ATT TAT GTG AGC AGT GGG GCA     1120
Leu Tyr Lys His Ser Pro Thr Thr Gln Ile Tyr Val Ser Ser Gly Ala
    330                 335                 340

GGG TAT TGG GGG ATT CCT TTA AGG TTT TTA GCC CCT AGC GAG ATC GCA     1168
Gly Tyr Trp Gly Ile Pro Leu Arg Phe Leu Ala Pro Ser Glu Ile Ala
345                 350                 355                 360

TAC CTT AGG CTT TTA CCT AAA AAT CAA GCT TAGTTAAACA AAATCTTAAA ATC   1221
Tyr Leu Arg Leu Leu Pro Lys Asn Gln Ala
                365                 370

TTAATCGTAA TCAAGCGGTT AAAAATAAGA A                                  1252
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
Met Leu Ile Ser Ile Ala Phe Leu Leu Val Leu Tyr Leu Leu Asn Tyr
 1               5                  10                  15
Ser Ser Phe Arg Met Leu Lys Ser Phe Leu Thr Leu Lys Lys Ile Ser
            20                  25                  30
Gln Tyr Ala Tyr Leu Trp Phe Phe Ile Leu Leu Ser Ile Gly Glu Ala
        35                  40                  45
Ala Phe Val Phe Tyr Arg Asn Ile Met Pro Ser His Leu Phe Val Leu
    50                  55                  60
Thr Ser Ala Cys Ser Phe Val Ser Phe Ile Ile Phe Ile Leu Ser Leu
65                  70                  75                  80
Ser Phe Tyr Gly Phe Ser Tyr Ser Ile Glu Lys Ile Asp Phe Leu His
                85                  90                  95
Ser Arg Arg Lys Ser Leu Lys Asn Phe Leu Lys Leu Gly Phe Tyr Leu
            100                 105                 110
Ala Leu Leu Gly Tyr Phe Trp Arg Gly Phe Tyr Glu Gly Leu Ala Arg
        115                 120                 125
Pro Lys Ile Lys Glu Thr Pro Ile Tyr Leu Asp Lys Leu Asp Lys Glu
    130                 135                 140
Leu Lys Ile Ile Leu Leu Thr Asp Met His Val Gly Ser Leu Leu Gln
```

```
145                 150                 155                 160
Lys Asp Phe Val Asp Tyr Ile Val Glu Glu Val Asn Gln Lys Glu Val
                165                 170                 175
Asp Met Val Leu Ile Gly Gly Asp Leu Val Asp Glu Ser Ile Glu Lys
            180                 185                 190
Val Lys Ser Phe Leu Leu Pro Leu Asn Asn Leu Lys Ser Thr His Gly
        195                 200                 205
Thr Phe Tyr Val Pro Gly Asn His Glu Tyr Tyr His Gly Ile Glu Pro
    210                 215                 220
Ile Leu Ser Phe Leu Asp Thr Leu Asn Leu Thr Ile Leu Gly Asn Glu
225                 230                 235                 240
Cys Val His Leu Gly Gly Ile Asn Leu Cys Gly Val Tyr Asp Tyr Phe
                245                 250                 255
Ala Arg Lys Arg Gln Asn Phe Ala Pro Asp Ile Asp Lys Ala Leu Lys
            260                 265                 270
Lys Arg Asn Glu Ser Lys Pro Thr Ile Leu Leu Ala His Gln Pro Lys
        275                 280                 285
Gln Ile Arg Ser Leu Lys Glu Ser His Ser Val Asp Leu Val Leu Ser
    290                 295                 300
Gly His Thr His Ala Gly Gln Ile Phe Pro Phe Ser Leu Leu Val Lys
305                 310                 315                 320
Leu Ala Gln Thr Tyr Leu His Gly Leu Tyr Lys His Ser Pro Thr Thr
                325                 330                 335
Gln Ile Tyr Val Ser Ser Gly Ala Gly Tyr Trp Gly Ile Pro Leu Arg
            340                 345                 350
Phe Leu Ala Pro Ser Glu Ile Ala Tyr Leu Arg Leu Leu Pro Lys Asn
        355                 360                 365
Gln Ala
    370
```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 103...381
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
AGTCTTTGCC CGCTATCAAA AAAGAGATTT TTTGCAATAT TTTCATAAGC ACCGAAGAAA     60
GCTTGCTTTA GCGAGTTTGT GGGTGAAACG TACGCCTTGC TC ATG ATT TTT GTC      114
                                              Met Ile Phe Val
                                               1

AAT AAA TAT CTC TAT GGG ATT AAA AGC GTT GTG CCT TTG GCG GTT GGT     162
Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Val Gly
 5                  10                  15                  20
```

```
TTT AGC AAA TAC CCT TTA AAA AAG TTT TTA TGG CTT AAT GTT TTT TCC      210
Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
                25                  30                  35

AGT TTT TTG TGG GCG CTC ATC GTG GGG AGC GTT TCT TTT CAA GCG AGC      258
Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
            40                  45                  50

GAT TGG GTG AAA ACG CTG TAT GAA AGG CTT TCT CAT TAC ACT TCG TTT      306
Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
        55                  60                  65

TTT ATC ATA AGT TTT GTT CTT ATA GCG CTT TTA ATA TGG TTT TTA TTG      354
Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
    70                  75                  80

AAA CGA TAT TCG CGC AAA ATG GGT TTT TAAGCAAGAT GTTTAATTAA ATGCGCT    408
Lys Arg Tyr Ser Arg Lys Met Gly Phe
85                  90

AGACTACGCC CACAAGCATT CGC                                           431
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro
 1               5                  10                  15
Leu Ala Val Gly Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu
            20                  25                  30
Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser
        35                  40                  45
Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His
    50                  55                  60
Tyr Thr Ser Phe Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile
65                  70                  75                  80
Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly Phe
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 70...1227
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
TAGCATCAAT ACCCCTTAAA TAAAAGATAT AATGCTGTAT TATAAGCTAG TTTTAATTAC      60
AATTTTCAA ATG TTA AGG AAA AAC ATT TTA GCT TAC TAT GGG GCG AAT TTT     111
          Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe
           1               5                  10

CTC TTA ATC ATC GCT CAA AGC TTA CCC CAT GCG ATT TTA ACC CCC TTG      159
Leu Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu
15                  20                  25                  30

TTG CTT TCT AAA GGG CTT AGT TTG AGT GAA ATC TTG CTC GTG CAA ACC      207
Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr
                35                  40                  45

TTT TTT AGC TTT TGC GTG CTA GTG GCT GAA TAC CCA AGC GGC GTT TTA      255
Phe Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu
            50                  55                  60

GCG GAT TTG ATG AGC CGA AAA AAT TTA TTC CTG GTT TCT AAT GCC TTT      303
Ala Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe
        65                  70                  75

TTA ATC GCT AGT TTT TCG TTT GTG CTG TTT TTT GAT AGC TTT ATT TTC      351
Leu Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe
    80                  85                  90

ATG CTT TTA GCG TGG GGG TTG TAT GGT TTG TAT AGC GCA TGC TCT AGC      399
Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser
95                  100                 105                 110

GGC ACG ATT GAA GCT TCA CTC ATC ACA GAC ATT AAG GAA AAC AAA AAA      447
Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys
                115                 120                 125

GAT TTA TCC AAG TTT TTA GCC AAA AAC AAT CAA ATT ACT TAT TTA GGC      495
Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly
            130                 135                 140

ATG ATT ATA GGG AGT TCT TTG GGA TCG TTT TTG TAT CTC AAA GTC CAT      543
Met Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His
        145                 150                 155

GCG ATG CTG TAT ATT GTG GGG ATT TTT TTA ATC ATG CTC TGT GTG CTA      591
Ala Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu
    160                 165                 170

ACG ATC ATT TTT TAT TTT AAA GAG AAA GAA GGG GAT TTT AAA AGC CAA      639
Thr Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln
175                 180                 185                 190

AAA AGC CTG AAA CTC CTT AAA GAG CAA GTC AAA GGC AGT CTT AAA GAG      687
```

```
Lys Ser Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu
                195                 200                 205

CTT AAA GAT AAC CCC AAA CTT AAA ATT CTG TTA GTG GGG CAT TTG ATT      735
Leu Lys Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile
            210                 215                 220

ACG CCC GTC TTT TTT ATG AGC CAT TTT CAA ATG TGG CAA GCG TAT TTT      783
Thr Pro Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe
        225                 230                 235

TTA AAA CAA GGC GTT AAA GAG CAA TAC CTT TTT GTG TTT TAT ATC GCT      831
Leu Lys Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala
    240                 245                 250

TTT CAA GTG ATT TCT ATT CTC ATT CAT TTT TTA AAA GCC TCT AGT TAT      879
Phe Gln Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr
255                 260                 265                 270

AGC CAA AAA ATC GCC TTG AGT TCG CTT GTG GTG TTG TTA GGC GTT AGC      927
Ser Gln Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser
                275                 280                 285

CCC TTA TTG CTT AGC AAT ATC CCT TAT TGT TTC ATA GGG GTG TAT GCG      975
Pro Leu Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala
            290                 295                 300

CTC ATG GTG GCG TTT TTC ACT TAC ATG AGC TAT TGC TTA AAC TAT CAA     1023
Leu Met Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln
        305                 310                 315

TTC TCC AAA TTC GTT TCT AAA AAC AAC ATT TCC TCG CTC TCA TCG CTT     1071
Phe Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu
    320                 325                 330

TTA TCA AGC TGT GTG CGC GTG GTC TCT GTG CTA ATC TTA TCG CTC AGC     1119
Leu Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser
335                 340                 345                 350

AGT CTG GAA CTG CGT TAC TTC TCA CCC CTA ACT ATC ATA ACC ATG CAT     1167
Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His
                355                 360                 365

TTT GCC TTG ACG CTT ATC ATC CTC TTT TTC TTT TTG TAT AAG GCT AAG     1215
Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys
            370                 375                 380

CCG TTT GAT GAG TGAGCGGCTT TAAGAGTGCA ACCTTTTAGC GATTTCTATA GCAAC  1272
Pro Phe Asp Glu
        385

ATCATAGCC                                                          1281
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
 1               5                  10                  15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
            20                  25                  30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
        35                  40                  45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
    50                  55                  60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu Ile
65                  70                  75                  80
Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met Leu
                85                  90                  95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
            100                 105                 110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
        115                 120                 125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
    130                 135                 140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145                 150                 155                 160
Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr Ile
                165                 170                 175
Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Ser
            180                 185                 190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
        195                 200                 205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
    210                 215                 220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225                 230                 235                 240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
                245                 250                 255
Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser Gln
            260                 265                 270
Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro Leu
        275                 280                 285
Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu Met
    290                 295                 300
Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe Ser
305                 310                 315                 320
Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu Ser
                325                 330                 335
Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser Leu
            340                 345                 350
Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe Ala
        355                 360                 365
Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro Phe
    370                 375                 380
Asp Glu
385
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 77...2167
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
GAAGTTTATG AGCCGTTTTG CCACTATTCA AAGAAATTTT GGATTATAAT AAAAAAACTG      60
GCTGAAATTA ACAACA ATG ATT AAA CAA TCA TTA AAT GGA GAG GAC ATG CAA     112
                  Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln
                   1               5                  10

AAA AGT TTA GTT TCT TTG GCT TGG GTT TTT GTA GCT ATT TTA GGG GCG      160
Lys Ser Leu Val Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala
        15                  20                  25

ATC TGT TTA GGG GTG TTA GCC TTA CAC AAG GGT GAG AGC ATT AAC ACG      208
Ile Cys Leu Gly Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr
    30                  35                  40

CTA TGG CTT GTA GTA GCG AGC GCT TGT ATT TAT AGC ATA GGC TAT CGT      256
Leu Trp Leu Val Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg
45                  50                  55                  60

TTT TAT AGC CAT TTT ATC GCT TAT AAG GTG TTA AAG CTA GAT GAT AGC      304
Phe Tyr Ser His Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser
                65                  70                  75

AGA GCC ACG CCC GCA TGC GTA AGG AAT GAT GGC AAG GAT TTT GTG CCA      352
Arg Ala Thr Pro Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro
            80                  85                  90

ACC GAT AAA GCG ATC ACT TTT GGG CAC CAT TTC GCC GCT ATT GCT GGG      400
Thr Asp Lys Ala Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly
        95                  100                 105

GCT GGC CCT TTA GTA GGC CCG ATA CTA GCC GCT CAA ATG GGT TAC TTG      448
Ala Gly Pro Leu Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu
    110                 115                 120

CCC TCT ATC TTA TGG ATT TTG ATA GGC TCG GTT TTA GGG GGT TGC GTG      496
Pro Ser Ile Leu Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val
125                 130                 135                 140

CAT GAT TTT GTG GTG CTT TTT GCT TCT ATT AGG CGC GAT GGC AAG TCT      544
His Asp Phe Val Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser
```

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                    145                 150                 155

TTA GGC GAA ATG ATC AAA CTT GAA ATG GGC CAA TTT GTA GGC ATG ATC      592
Leu Gly Glu Met Ile Lys Leu Glu Met Gly Gln Phe Val Gly Met Ile
            160                 165                 170

GCA AGT CTG GGC ATT TTA GGG ATC ATG CTC ATT ATC ATT GCG ATT TTA      640
Ala Ser Leu Gly Ile Leu Gly Ile Met Leu Ile Ile Ile Ala Ile Leu
        175                 180                 185

GCG ATG GTG GTG GTG AAG GCT TTA GCG CAT TCG CCT TGG GGC TTT TTT      688
Ala Met Val Val Val Lys Ala Leu Ala His Ser Pro Trp Gly Phe Phe
    190                 195                 200

ACG ATC GCA ATG ACT ATT CCC ATT GCG ATT CTT ATG GGG CTT TAC ATG      736
Thr Ile Ala Met Thr Ile Pro Ile Ala Ile Leu Met Gly Leu Tyr Met
205                 210                 215                 220

CGG TTT TTC AGG CCA CAC AAG ATT TTA GAG GTT TCT GTT ATT GGC TTT      784
Arg Phe Phe Arg Pro His Lys Ile Leu Glu Val Ser Val Ile Gly Phe
                225                 230                 235

ATC CTA TTG ATT ATA GCG ATT TAT GCG GGT AAA TAC GTT TCT TTA GAT      832
Ile Leu Leu Ile Ile Ala Ile Tyr Ala Gly Lys Tyr Val Ser Leu Asp
            240                 245                 250

CCT AAA TTA GCG TCA ATA TTC ACT TTT GAG GCC AGT TCT TTA GCG TGG      880
Pro Lys Leu Ala Ser Ile Phe Thr Phe Glu Ala Ser Ser Leu Ala Trp
        255                 260                 265

ATG ATC ATG GGC TAT GGG TTT GTG GCT TCT ATT TTA CCG GTA TGG TTT      928
Met Ile Met Gly Tyr Gly Phe Val Ala Ser Ile Leu Pro Val Trp Phe
    270                 275                 280

TTA CTC GCT CCA CGA GAT TAT CTA AGC ACT TTT TTA AAA ATT GGC GTT      976
Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Leu Lys Ile Gly Val
285                 290                 295                 300

ATA GGG GTG TTG GTT GTG GCC ATT ATT TTT GTC GCT CCG CCT TTA CAA     1024
Ile Gly Val Leu Val Val Ala Ile Ile Phe Val Ala Pro Pro Leu Gln
                305                 310                 315

ATC CCT AAA ATC ACG CCC TTT GTA GAT GGC AGT GGG CCT GTG TTT GCA     1072
Ile Pro Lys Ile Thr Pro Phe Val Asp Gly Ser Gly Pro Val Phe Ala
            320                 325                 330

GGA AGC GTG TTC CCT TTC TTG TTT ATC ACG GTG GCT TGC GGG ACG ATT     1120
Gly Ser Val Phe Pro Phe Leu Phe Ile Thr Val Ala Cys Gly Thr Ile
        335                 340                 345

AGC GGA TTC CAT GCT TTA ATT TCT TCA GGC ACG ACC CCT AAA ATG CTC     1168
Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Met Leu
    350                 355                 360

GCT AAA GAA AGC GAC GCA AGG CTA GTG GGC TAT GGC TCT ATG GTG ATG     1216
Ala Lys Glu Ser Asp Ala Arg Leu Val Gly Tyr Gly Ser Met Val Met
365                 370                 375                 380
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GAG AGC GTT GTG GCT CTT ATG GCG TTG GTG TGC GCA GGG ATC TTG CAC    1264
Glu Ser Val Val Ala Leu Met Ala Leu Val Cys Ala Gly Ile Leu His
                385                 390                 395

CCA GGG CTT TAT TTC GCT ATC AAT TCG CCA GAA GTG AGC ATC GGT AAA    1312
Pro Gly Leu Tyr Phe Ala Ile Asn Ser Pro Glu Val Ser Ile Gly Lys
            400                 405                 410

GAT ATA GCT GAT GCG GCT TCA GTG ATT AGC TCA TGG GGG TTT AAT ATC    1360
Asp Ile Ala Asp Ala Ala Ser Val Ile Ser Ser Trp Gly Phe Asn Ile
        415                 420                 425

AGC GCT GAA GAA ATT CGT GAG ATG ACT AAA AAC ATC GGC GAA AGC TCC    1408
Ser Ala Glu Glu Ile Arg Glu Met Thr Lys Asn Ile Gly Glu Ser Ser
    430                 435                 440

ATT TTG AGC CGC ACC GGT GGG GCG CCC ACT TTT GCG ATC GGT TTA GCG    1456
Ile Leu Ser Arg Thr Gly Gly Ala Pro Thr Phe Ala Ile Gly Leu Ala
445                 450                 455                 460

ATG ATT GTG TAT CAC ATT TTA GGG GAT CCA AGC GTG ATG GCG TTT TGG    1504
Met Ile Val Tyr His Ile Leu Gly Asp Pro Ser Val Met Ala Phe Trp
                465                 470                 475

TAT CAT TTT GCG ATT TTG TTT GAA GCT TTG TTC ATT TTA ACC GCT GTG    1552
Tyr His Phe Ala Ile Leu Phe Glu Ala Leu Phe Ile Leu Thr Ala Val
            480                 485                 490

GAT GCT GGC ACA CGA ACC GCT CGT TTC ATG ATT CAA GAT TTG CTC GGT    1600
Asp Ala Gly Thr Arg Thr Ala Arg Phe Met Ile Gln Asp Leu Leu Gly
        495                 500                 505

AAT GTT TAT AAG CCT TTG GGC GAT CTT AGC TCT TAT AAG GCT GGG ATT    1648
Asn Val Tyr Lys Pro Leu Gly Asp Leu Ser Ser Tyr Lys Ala Gly Ile
    510                 515                 520

TTT GCC ACT CTT TTG TGC GTG GCA GGG TGG GGG TAT TTC TTG TAT CAA    1696
Phe Ala Thr Leu Leu Cys Val Ala Gly Trp Gly Tyr Phe Leu Tyr Gln
525                 530                 535                 540

GGC ACG ATT GAT CCT AAA GGG GGG ATT TAT ACG CTA TGG CCT TTA TTT    1744
Gly Thr Ile Asp Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe
                545                 550                 555

GGC GTG AGC AAT CAG ATG TTA GCG GGC ATG GCG TTG TTG TTG GTC ACG    1792
Gly Val Ser Asn Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr
            560                 565                 570

GTG GTG TTG TTT AAA ATG GGG CGT TTT AAG GGG GCG ATG ATA AGC GCC    1840
Val Val Leu Phe Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala
        575                 580                 585

TTA CCG GCA GTT TTG ATT TTA TCC ATC ACT TTT TAT AGC GGT ATT TTA    1888
Leu Pro Ala Val Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu
    590                 595                 600

AAG GTG GTG CCA AAG AGC GAT AAC AGC GTG CTG AAT AAT GTT TCC CAT    1936
Lys Val Val Pro Lys Ser Asp Asn Ser Val Leu Asn Asn Val Ser His
```

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605                 610                 615                 620

GTG GCG CAA ATG CAA ATC ATC AAA GAA AAA ATG GCT ACC ACT ACC GAT    1984
Val Ala Gln Met Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp
                625                 630                 635

GAA AAA GCG CTC AAA ACG CTC CAA AAA TCC TTT TTT AAC CAC GCT ATT    2032
Glu Lys Ala Leu Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile
            640                 645                 650

GAT GCG ATT TTG TGC GTG TTT TTC ATG CTT GTG GCG CTA TTG GTT TTA    2080
Asp Ala Ile Leu Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu
        655                 660                 665

ATC GTG AGC GTT AGG ATT TGC TCA AAC GCT TAT TTT AAA AAC AAA ATT    2128
Ile Val Ser Val Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile
    670                 675                 680

TAC CCA CCG CTG GCT GAA ACG CCC TAC ATC AAA GCC TCT TGAATAAAAA AG  2179
Tyr Pro Pro Leu Ala Glu Thr Pro Tyr Ile Lys Ala Ser
685                 690                 695

GGGTTTTAAC CCCCTTTAAA TCCATAGAAA AAAGTTTGA                         2218
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 697 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln Lys Ser Leu Val
 1               5                  10                  15
Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala Ile Cys Leu Gly
            20                  25                  30
Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr Leu Trp Leu Val
        35                  40                  45
Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg Phe Tyr Ser His
    50                  55                  60
Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser Arg Ala Thr Pro
65                  70                  75                  80
Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro Thr Asp Lys Ala
                85                  90                  95
Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu
            100                 105                 110
Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu Pro Ser Ile Leu
        115                 120                 125
Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val His Asp Phe Val
    130                 135                 140
Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser Leu Gly Glu Met
145                 150                 155                 160
Ile Lys Leu Glu Met Gly Gln Phe Val Gly Met Ile Ala Ser Leu Gly
```

```
                 165                 170                 175
Ile Leu Gly Ile Met Leu Ile Ile Ile Ala Ile Leu Ala Met Val Val
            180                 185                 190
Val Lys Ala Leu Ala His Ser Pro Trp Gly Phe Phe Thr Ile Ala Met
        195                 200                 205
Thr Ile Pro Ile Ala Ile Leu Met Gly Leu Tyr Met Arg Phe Phe Arg
    210                 215                 220
Pro His Lys Ile Leu Glu Val Ser Val Ile Gly Phe Ile Leu Leu Ile
225                 230                 235                 240
Ile Ala Ile Tyr Ala Gly Lys Tyr Val Ser Leu Asp Pro Lys Leu Ala
                245                 250                 255
Ser Ile Phe Thr Phe Glu Ala Ser Ser Leu Ala Trp Met Ile Met Gly
            260                 265                 270
Tyr Gly Phe Val Ala Ser Ile Leu Pro Val Trp Phe Leu Leu Ala Pro
        275                 280                 285
Arg Asp Tyr Leu Ser Thr Phe Leu Lys Ile Gly Val Ile Gly Val Leu
    290                 295                 300
Val Val Ala Ile Ile Phe Val Ala Pro Pro Leu Gln Ile Pro Lys Ile
305                 310                 315                 320
Thr Pro Phe Val Asp Gly Ser Gly Pro Val Phe Ala Gly Ser Val Phe
                325                 330                 335
Pro Phe Leu Phe Ile Thr Val Ala Cys Gly Thr Ile Ser Gly Phe His
            340                 345                 350
Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Met Leu Ala Lys Glu Ser
        355                 360                 365
Asp Ala Arg Leu Val Gly Tyr Gly Ser Met Val Met Glu Ser Val Val
    370                 375                 380
Ala Leu Met Ala Leu Val Cys Ala Gly Ile Leu His Pro Gly Leu Tyr
385                 390                 395                 400
Phe Ala Ile Asn Ser Pro Glu Val Ser Ile Gly Lys Asp Ile Ala Asp
                405                 410                 415
Ala Ala Ser Val Ile Ser Ser Trp Gly Phe Asn Ile Ser Ala Glu Glu
            420                 425                 430
Ile Arg Glu Met Thr Lys Asn Ile Gly Glu Ser Ser Ile Leu Ser Arg
        435                 440                 445
Thr Gly Gly Ala Pro Thr Phe Ala Ile Gly Leu Ala Met Ile Val Tyr
    450                 455                 460
His Ile Leu Gly Asp Pro Ser Val Met Ala Phe Trp Tyr His Phe Ala
465                 470                 475                 480
Ile Leu Phe Glu Ala Leu Phe Ile Leu Thr Ala Val Asp Ala Gly Thr
                485                 490                 495
Arg Thr Ala Arg Phe Met Ile Gln Asp Leu Leu Gly Asn Val Tyr Lys
            500                 505                 510
Pro Leu Gly Asp Leu Ser Ser Tyr Lys Ala Gly Ile Phe Ala Thr Leu
        515                 520                 525
Leu Cys Val Ala Gly Trp Gly Tyr Phe Leu Tyr Gln Gly Thr Ile Asp
    530                 535                 540
Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe Gly Val Ser Asn
545                 550                 555                 560
Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr Val Val Leu Phe
                565                 570                 575
Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala Leu Pro Ala Val
            580                 585                 590
Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu Lys Val Val Pro
        595                 600                 605
Lys Ser Asp Asn Ser Val Leu Asn Asn Val Ser His Val Ala Gln Met
    610                 615                 620
Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp Glu Lys Ala Leu
```

```
625                 630                 635                 640
Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile Asp Ala Ile Leu
                645                 650                 655
Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu Ile Val Ser Val
            660                 665                 670
Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile Tyr Pro Pro Leu
        675                 680                 685
Ala Glu Thr Pro Tyr Ile Lys Ala Ser
    690                 695
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 121...861
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
TAAGGGGCTT TGCATTTTTT ACTCATTTCA TGCCTCTTTT TCTTTATTTA GACAGATTAT      60
TATCTTAAAA TAATTGTAAT ATCATTATTA TTATATCAAC TCAATAAAAA AGGAGAAGGT     120
 ATG CAA AAA ACT TCT AAC ACT CTG GCG CTG GGG AGT TTG ACA GCG CTA      168
 Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu
  1               5                  10                  15

TTC TTT CTA ATG GGT TTT ATC ACG GTT TTA AAC GAT ATT TTA ATC CCA      216
Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro
            20                  25                  30

CAC TTA AAG CCC ATT TTT GAC TTG ACC TAT TTT GAA GCT TCA CTC ATT      264
His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile
        35                  40                  45

CAA TTT TGC TTT TTT GGG GCG TAT TTC ATC ATG GGA GGA GTT TTT GGG      312
Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly
    50                  55                  60

AAT GTG ATC AGT AAA ATC GGC TAC CCT TTT GGC GTG GTG CTT GGT TTT      360
Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe
65                  70                  75                  80

GTG ATC ACA GCG ACG GGG TGC GCG TTG TTT TAT CCG GCG GCG CAT TTT      408
Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe
                85                  90                  95

GGA TCC TAT GGG TTT TTT TTA GGA GCG TTG TTT ATT TTA GCG AGC GGG      456
Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly
            100                 105                 110
```

```
ATT GTG TGC TTG CAA ACC GCT GGT AAT CCC TTT GTA ACC TTG CTT TCT      504
Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser
        115                 120                 125

AAA GGT AAA GAA GCC AGA AAT TTG GTT TTA GTC CAG GCG TTC AAT TCG      552
Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser
    130                 135                 140

CTT GGC ACA ACT TTA GGG CCT ATT TTT GGG AGC TTG TTG ATT TTT AGC      600
Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser
145                 150                 155                 160

ACG ACT AAA ATG GGC GAT AAT GCA AGT TTG ATA GAT AAA TTA GCG GAC      648
Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp
                165                 170                 175

GCT AAA AGC GTT CAA ATG CCT TAT TTG GGC TTG GCG GTG TTT TCG CTT      696
Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu
            180                 185                 190

CTT TTA GCG CTC ATC ATG TAT CTT TTG AAA TTG CCT GAT GTG GAA AAA      744
Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys
        195                 200                 205

GAA ATG CCC AAA GAG ACG ACT CAA AAA AGC TTG TTT TCG CAC AAA CAC      792
Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His
    210                 215                 220

TTT GTT TTT GGG GCT TGG GGA TCT TTT TTT ATG TGG GGG GAG AAN TGG      840
Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp
225                 230                 235                 240

CGA TTG GCT CAT TCT TGG TGC TAAGCTTTGA AAAGCTTTTG AATTTAGACT CTCA    895
Arg Leu Ala His Ser Trp Cys
                245

ATCAAGCGCG CATTAC                                                   911
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu
 1               5                  10                  15
Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro
            20                  25                  30
His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile
        35                  40                  45
Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly
```

```
    50                  55                  60
Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe
65                  70                  75                  80
Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe
                85                  90                  95
Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly
            100                 105                 110
Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser
        115                 120                 125
Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser
    130                 135                 140
Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser
145                 150                 155                 160
Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp
                165                 170                 175
Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu
            180                 185                 190
Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys
        195                 200                 205
Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His
    210                 215                 220
Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp
225                 230                 235                 240
Arg Leu Ala His Ser Trp Cys
                245
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3084 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 49...3027
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

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GAATTAATGC ATTAAATAAC TCAAAATTTT TGATCAAAGG CTTGAAAT ATG TCA AAA     57
                                                      Met Ser Lys
                                                       1

AAA ATT CCC CTA AAA AAC CGC TTG AGA GCT GAT TTT ACA AAA ACC CCA     105
Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr Lys Thr Pro
 5                  10                  15

ACA GAT TTA GAA GTC CCT AAT TTA TTA TTA TTA CAA CGA GAC AGC TAT     153
Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg Asp Ser Tyr
20                  25                  30                  35

GAT TCT TTC TTG TAT TCT AAA GAG GGT AAA GAG AGC GGG ATT GAA AAG     201
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Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly Ile Glu Lys
                 40                  45                  50

GTT TTT AAA TCC ATT TTC CCT ATC CAA GAT GAG CAT AAC CGC ATC ACT      249
Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn Arg Ile Thr
            55                  60                  65

TTA GAA TAC GCG GGT TGC GAA TTT GGC AAG TCT AAA TAC ACC GTT AGA      297
Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr Thr Val Arg
        70                  75                  80

GAA GCG ATG GAG AGG GGC ATT ACC TAC TCT ATC CCT CTC AAA ATT AAG      345
Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu Lys Ile Lys
    85                  90                  95

GTG CGC TTG ATC TTG TGG GAA AAA GAT ACC AAG AGT GGC GAA AAG AAC      393
Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly Glu Lys Asn
100                 105                 110                 115

GGC ATT AAG GAT ATT AAA GAA CAA AGC ATT TTC ATT CGT GAG ATC CCT      441
Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg Glu Ile Pro
                120                 125                 130

TTG ATG ACA GAA CGC ACT TCA TTT ATT ATT AAT GGG GTG GAG CGC GTG      489
Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val Glu Arg Val
            135                 140                 145

GTG GTC AAT CAA CTC CAC AGA AGC CCC GGT GTG ATT TTC AAA GAA GAA      537
Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe Lys Glu Glu
        150                 155                 160

GAG TCT AGC ACT TCT TTA AAC AAG CTC ATT TAC ACA GGG CAA ATC ATT      585
Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile
    165                 170                 175

CCT GAT AGG GGT TCG TGG TTG TAT TTT GAA TAC GAT TCT AAA GAT GTT      633
Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val
180                 185                 190                 195

TTA TAC GCT CGT ATC AAT AAA CGC CGT AAA GTG CCT GTT ACC ATT TTA      681
Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu
                200                 205                 210

TTC AGG GCG ATG GAT TAT CAA AAA CAA GAC ATC ATC AAA ATG TTC TAC      729
Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr
            215                 220                 225

CCG CTT GTT AAA GTG CGT TAT GAA AAC GAT AAA TAT TTG ATC CCG TTT      777
Pro Leu Val Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu Ile Pro Phe
        230                 235                 240

GCT TCA TTA GAC GCC AAT CAA AGA ATG GAA TTT GAC TTG AAA GAT CCT      825
Ala Ser Leu Asp Ala Asn Gln Arg Met Glu Phe Asp Leu Lys Asp Pro
    245                 250                 255

CAA GGC AAG GTT ATT CTT TTA GCG GGT AAA AAG CTC ACT TCA AGA AAG      873
Gln Gly Lys Val Ile Leu Leu Ala Gly Lys Lys Leu Thr Ser Arg Lys
260                 265                 270                 275
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ATT AAA GAG CTT AAA GAA AAC CAT TTA GAA TGG GTG GAA TAC CCT ATG      921
Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met
                280                 285                 290

GAT ATT TTA CTC AAT CGC CAT TTA GCT GAG CCT GTT ATG GTA GGG AAA      969
Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys
            295                 300                 305

GAA GTC TTA TTG GAC ATG CTC ACT CAG CTA GAT AAA AAC AAA TTA GAA     1017
Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu
        310                 315                 320

AAA ATC CAC GAT TTA GGC GTG CAA GAA TTT GTG ATC ATC AAC GAT CTG     1065
Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu
    325                 330                 335

GCG TTA GGG CAT GAC GCT TCC ATT ATC CAA TCT TTT TCA GCC GAT TCT     1113
Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser
340                 345                 350                 355

GAG TCT TTG AAA TTA CTC AAG CAA ACC GAA AAA ATT GAT GAT GAA AAC     1161
Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn
                360                 365                 370

GCT CTA GCG GCG ATT CGT ATC CAT AAG GTT ATG AAA CCA GGC GAT CCC     1209
Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro
            375                 380                 385

GTT ACG ACT GAA GTG GCT AAG CAG TTT GTC AAA AAA CTT TTC TTT GAT     1257
Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp
        390                 395                 400

CCA GAA CGC TAT GAT TTG ACC ATG GTG GGC CGC ATG AAA ATG AAT CAC     1305
Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His
    405                 410                 415

AAG TTA GGC TTG CAT GTG CCT GAT TAC ATT ACG ACT TTA ACG CAT GAA     1353
Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu
420                 425                 430                 435

GAT ATT ATC ACC ACC GTT AAA TAC CTC ATG AAG ATC AAA AAC AAT CAA     1401
Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn Gln
                440                 445                 450

GGC AAG ATT GAT GAC AGG GAC CAC TTG GGC AAT CGT AGG ATT AGG GCG     1449
Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg Ile Arg Ala
            455                 460                 465

GTA GGG GAA TTG TTG GCC AAT GAA TTG CAT TCA GGT TTA GTG AAA ATG     1497
Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu Val Lys Met
        470                 475                 480

CAA AAG ACC ATT AAA GAC AAG CTC ACT ACC ATG AGC GGG GCT TTT GAT     1545
Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly Ala Phe Asp
    485                 490                 495

TCG CTC ATG CCC CAT GAC TTG GTC AAT TCT AAA ATG ATC ACA AGC ACC     1593
Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile Thr Ser Thr
```

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500                 505                 510                 515

ATC ATG GAA TTT TTC ATG GGC GGT CAG CTC TCG CAA TTT ATG GAT CAA    1641
Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe Met Asp Gln
                520                 525                 530

ACG AAT CCC TTG AGT GAG GTT ACG CAC AAG CGC CGC CTT TCA GCG CTC    1689
Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu Ser Ala Leu
        535                 540                 545

GGC GAA GGG GGG TTG GTG AAA GAC AGA GTG GGG TTT GAA GCC AGG GAT    1737
Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu Ala Arg Asp
    550                 555                 560

GTG CAC CCC ACG CAT TAT GGC CGA ATT TGT CCC ATT GAG ACC CCA GAA    1785
Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu
565                 570                 575

GGT CAA AAT ATC GGT CTG ATC AAC ACC CTT TCC ACT TTC ACA AGA GTG    1833
Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe Thr Arg Val
580                 585                 590                 595

AAT GAT TTA GGC TTT ATT GAA GCC CCT TAT AAA AAG GTT GTG GAT GGC    1881
Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val Val Asp Gly
                600                 605                 610

AAG GTC GTG GGT GAG ACG ATT TAT TTG ACC GCT ATT CAA GAA GAC AGC    1929
Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln Glu Asp Ser
        615                 620                 625

CAC ATC ATC GCT CCC GCA AGC ACC CCC ATT GAT GAA GAG GGG AAT ATT    1977
His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu Gly Asn Ile
    630                 635                 640

TTG GGC GAT TTG ATT GAA ACG CGC GTG GAA GGC GAG ATC GTT TTA AAC    2025
Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile Val Leu Asn
645                 650                 655

GAA AAA AGC AAA GTA ACC TTA ATG GAT TTA AGC TCT AGC ATG CTA GTG    2073
Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser Met Leu Val
660                 665                 670                 675

GGG GTA GCC GCA TCG CTC ATT CCT TTC TTA GAG CAT GAT GAC GCC AAC    2121
Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn
                680                 685                 690

CGT GCC TTA ATG GGG ACT AAC ATG CAG CGC CAA GCG GTG CCC TTA TTA    2169
Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val Pro Leu Leu
        695                 700                 705

AGA AGC GAC GCT CCC ATT GTA GGC ACG GGG ATT GAA AAA ATT ATT GCT    2217
Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala
    710                 715                 720

AGG GAT TCT TGG GGA GCG ATC AAA GCC AAT CGC GCA GGC GTT GTA GAA    2265
Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu
725                 730                 735
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AAA ATT GAT TCT AAA AAT ATT TAT ATT TTA GGC GAA AGC AAA GAA GAA     2313
Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu
740                 745                 750                 755

GCC TAT ATT GAT GCG TAT TCT TTG CAA AAA AAC TTG CGC ACC AAC CAA     2361
Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln
                760                 765                 770

AAC ACC AGT TTC AAT CAA GTC CCT ATC GTT AAA GTG GGC GAT AAA GTG     2409
Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val
            775                 780                 785

GGA GCC GGG CAA ATC ATC GCT GAT GGC CCT AGC ATG GAT AGA GGC GAG     2457
Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu
        790                 795                 800

TTG GCG TTA GGG AAA AAT GTG CGC GTG GCG TTC ATG CCT TGG AAT GGC     2505
Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly
    805                 810                 815

TAT AAC TTT GAA GAC GCG ATC GTG GTG AGT GAG TGC ATC ACT AAA GAT     2553
Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp
820                 825                 830                 835

GAT ATT TTC ACT TCC ACC CAC ATT TAT GAA AAA GAA GTG GAT GCT AGG     2601
Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg
                840                 845                 850

GAG CTT AAG CAT GGT GTG GAA GAA TTT ACC GCT GAT ATT CCT GAT GTG     2649
Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val
            855                 860                 865

AAA GAA GAA GCG CTC GCT CAT CTT GAT GAA AGC GGG ATC GTT AAA GTC     2697
Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val
        870                 875                 880

GGT ACT TAT GTG AGC GCT GGC ATG ATT TTG GTG GGC AAA ACT TCT CCT     2745
Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro
    885                 890                 895

AAA GGC GAG ATT AAA AGC ACG CCT GAA GAG CGG CTT TTA AGG GCT ATT     2793
Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile
900                 905                 910                 915

TTT GGG GAT AAA GCC GGG CAT GTG GTC AAT AAG AGT TTG TAT TGC CCT     2841
Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro
                920                 925                 930

CCC AGT TTG GAA GGC ACG GTG ATT GAT GTG AAA GTC TTC ACT AAA AAA     2889
Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys
            935                 940                 945

GGC TAT GAG AAA GAC GCG CGA GTT TTG AGC GCG TAT GAA GAA GAA AAA     2937
Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys
        950                 955                 960

GCC AAG CTT GAT ATG GAG CAT TTT GAT CGC TTG ACC ATG CTC AAT AGA     2985
Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg
```

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    965                 970                 975

GAA GAA TTG TTG CGC GTT ACT CGC TCC TTT CTC AAG CGA TTT TAGAAGAGC  3036
Glu Glu Leu Leu Arg Val Thr Arg Ser Phe Leu Lys Arg Phe
980                 985                 990

CTTTCAGCCA TAACGGCAAG GATTATAAAG AAGGCGATCA AATCCCTA              3084
```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
Met Ser Lys Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr
 1               5                  10                  15
Lys Thr Pro Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg
            20                  25                  30
Asp Ser Tyr Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly
        35                  40                  45
Ile Glu Lys Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn
    50                  55                  60
Arg Ile Thr Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr
65                  70                  75                  80
Thr Val Arg Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu
                85                  90                  95
Lys Ile Lys Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly
            100                 105                 110
Glu Lys Asn Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg
        115                 120                 125
Glu Ile Pro Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val
    130                 135                 140
Glu Arg Val Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe
145                 150                 155                 160
Lys Glu Glu Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly
                165                 170                 175
Gln Ile Ile Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser
            180                 185                 190
Lys Asp Val Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val
        195                 200                 205
Thr Ile Leu Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys
    210                 215                 220
Met Phe Tyr Pro Leu Val Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu
225                 230                 235                 240
Ile Pro Phe Ala Ser Leu Asp Ala Asn Gln Arg Met Glu Phe Asp Leu
                245                 250                 255
Lys Asp Pro Gln Gly Lys Val Ile Leu Leu Ala Gly Lys Lys Leu Thr
            260                 265                 270
Ser Arg Lys Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu
        275                 280                 285
Tyr Pro Met Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met
```

290 295 300
Val Gly Lys Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn
305 310 315 320
Lys Leu Glu Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile
325 330 335
Asn Asp Leu Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser
340 345 350
Ala Asp Ser Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp
355 360 365
Asp Glu Asn Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro
370 375 380
Gly Asp Pro Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu
385 390 395 400
Phe Phe Asp Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys
405 410 415
Met Asn His Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu
420 425 430
Thr His Glu Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys
435 440 445
Asn Asn Gln Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg
450 455 460
Ile Arg Ala Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu
465 470 475 480
Val Lys Met Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly
485 490 495
Ala Phe Asp Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile
500 505 510
Thr Ser Thr Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe
515 520 525
Met Asp Gln Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu
530 535 540
Ser Ala Leu Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu
545 550 555 560
Ala Arg Asp Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu
565 570 575
Thr Pro Glu Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe
580 585 590
Thr Arg Val Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val
595 600 605
Val Asp Gly Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln
610 615 620
Glu Asp Ser His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu
625 630 635 640
Gly Asn Ile Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile
645 650 655
Val Leu Asn Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser
660 665 670
Met Leu Val Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp
675 680 685
Asp Ala Asn Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val
690 695 700
Pro Leu Leu Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys
705 710 715 720
Ile Ile Ala Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly
725 730 735
Val Val Glu Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser
740 745 750
Lys Glu Glu Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg

```
        755                 760                 765
Thr Asn Gln Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly
    770                 775                 780
Asp Lys Val Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp
785                 790                 795                 800
Arg Gly Glu Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro
                805                 810                 815
Trp Asn Gly Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile
            820                 825                 830
Thr Lys Asp Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val
        835                 840                 845
Asp Ala Arg Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile
    850                 855                 860
Pro Asp Val Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile
865                 870                 875                 880
Val Lys Val Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys
                885                 890                 895
Thr Ser Pro Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu
            900                 905                 910
Arg Ala Ile Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu
        915                 920                 925
Tyr Cys Pro Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe
    930                 935                 940
Thr Lys Lys Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu
945                 950                 955                 960
Glu Glu Lys Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met
                965                 970                 975
Leu Asn Arg Glu Glu Leu Leu Arg Val Thr Arg Ser Phe Leu Lys Arg
            980                 985                 990
Phe
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 49...525
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
AGGTTAAAGT TTAAGACAAA CCAAAGAGTT TGTCTTGTTT GTTTTTGA ATG CAC TCT      57
                                                      Met His Ser
                                                       1

CCA AAT TTA GAA AAA GAA GAA ACC GAA ATC ATA GAA ACA CTC CTT ATG      105
Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr Leu Leu Met
 5                  10                  15
```

```
CGT GAA AAA ATG CGT TTA TGC CCC TTG TAT TGG CGC ATC TTA GCG TTT      153
Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile Leu Ala Phe
20                  25                  30                  35

TTA ACC GAT GGT TTG TTA GTG GCG TTT TTA TTG AGC GAT CTT TTA GAC      201
Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp Leu Leu Asp
                40                  45                  50

GCA TGC GAT TTC TTG CAT TCT TTA TAT TGG CTA GCT AAC CCT ATT TAT      249
Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn Pro Ile Tyr
            55                  60                  65

CAC AGC GCA TTT GTT GCG ATG GGT TTT ATC ATC TTG TAT GGC GTT TAT      297
His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr Gly Val Tyr
        70                  75                  80

GAA ATC TTT TTT GTG TGT TTG TGC AAG ATG AGC TTG GCT AAA CTG GTT      345
Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala Lys Leu Val
    85                  90                  95

TTT AGG ATT AAG ATT ATT GAT ATT TAT TTG GCA GAT TGC CCC AGT AGG      393
Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys Pro Ser Arg
100                 105                 110                 115

GCT ATT TTA TTG AAG CGT TTA GGG TTA AAG ATC GTG GTT TTT CTA TGC      441
Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val Phe Leu Cys
                120                 125                 130

CCC TTT TTA TGG TTT GTT GCG TTT AAA AAC CCC TAT CAT AGG GCG TGG      489
Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His Arg Ala Trp
            135                 140                 145

CAT GAA GAA AAA AGC AAA AGT CTT TTG GTA TTG TTT TAATCATGAT TTATTG    541
His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe
        150                 155

GTTGTATTTG GCGGTCTTTT TTTTGTTGAG CGCATTAGAC                          581
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr
 1               5                  10                  15
Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile
            20                  25                  30
Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp
        35                  40                  45
Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn
```

```
    50                  55                  60
Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr
65                  70                  75                  80
Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala
                85                  90                  95
Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys
            100                 105                 110
Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val
        115                 120                 125
Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His
    130                 135                 140
Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 901 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 67...852
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
GAATTTAAGC GGCAGAGGGG ATAAGGATTT AAGCACCGTT TATAACGCTT TAAAAGGAGG    60
TTTAAA ATG AGG TAT CAA AAC ATG TTT GAA ACC TTA AAA AAA CAC GAA       108
       Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu
        1               5                   10

AAA ATG GCG TTT ATC CCG TTT GTA ACC TTG GGC GAT CCT AAT TAT GAA     156
Lys Met Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu
15                  20                  25                  30

TTG AGT TTT GAA ATC ATT AAA ACC CTA ATT ATT AGC GGG GTG AGC GCT     204
Leu Ser Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala
                35                  40                  45

TTA GAA TTG GGT CTT GCT TTT TCT GAT CCT GTG GCG GAT GGC ATT ACC     252
Leu Glu Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr
            50                  55                  60

ATA CAA GCG AGC CAT TTA AGG GCG TTA AAA CAC GCT AGC ATG GCT AAA     300
Ile Gln Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys
        65                  70                  75

AAT TTC CAG CTT TTA AAA AAG ATT AGA GAT TAC AAC CAC AAT ATT CCC     348
Asn Phe Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro
    80                  85                  90
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ATA GGG CTT TTA GCG TAT GCG AAT TTA ATT TTT TCT TAT GGC GTT GAT      396
Ile Gly Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp
95                  100                 105                 110

GGC TTT TAC GCT CAA GCT AAA GAA TGC GGT ATA GAT AGC GTT TTA ATA      444
Gly Phe Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile
                115                 120                 125

GCG GAC ATG CCC CTA ATA GAA AAA GAA TTA GTC ATC AAA TCC GCT CAA      492
Ala Asp Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln
            130                 135                 140

AAA CAC CAA ATC AAG CAA ATC TTT ATC GCC AGC CCC AAT GCG AGC AGT      540
Lys His Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser
        145                 150                 155

AAA GAT TTA GAA CAA GTC GCT ACG CAT TCG CAA GGC TAT ATC TAC GCT      588
Lys Asp Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala
    160                 165                 170

TTA GCC AGG AGT GGG GTT ACA GGG GCG AGC CGT ATT TTA GAG AAT GAT      636
Leu Ala Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp
175                 180                 185                 190

TCG AGT GCT ATT ATT AAA ACC TTA AAA GCT TTT AGC CCT ACC CCA GCC      684
Ser Ser Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala
                195                 200                 205

TTA CTG GGC TTT GGC ATT TCC AAA AAA GAA CAC ATC ACA AAC GCT AAA      732
Leu Leu Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys
            210                 215                 220

GGC ATG GGT GCT GAT GGC GTG ATT TGC GGA TCA GCG TTA GTC AAA ATC      780
Gly Met Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile
        225                 230                 235

ATA GAA GAA AAT TTA AAC AAT GAA AAC GCC ATG CTG GAA AAA ATT AAA      828
Ile Glu Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys
    240                 245                 250

GGG TTT ATA GGA GGA ATG ATT TTT TAAGGCTTTT AGGCTTTGTT GCGTTAAAAA     882
Gly Phe Ile Gly Gly Met Ile Phe
255                 260

TTAAAGATCA CAGATTAAC                                                901
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu Lys Met
 1               5                  10                  15
Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu Leu Ser
            20                  25                  30
Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala Leu Glu
        35                  40                  45
Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr Ile Gln
    50                  55                  60
Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys Asn Phe
65                  70                  75                  80
Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro Ile Gly
                85                  90                  95
Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp Gly Phe
            100                 105                 110
Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile Ala Asp
        115                 120                 125
Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln Lys His
    130                 135                 140
Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser Lys Asp
145                 150                 155                 160
Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala Leu Ala
                165                 170                 175
Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp Ser Ser
            180                 185                 190
Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala Leu Leu
        195                 200                 205
Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys Gly Met
    210                 215                 220
Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile Ile Glu
225                 230                 235                 240
Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys Gly Phe
                245                 250                 255
Ile Gly Gly Met Ile Phe
            260
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 49...954
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
AAGTAATGCC CCTGTTGTAT CAGCTTGATT TAAGAGGAAT AAGTTATT ATG AAT AAA     57
                                                     Met Asn Lys
                                                      1

GCT ATT GCT AGT AAG ATA CTC ATC ACT TTG GGT TTT TTA TTT CTC TAC     105
```

```
Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu Phe Leu Tyr
     5                  10                  15

AGA GTC TTA GCT TAT ATC CCC ATT CCT GGC GTA GAT TTA GCA GCG ATC      153
Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu Ala Ala Ile
20                  25                  30                  35

AAG GCT TTT TTT GAC AGC AAT TCC AAC AAC GCT TTG GGG TTG TTT AAT      201
Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly Leu Phe Asn
                40                  45                  50

ATG TTT AGC GGG AAT GCG GTT TCT CGC TTG AGC ATC ATC TCG TTG GGT      249
Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile Ser Leu Gly
            55                  60                  65

ATC ATG CCC TAT ATC ACT TCT TCA ATT ATC ATG GAG CTT TTG AGC GCG      297
Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu Leu Ser Ala
        70                  75                  80

ACT TTC CCT AAC CTG GCT AAA ATG AAA AAA GAG CGG GAT GGC ATG CAA      345
Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp Gly Met Gln
    85                  90                  95

AAA TAC ATG CAA ATC GTG CGT TAT TTG ACC ATT TTA ATC ACC CTA ATC      393
Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile Thr Leu Ile
100                 105                 110                 115

CAA GCG GTG AGC GTT TCA GTA GGC TTA AGG AGC ATT AGT GGA GGA GCC      441
Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser Gly Gly Ala
                120                 125                 130

AAT GGG GCG ATC ATG ATT GAT ATG CAA GTT TTT ATG ATC GTT TCA GCG      489
Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile Val Ser Ala
            135                 140                 145

TTT TCT ATG CTT ACA GGA ACG ATG CTA CTC ATG TGG ATA GGG GAG CAA      537
Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile Gly Glu Gln
        150                 155                 160

ATC ACG CAA AGG GGC GTG GGG AAT GGG ATC AGT CTC ATT ATT TTT GCC      585
Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile Ile Phe Ala
    165                 170                 175

GGG ATT GTT TCA GGG ATC CCA TCA GCT ATT TCA GGC ACA TTC AAT TTG      633
Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr Phe Asn Leu
180                 185                 190                 195

GTC AAT ACG GGC GTT ATT AAT ATC TTA ATG CTC ATT GGT ATT GTG CTG      681
Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly Ile Val Leu
                200                 205                 210

ATT GTT TTA GCG ACT ATT TTT GCG ATT ATC TAT GTG GAA TTA GCT GAG      729
Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu Leu Ala Glu
            215                 220                 225

CGC AGG ATC CCT ATT TCT TAT GCG CGT AAA GTG GTG ATG CAA AAC CAA      777
Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met Gln Asn Gln
        230                 235                 240
```

```
AAC AAG CGC ATC ATG AAT TAC ATT CCT ATT AAG TTG AAT TTA AGT GGG      825
Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn Leu Ser Gly
    245                 250                 255

GTG ATC CCC CCT ATT TTC GCT TCA GCT TTG CTC GTG TTC CCT TCT ACG      873
Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe Pro Ser Thr
260                 265                 270                 275

ATT TTG CAG CAA GCC ACA AGC AAC AAA ACC TTG CAA GCG GTT GCG NAT      921
Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala Val Ala Xaa
                280                 285                 290

TTT TTA AGC CCG CAA GGT ATG CGT ATA ATA TTT TGATGTTCTT GCTCATCATC     974
Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe
            295                 300

TTTTTTGCTT ACTTTTATTC TTCTATTGTG TTCAATTCTA AGGATATTGC GGATAATTTG    1034
AGGCGTAATG GCGGGTATAT TCCAGGGCTT AGGCCTGGAG AGGGGAC                  1081
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
Met Asn Lys Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu
 1               5                  10                  15
Phe Leu Tyr Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu
            20                  25                  30
Ala Ala Ile Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly
        35                  40                  45
Leu Phe Asn Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile
    50                  55                  60
Ser Leu Gly Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu
65                  70                  75                  80
Leu Ser Ala Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp
                85                  90                  95
Gly Met Gln Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile
            100                 105                 110
Thr Leu Ile Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser
        115                 120                 125
Gly Gly Ala Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile
    130                 135                 140
Val Ser Ala Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile
145                 150                 155                 160
Gly Glu Gln Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile
                165                 170                 175
Ile Phe Ala Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr
            180                 185                 190
Phe Asn Leu Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly
        195                 200                 205
```

```
Ile Val Leu Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu
    210                 215                 220
Leu Ala Glu Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met
225                 230                 235                 240
Gln Asn Gln Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn
                245                 250                 255
Leu Ser Gly Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe
            260                 265                 270
Pro Ser Thr Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala
        275                 280                 285
Val Ala Xaa Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 109...363
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
AATGGGGCAA TTCAAGGCGA TAGAAGCTTG AATGAGGGCT TCTTCTAAGG TTTTGGCTTT     60
GATTTCAATA AAATTTTGCA TCAATGTTCC TTTTTGTTTT GCGCATGC ATG CGT TTT    117
                                                      Met Arg Phe
                                                       1

TTA TTC TCT AAG ACT TTA TTG ATG ATG AGT TGT TGC AAC ACC GAA AGG     165
Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn Thr Glu Arg
 5                  10                  15

ATG TTG TTC GTG GTC CAA TAC AAG ACT AAC CCT GCC GGG AAA GTG ATT     213
Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly Lys Val Ile
20                  25                  30                  35

AAA AAG ATT GTG AAT AAT AGG GGT AAG AGT TTA AAA ATC TTT GCT TGC     261
Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile Phe Ala Cys
                40                  45                  50

ATG GGA TCG GTC ATG GTG TTT GGC GTA ACG CTT TGG TGC CAA TAC ATA     309
Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys Gln Tyr Ile
            55                  60                  65

GAC GCT CCC ATA AGA AGC GGT AAA ATA AAA TAC GGA TCC ATG ATG GAT     357
Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser Met Met Asp
        70                  75                  80

AAA TCA TGAATCCATA AGATCCACTC TGAGCTTTTC AATTCCACAG CGTTATAAAG CA   415
Lys Ser
```

85

CTCTATAA 423

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
Met Arg Phe Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn
 1               5                  10                  15
Thr Glu Arg Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly
            20                  25                  30
Lys Val Ile Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile
        35                  40                  45
Phe Ala Cys Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys
    50                  55                  60
Gln Tyr Ile Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser
65                  70                  75                  80
Met Met Asp Lys Ser
                85
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 59...688
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
TTTAAAATTA GAAACAGATG TATCTGTTTT AAATTTTGAA TAGGGAGTTT CTATCATT      58

ATG TTA TTG AAA ACA AAA TTA AAA ATT ATA AGC TCG GTG ATT TTG AGC      106
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser
 1               5                  10                  15

GCT TTA TTG TGG GTG GGT TGC TCA AGC GAA ATG GCA ACT TAT CAA AAC      154
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn
```

```
                20                  25                  30

GTG AAT GAT GCC ACT AAA AAT ACG ACT GCA AGC ATT AAT AGC ACG GAT      202
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp
        35                  40                  45

TTA TTG CTA ACC GCT AAC GCG ATG TTA GAT TCC ATG TTT AGC GAC CCT      250
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro
    50                  55                  60

AAT TTT GAG CAA CTC AAG GGC AAG CAT TTG ATT GAA GTT TCA GAT GTG      298
Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val
65                  70                  75                  80

ATT AAC GAC ACC ACG CAG CCC AAT TTG GAC ATG AAT CTT TTG ACG ACT      346
Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr
                85                  90                  95

GAA ATC GCG CGG CAG TTG CGG TTG CGA TCT AAT GGG AGG TTC AAT ATC      394
Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile
            100                 105                 110

ACA AGG GCG AGC GGA GGG AGT GGC ATT GCA GCC GAT AGC AGA ATG GTG      442
Thr Arg Ala Ser Gly Gly Ser Gly Ile Ala Ala Asp Ser Arg Met Val
        115                 120                 125

AAA CAG CGC GAA AAA GAA CGA GAG AGC GAA GAG TAT AAT CAA GAC ACC      490
Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr
    130                 135                 140

ACT GTA GAA AAA GGC ACT TTA AAA GCC GCT GAT TTA TCT TTA AGT GGT      538
Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly
145                 150                 155                 160

AAA GTA TCT AGT ATC GCA GCC TCT ATT AGT AGT TCT AGG CAG CGC TTG      586
Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu
                165                 170                 175

GAC TAT GAC TTC ACC CTA AGC CTT ACC AAC AGG AAA ACG GGT GAA GAG      634
Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu
            180                 185                 190

GTA TGG AGC GAT GTT AAG CCT ATT GTG AAG AAC GCT AGC AAT AAG CGT      682
Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg
        195                 200                 205

ATG TTT TAAATTTATA TTTGAAAGGA TGAACAATGA AAAATCAAGT TAAAAAAATT TT    740
Met Phe
    210
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser
 1               5                  10                  15
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn
            20                  25                  30
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp
        35                  40                  45
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro
    50                  55                  60
Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val
65                  70                  75                  80
Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr
                85                  90                  95
Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile
            100                 105                 110
Thr Arg Ala Ser Gly Gly Ser Gly Ile Ala Ala Asp Ser Arg Met Val
        115                 120                 125
Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr
    130                 135                 140
Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly
145                 150                 155                 160
Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu
                165                 170                 175
Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu
            180                 185                 190
Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg
        195                 200                 205
Met Phe
    210
```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 84...1214
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
TTATCATTGT GTTAAAATAG TCGTTTTAAC AAACAAAATT TTGTTAATAG ATTTTACCTA    60
ATCTGAGAGA GAATTATATT TTA ATG AAG ACA GAG AAA CAA AAA TTT TTA GAG   113
                          Met Lys Thr Glu Lys Gln Lys Phe Leu Glu
                           1               5                  10
```

```
ATG CGT AAA GAT GGG GCG AAC TCT GTG CTG ATT TTA AGA GGG GAT TGG      161
Met Arg Lys Asp Gly Ala Asn Ser Val Leu Ile Leu Arg Gly Asp Trp
                15                  20                  25

GAT TTT AAA ACG AGC GTG TTT CGT TTA GAT GAG TTG AAA AAA AAT TTA      209
Asp Phe Lys Thr Ser Val Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu
            30                  35                  40

TTA GAT CAT CAA GGG CCT TTA AAA ATG GAT TTT TCA GGG TGC CAA AAA      257
Leu Asp His Gln Gly Pro Leu Lys Met Asp Phe Ser Gly Cys Gln Lys
        45                  50                  55

GTG GAT TTT GTT TTT GGC ATG TTT TTA TTT GAT TTA GTT AAG GAG CGT      305
Val Asp Phe Val Phe Gly Met Phe Leu Phe Asp Leu Val Lys Glu Arg
    60                  65                  70

TCT TTA AAC ATT GAA TTG TGT AAC GTG AGT GAG AAT AAC GCA TGC GCT      353
Ser Leu Asn Ile Glu Leu Cys Asn Val Ser Glu Asn Asn Ala Cys Ala
75                  80                  85                  90

TTG AAA GTG GTT AAA GAC TGG CTT GAA AAA GAA GAG GAT TTA GAG TCT      401
Leu Lys Val Val Lys Asp Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser
                95                  100                 105

AAA AAA GCG GGC AAA CAC TAC GAA CTT TTG ATC ACT AAA TTG GGT AAG      449
Lys Lys Ala Gly Lys His Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys
            110                 115                 120

AGT ATC GTA GAG ACT TAT AAT ACC TTT TTA AAC GCA TTC AAT TTT TGC      497
Ser Ile Val Glu Thr Tyr Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys
        125                 130                 135

GGC ATG ATT TTA TTC TAC TTC ATT AAA AGC GTT TTC AAC CCC AAA CGC      545
Gly Met Ile Leu Phe Tyr Phe Ile Lys Ser Val Phe Asn Pro Lys Arg
    140                 145                 150

TTT TGT ATC ACT CCT TTG CTC TAT CAT ATC AAT GAA TCC GGG TTT AAG      593
Phe Cys Ile Thr Pro Leu Leu Tyr His Ile Asn Glu Ser Gly Phe Lys
155                 160                 165                 170

GTT TTG CCA GTG AGT ATT TTA ACG GTG TTT ATC GTG GGG TTT GCC GTT      641
Val Leu Pro Val Ser Ile Leu Thr Val Phe Ile Val Gly Phe Ala Val
                175                 180                 185

GCT TTA CAA GGG GCT TTA CAA TTA CAA GAC ATG GGC GCG CCT TTA ATG      689
Ala Leu Gln Gly Ala Leu Gln Leu Gln Asp Met Gly Ala Pro Leu Met
            190                 195                 200

TCG GTG GAA ATG ACG GCT AAA CTC GCT TTA AGA GAA ATC GGC CCT TTT      737
Ser Val Glu Met Thr Ala Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe
        205                 210                 215

ATT TTA ACC CTT GTG GTG GCC GGG AGG AGC GCG AGC AGT TTT ACC GCG      785
Ile Leu Thr Leu Val Val Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala
    220                 225                 230

CAA ATT GGG GTG ATG AAG ATC ACT GAG GAA TTA GAC GCG ATG AAA ACC      833
Gln Ile Gly Val Met Lys Ile Thr Glu Glu Leu Asp Ala Met Lys Thr
```

```
235                 240                 245                 250

ATG GGC TTT AAC CCT TTT GAA TTT TTA GTG TTG CCT AGG GTG TTA GCC      881
Met Gly Phe Asn Pro Phe Glu Phe Leu Val Leu Pro Arg Val Leu Ala
                255                 260                 265

TTA GTG ATT GTT TTG CCT TTA TTG GTG TTT ATT GCC GAT GCG TTC GCC      929
Leu Val Ile Val Leu Pro Leu Leu Val Phe Ile Ala Asp Ala Phe Ala
            270                 275                 280

ATT CTT GGG GGC ATG TTT GCG ATT AAA TAC CAA TTG GAT TTA GGC TTC      977
Ile Leu Gly Gly Met Phe Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe
        285                 290                 295

CCG AGC TAT ATT GAC AGA TTC CAT GAC ACA GTG GGT TGG AAC CAT TTT     1025
Pro Ser Tyr Ile Asp Arg Phe His Asp Thr Val Gly Trp Asn His Phe
    300                 305                 310

TTG GTA GGG ATT GTC AAA GCC CCT TTT TGG GGG TTT GCG ATT GCG ATG     1073
Leu Val Gly Ile Val Lys Ala Pro Phe Trp Gly Phe Ala Ile Ala Met
315                 320                 325                 330

GTA GGG TGC ATG CGC GGG TTT GAA GTC AAG GGG GAT ACT GAG AGC ATT     1121
Val Gly Cys Met Arg Gly Phe Glu Val Lys Gly Asp Thr Glu Ser Ile
                335                 340                 345

GGG CGC TTG ACC ACT ATT AGC GTC GTG AAC GCT TTG TTT TGG ATC ATT     1169
Gly Arg Leu Thr Thr Ile Ser Val Val Asn Ala Leu Phe Trp Ile Ile
            350                 355                 360

TTC TTA GAC GCT ATT TTT TCT ATC ATC TTT TCT AAG TTG AAC ATA TAATG   1219
Phe Leu Asp Ala Ile Phe Ser Ile Ile Phe Ser Lys Leu Asn Ile
        365                 370                 375

AACGCTACTA ACAATCAAGT CTTAATTGAA GTGAAGGATC TCCATAGCGC              1269
```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
Met Lys Thr Glu Lys Gln Lys Phe Leu Glu Met Arg Lys Asp Gly Ala
 1               5                  10                  15
Asn Ser Val Leu Ile Leu Arg Gly Asp Trp Asp Phe Lys Thr Ser Val
            20                  25                  30
Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu Leu Asp His Gln Gly Pro
        35                  40                  45
Leu Lys Met Asp Phe Ser Gly Cys Gln Lys Val Asp Phe Val Phe Gly
    50                  55                  60
Met Phe Leu Phe Asp Leu Val Lys Glu Arg Ser Leu Asn Ile Glu Leu
```

```
65                  70                  75                  80
Cys Asn Val Ser Glu Asn Asn Ala Cys Ala Leu Lys Val Val Lys Asp
                85                  90                  95
Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser Lys Lys Ala Gly Lys His
            100                 105                 110
Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys Ser Ile Val Glu Thr Tyr
        115                 120                 125
Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys Gly Met Ile Leu Phe Tyr
    130                 135                 140
Phe Ile Lys Ser Val Phe Asn Pro Lys Arg Phe Cys Ile Thr Pro Leu
145                 150                 155                 160
Leu Tyr His Ile Asn Glu Ser Gly Phe Lys Val Leu Pro Val Ser Ile
                165                 170                 175
Leu Thr Val Phe Ile Val Gly Phe Ala Val Ala Leu Gln Gly Ala Leu
            180                 185                 190
Gln Leu Gln Asp Met Gly Ala Pro Leu Met Ser Val Glu Met Thr Ala
        195                 200                 205
Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe Ile Leu Thr Leu Val Val
    210                 215                 220
Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala Gln Ile Gly Val Met Lys
225                 230                 235                 240
Ile Thr Glu Glu Leu Asp Ala Met Lys Thr Met Gly Phe Asn Pro Phe
                245                 250                 255
Glu Phe Leu Val Leu Pro Arg Val Leu Ala Leu Val Ile Val Leu Pro
            260                 265                 270
Leu Leu Val Phe Ile Ala Asp Ala Phe Ala Ile Leu Gly Gly Met Phe
        275                 280                 285
Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe Pro Ser Tyr Ile Asp Arg
    290                 295                 300
Phe His Asp Thr Val Gly Trp Asn His Phe Leu Val Gly Ile Val Lys
305                 310                 315                 320
Ala Pro Phe Trp Gly Phe Ala Ile Ala Met Val Gly Cys Met Arg Gly
                325                 330                 335
Phe Glu Val Lys Gly Asp Thr Glu Ser Ile Gly Arg Leu Thr Thr Ile
            340                 345                 350
Ser Val Val Asn Ala Leu Phe Trp Ile Ile Phe Leu Asp Ala Ile Phe
        355                 360                 365
Ser Ile Ile Phe Ser Lys Leu Asn Ile
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 60...503
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
CACAAGAGAA AATTTGCAAG CGTTTTTACA ACAAAATAAG ATAAATTAGG GAGAGTGGT     59

ATG GGA TTT TTG AAT GGG TAT TTT TTA TGG GTT AAG GCT TTC CAT GTG      107
Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1               5                  10                  15

ATA GCG GTC ATT TCG TGG ATG GCA GCG TTG TTT TAT TTG CCG CGC CTT      155
Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
            20                  25                  30

TTT GTC TAT CAT GCA GAA AAC GCG CAT AAA AAA GAG TTT GTA GGA GTG      203
Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
        35                  40                  45

GTT CAA ATC CAA GAA AAA AAG CTT TAT TCC TTT ATC GCT TCA CCG GCT      251
Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
    50                  55                  60

ATG GGT TTT ACG CTT ATT ACA GGG ATT TTA ATG CTG TTG ATA GAG CCT      299
Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
65                  70                  75                  80

ACG CTC TTT AAA AGT GGG GGT TGG TTG CAT GCT AAA TTG GCT TTA GTG      347
Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
                85                  90                  95

GTT TTA CTT TTA GCC TAT CAT TTT TAT TGC AAA AAA TGC ATG CGC GAG      395
Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
            100                 105                 110

CTG GAA AAA GAC CCC ACA AGG AGA AAC GCA AGG TTT TAT CGC GTG TTT      443
Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe
        115                 120                 125

AAT GAG GCG CCA ACG ATT TTA ATG ATC CTC ATT GTG ATT TTA GTG GTT      491
Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
    130                 135                 140

GTC AAG CCT TTT TAAAGACAAG CCATGAAAAA AGAAAAGTCA TGAAAAAAGA AAAGCA   549
Val Lys Pro Phe
145

TCTCAAGC                                                            557
```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1               5                  10                  15
Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
            20                  25                  30
Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
        35                  40                  45
Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
    50                  55                  60
Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
65                  70                  75                  80
Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
                85                  90                  95
Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
            100                 105                 110
Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe
        115                 120                 125
Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
    130                 135                 140
Val Lys Pro Phe
145
```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...1624
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
CAAAATTATC TGGTGCTAAG ACTTTGAAAC AACGCCAAAT AACAACTGA ATG AAA CTT     58
                                                      Met Lys Leu
                                                       1

TTT AAC GCT CGT TTA ATC GTT TTT ATT GGC GCG CTT CTT TTA GGG GTA      106
Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu Leu Gly Val
     5                  10                  15

GGG TTT TCT GTG CCT TCT TTA CTA GAA ACT AAA GGC CCT AAA ATC ACT      154
Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro Lys Ile Thr
20                  25                  30                  35

TTA GGT TTG GAT TTA AGG GGG GGG TTG AAC ATG CTT TTA GGG GTA CAA      202
Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu Gly Val Gln
                40                  45                  50

ACC GAT GAG GCT TTA AAA AAC AAG TAT TTA AGC TTG GCG TCC GCT TTA      250
Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala Ser Ala Leu
```

```
                55                  60                  65

GAA TAC AAC GCT AAA AAG CAA AAT ATC TTG CTT AAA GAT ATT AAA TCC     298
Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp Ile Lys Ser
        70                  75                  80

AAT TTA GAA GGG ATC AGT TTT GAG CTT TTA GAT GAA GAT GAA GCG AAA     346
Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp Glu Ala Lys
    85                  90                  95

AAA TTA GAC GCG CTT TTA TTG GAA TTG CAA GGC CAT AGC CAG TTT GAA     394
Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser Gln Phe Glu
100                 105                 110                 115

ATC AAA AAG GAA GCG GGG TTT TAT AGC GTG AAT CTC ACC CCT TTA GAG     442
Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr Pro Leu Glu
                120                 125                 130

CAA GAA GAA TTG CGT AAA AAC ACG ATT TTG CAA GTG ATA GGG ATC ATT     490
Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile Gly Ile Ile
            135                 140                 145

CGT AAC CGC TTG GAT CAA TTT GGT TTG GCA GAG CCT GTA GTC ATT CAG     538
Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val Val Ile Gln
        150                 155                 160

CAA GGT AAA GAA GAA ATT TCG GTG CAA TTG CCT GGC ATT AAG ACT TTA     586
Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile Lys Thr Leu
    165                 170                 175

GAA GAA GAA CGG CGC GCT AAA GAC TTG ATT TCA AGA TCC GCT CAT TTG     634
Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser Ala His Leu
180                 185                 190                 195

CAG ATG ATG GCG GTG GAT GAA GAA CAC AAT AAA GAT GCG ATG AAA ATG     682
Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala Met Lys Met
                200                 205                 210

ACG GAT TTA GAG GCT CAA AAA TTA GGC AGC GTG TTG TTG TCT GAT GTG     730
Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu Ser Asp Val
            215                 220                 225

GAA ATG GGG GGT AAA ATC TTG CTC AAA GCG ATC CCC ATT TTA GAT GGC     778
Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile Leu Asp Gly
        230                 235                 240

GAA ATG CTT ACA GAT GCG AAA GTG GTG TAT GAC CAA AAC AAC CAG CCG     826
Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn Asn Gln Pro
    245                 250                 255

GTG GTG AGC TTC ACG CTG GAT GCG CAA GGG GCT AAG ATT TTT GGG GAT     874
Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile Phe Gly Asp
260                 265                 270                 275

TTC TCA GGT GCG AAT GTG GGC AAA CGC ATG GCG ATT GTT TTA GAC AAT     922
Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val Leu Asp Asn
                280                 285                 290
```

```
AAG GTC TAT TCA GCC CCG GTG ATT AGG GAG CGT ATC GGT GGG GGG AGC      970
Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly Gly Gly Ser
            295                 300                 305

GGG CAG ATT AGC GGG AAT TTT AGC GTG GCT CAA GCG AGC GAT TTA GCG     1018
Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser Asp Leu Ala
        310                 315                 320

ATC GCT TTA AGG AGT GGG GCG ATG AGC GCT CCC ATT CAG GTT TTA GAA     1066
Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln Val Leu Glu
    325                 330                 335

AAA AGA ATT ATA GGC CCA AGT TTA GGG AAA GAC AGC GTT AAA ACT TCC     1114
Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val Lys Thr Ser
340                 345                 350                 355

ATT ATC GCT CTA GTT GGG GGC TTT ATT TTA GTG ATG GGC TTT ATG GTG     1162
Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly Phe Met Val
                360                 365                 370

CTT TAT TAC TCT ATG GCG GGG GTG ATC GCT TGT TTG GCG TTA GTG GTC     1210
Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala Leu Val Val
            375                 380                 385

AAT CTT TTT TTG ATT GTG GCG GTC ATG GCG ATT TTT GGA GCG ACG CTG     1258
Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly Ala Thr Leu
        390                 395                 400

ACT TTA CCG GGA ATG GCG GGG ATT GTT TTA ACC GTG GGG ATT GCC GTG     1306
Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly Ile Ala Val
    405                 410                 415

GAT GCT AAT ATC ATC ATC AAC GAG CGC ATT AGA GAA GTC TTA AGA GAG     1354
Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val Leu Arg Glu
420                 425                 430                 435

AAT GAG GGC ATC GCT AAA GCG ATC CAT TTA GGC TAT ATC AAT GCG AGC     1402
Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile Asn Ala Ser
                440                 445                 450

CGG GCG ATT TTT GAT TCT AAT ATC ACT TCT TTG ATC GCT TCA GTG TTA     1450
Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala Ser Val Leu
            455                 460                 465

TTA TAC GCT TAT GGC ACA GGA GCG ATT AAA GGC TTT GCC CTA ACT ACA     1498
Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala Leu Thr Thr
        470                 475                 480

GGC ATT GGG ATT TTA GCC TCT ATT ATC ACC GCT ATT GTT GGC ACG CAA     1546
Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val Gly Thr Gln
    485                 490                 495

GGG ATT TAT CAA GCC CTT TTA CCT AAA CTC ACT CAA ACA AAA AGC CTT     1594
Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr Lys Ser Leu
500                 505                 510                 515

TAC TTT TGG TTT GGC GTG AAT AAA AGA GCT TAGGAGGTTT TATGGAATTA TTC  1647
Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala
```

520 525

AAACGAACTA GAATCTTAAG CTTC 1671

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
Met Lys Leu Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu
 1               5                  10                  15
Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro
            20                  25                  30
Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu
        35                  40                  45
Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala
    50                  55                  60
Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp
65                  70                  75                  80
Ile Lys Ser Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp
                85                  90                  95
Glu Ala Lys Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser
            100                 105                 110
Gln Phe Glu Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr
        115                 120                 125
Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile
    130                 135                 140
Gly Ile Ile Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val
145                 150                 155                 160
Val Ile Gln Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile
                165                 170                 175
Lys Thr Leu Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser
            180                 185                 190
Ala His Leu Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala
        195                 200                 205
Met Lys Met Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu
    210                 215                 220
Ser Asp Val Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile
225                 230                 235                 240
Leu Asp Gly Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn
                245                 250                 255
Asn Gln Pro Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile
            260                 265                 270
Phe Gly Asp Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val
        275                 280                 285
Leu Asp Asn Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly
    290                 295                 300
Gly Gly Ser Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser
305                 310                 315                 320
Asp Leu Ala Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln
```

```
                325                 330                 335
Val Leu Glu Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val
            340                 345                 350
Lys Thr Ser Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly
        355                 360                 365
Phe Met Val Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala
    370                 375                 380
Leu Val Val Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly
385                 390                 395                 400
Ala Thr Leu Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly
                405                 410                 415
Ile Ala Val Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val
            420                 425                 430
Leu Arg Glu Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile
        435                 440                 445
Asn Ala Ser Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala
    450                 455                 460
Ser Val Leu Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala
465                 470                 475                 480
Leu Thr Thr Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val
                485                 490                 495
Gly Thr Gln Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr
            500                 505                 510
Lys Ser Leu Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala
        515                 520                 525
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 64...654
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
CAGGGGGCAA GGGGGCTGTT AGGGAAGCGA TTGATTATCT TTTAACATTA GAAGGCTTGC     60
AAG ATG AAG CGC TCA AGC TTT ACC TCT AAT AGC GTT TTA AAC TTT TTT     108
    Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe
     1               5                  10                  15

GTA GTT TTG TCT TTC ATT ACG ATA GGA TTA GTG TTT TTC TTT TTG CGT     156
Val Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg
                20                  25                  30

TCC CAA CCC ACT AGC GTA GTT TCT AAA GAA AAT ATC CCT AAA ATT GAA     204
Ser Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu
            35                  40                  45
```

```
TTA GAA AAT TTT AAA GCG TTT CAA ATC AAC GAT AAA ATC CTT GAT CTG      252
Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu
        50                  55                  60

TCC ATA GAG GGC AAA AAA GCC CTA CAA TAC GAT GAT CAT GAA ATC TTT      300
Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe
    65                  70                  75

TTT GAT TCC AAA ATC AAG CGC TAT GAT GAA GAC ACC ATT GAA AGC GTT      348
Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val
80                  85                  90                  95

GAG TCT CCT AAG GCC AAA CGG CAG CAG GAT TTG TAT TTC TTC CCT AAT      396
Glu Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn
                100                 105                 110

GGG GTT ACT TAT AAA AGA AGC GAT GAT TCC AGT TTT TGG AGT GAA ACA      444
Gly Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr
            115                 120                 125

GGG ATT TAT AAC CAT AAG GAG CAA AAT TTT AAA GGC AAG GGC CGT TTC      492
Gly Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe
        130                 135                 140

ATT CTC ACT TCA AAG GAC AGC AAG ATT GAA GGG CTT GAC ATT TCT TAT      540
Ile Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr
    145                 150                 155

TCG CAT GCA TTA GCT ATT ATT GAA GCT CAA AGC ATT CAA GCG CAT TTA      588
Ser His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu
160                 165                 170                 175

TTC TTA GAT GAA ATC AAA CAA AGC CAA AAA GAA AAG AAA AAA TTC CCC      636
Phe Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro
                180                 185                 190

ACT TTC AAA GGA GGT TTT TAATGCGTTG GTGGTGTTTT TTGGTGTGTT GTTTTGGT    692
Thr Phe Lys Gly Gly Phe
            195

ATTTTAAGCG TGAT                                                     706
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```
Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe Val
 1               5                  10                  15
Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg Ser
```

```
            20                  25                  30
Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu Leu
        35                  40                  45
Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu Ser
    50                  55                  60
Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe Phe
65                  70                  75                  80
Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val Glu
                85                  90                  95
Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn Gly
            100                 105                 110
Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr Gly
        115                 120                 125
Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe Ile
    130                 135                 140
Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr Ser
145                 150                 155                 160
His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu Phe
                165                 170                 175
Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro Thr
            180                 185                 190
Phe Lys Gly Gly Phe
        195
```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1010 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 130...957
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
AAGCGAGCAA GAATGAATTA AAAATTTTTG GTTGGCACTA CATCATAGAA ACAGGCAGGA     60
TTTATAATTA TAATTTTGAA AGCCATTTTT TTGAGCCGAT TGGAGAAACC ATTAAACAAA    120
GGAAAAGTC ATG AAA ACT TCT AAA ACA AAA ACC CCT AAA TCC GTT TTA ATC     171
          Met Lys Thr Ser Lys Thr Lys Thr Pro Lys Ser Val Leu Ile
           1               5                  10

GCT GGG CCA TGC GTC ATT GAG AGC TTA GAA AAT CTA AGA AGT ATC GCC      219
Ala Gly Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala
15                  20                  25                  30

ACT AAA TTG CAA CCC CTA GCC AAC AAC GAG CGG TTG GAT TTT TAT TTT      267
Thr Lys Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe
                35                  40                  45

AAA GCG AGT TTT GAT AAG GCG AAC CGC ACG AGT TTA GAG AGT TAC AGA      315
```

```
Lys Ala Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg
                50                  55                  60

GGG CCT GGT TTA GAA AAA GGC CTA GAA ATG TTA CAA ACG ATC AAA GAG      363
Gly Pro Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu
        65                  70                  75

GAA TTT GGT TAT AAA ATC TTA ACC GAT GTG CAT GAG AGT TAT CAA GCA      411
Glu Phe Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala
    80                  85                  90

AGC GTG GCA GCC AAA GTG GCG GAT ATT TTA CAA ATC CCG GCG TTT TTG      459
Ser Val Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu
95                  100                 105                 110

TGC CGC CAA ACG GAT CTG ATT GTA GAA GTG AGC CAG ACT AAC GCT ATT      507
Cys Arg Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile
                115                 120                 125

GTC AAT ATC AAA AAA GGG CAA TTC ATG AAC CCA AAA GAC ATG CAA TAT      555
Val Asn Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr
            130                 135                 140

TCT GTT CTA AAG GCC CTT AAA ACG AGA GAT AAA AGC ATT CAA AGC CCC      603
Ser Val Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro
        145                 150                 155

ACT TAT GAA ACA GCG TTA AAA AAT GGC GTG TGG CTG TGT GAA AGG GGG      651
Thr Tyr Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly
    160                 165                 170

AGC AGC TTT GGG TAT GGG AAT TTA GTG GTG GAT ATG CGC TCT TTA AAA      699
Ser Ser Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys
175                 180                 185                 190

ATC ATG CGA GAA TTT GCC CCT GTG ATT TTT GAC GCT ACC CAT AGC GTG      747
Ile Met Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val
                195                 200                 205

CAA ATG CCA GGG GGA GCG AAC GGG AAA AGT TCA GGA GAC AGC TCT TTT      795
Gln Met Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe
            210                 215                 220

GCC CCT ATT TTA GCG AGA GCT GCG GCG GCG GTG GGG ATT GAT GGG TTG      843
Ala Pro Ile Leu Ala Arg Ala Ala Ala Ala Val Gly Ile Asp Gly Leu
        225                 230                 235

TTT GCT GAA ACG CAT GTT GAT CCT AAA AAC GCC CTA AGC GAT GGA GCA      891
Phe Ala Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala
    240                 245                 250

AAC ATG CTA AAA CCT GAC GAG CTA GAA CAA TTA GTA ACC GAC ATG TTA      939
Asn Met Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu
255                 260                 265                 270

AAA ATC CAA AAT TTA TTT TAAAGGAATT TCATGCAAAT CATAGAAGGG AAATTGCA    995
Lys Ile Gln Asn Leu Phe
                275
```

ATTACAAGGG AATGA 1010

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```
Met Lys Thr Ser Lys Thr Lys Thr Pro Lys Ser Val Leu Ile Ala Gly
 1               5                  10                  15
Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala Thr Lys
            20                  25                  30
Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe Lys Ala
        35                  40                  45
Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg Gly Pro
    50                  55                  60
Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu Glu Phe
65                  70                  75                  80
Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala Ser Val
                85                  90                  95
Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu Cys Arg
            100                 105                 110
Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile Val Asn
        115                 120                 125
Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr Ser Val
    130                 135                 140
Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro Thr Tyr
145                 150                 155                 160
Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly Ser Ser
                165                 170                 175
Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys Ile Met
            180                 185                 190
Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val Gln Met
        195                 200                 205
Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe Ala Pro
    210                 215                 220
Ile Leu Ala Arg Ala Ala Ala Ala Val Gly Ile Asp Gly Leu Phe Ala
225                 230                 235                 240
Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala Asn Met
                245                 250                 255
Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu Lys Ile
            260                 265                 270
Gln Asn Leu Phe
        275
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 59...196
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
AACAATTCTT TTTTAAGCAA AAACAAAACA AAATTAAGGC ATAATCACTC TTTTTAAA     58

ATG AAA GGT CGC GTA GCT CAG TTG GTA GAG CAC TAC CTT GAC ATG GTA       106
Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
 1               5                  10                  15

GTG GCC GCT GGT TCA AGT CCA GTC GTG GCC ACC ATT ATC ACT CCA ATT       154
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
            20                  25                  30

TTA ATT CTC ATT TTT TTG CGA GTT TTT GAT CTT TAT AAA TTC TAAAGGGGTA    206
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
        35                  40                  45

TTAAACGCAC TTCTAATAAC GATTTTATAG CGCT                                240
```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
 1               5                  10                  15
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
            20                  25                  30
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 91...1329
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
ACCACCCCTT AATCTCAAAA AACCCCAATC ATAAAAAGCT TTATGCTACA ATGAAAGCTC     60
TTTAACACGA TAAAAGGGCG GTTTAATAGC  ATG GCA CAA GAA AAA GCA GTT CCA   114
                                  Met Ala Gln Glu Lys Ala Val Pro
                                   1               5

AGA GAT CCT AAA AAA CTC AAT GCG TTT GAT TTG CGT TGG ATG GTG TCC     162
Arg Asp Pro Lys Lys Leu Asn Ala Phe Asp Leu Arg Trp Met Val Ser
    10                  15                  20

TTA TTT GGC ACG GCG GTG GGG GCT GGG ATT TTA TTT TTG CCT ATT AGA     210
Leu Phe Gly Thr Ala Val Gly Ala Gly Ile Leu Phe Leu Pro Ile Arg
25                  30                  35                  40

GCC GGT GGG CAT GGG GTA TGG GCT ATT GTG GTA ATG AGC GCG ATC ATT     258
Ala Gly Gly His Gly Val Trp Ala Ile Val Val Met Ser Ala Ile Ile
                45                  50                  55

TTC CCT TTA ACT TAT CTA GGG CAT AGA GCT TTA GCT TAT TTC ATA GGA     306
Phe Pro Leu Thr Tyr Leu Gly His Arg Ala Leu Ala Tyr Phe Ile Gly
            60                  65                  70

TCT AAA GAC AAA GAA GAC ATT ACC ATG GTC GTT CGC TCT CAT TTT GGC     354
Ser Lys Asp Lys Glu Asp Ile Thr Met Val Val Arg Ser His Phe Gly
        75                  80                  85

GCT CAA TGG GGT TTT CTT ATC ACT TTG CTT TAT TTC TTA GCG ATT TAT     402
Ala Gln Trp Gly Phe Leu Ile Thr Leu Leu Tyr Phe Leu Ala Ile Tyr
    90                  95                  100

CCT ATT TGC TTG GTT TAT GGG GTG GGT ATC ACT AAC GTG TTT GAT CAT     450
Pro Ile Cys Leu Val Tyr Gly Val Gly Ile Thr Asn Val Phe Asp His
105                 110                 115                 120

TTT TTC ACT AAC CAG TTG CAT TTA GCG CCT TTT CAT CGG GGA TTA TTG     498
Phe Phe Thr Asn Gln Leu His Leu Ala Pro Phe His Arg Gly Leu Leu
                125                 130                 135

GCT GTA GCG TTA GTT TCT TTA ATG ATG TTG GTG ATG GTT TTT AAC GCT     546
Ala Val Ala Leu Val Ser Leu Met Met Leu Val Met Val Phe Asn Ala
            140                 145                 150

ACG ATT GTT ACG CGC ATT TGT AAC GCT TTA GTG TAT CCT TTA TGC TTG     594
Thr Ile Val Thr Arg Ile Cys Asn Ala Leu Val Tyr Pro Leu Cys Leu
        155                 160                 165

ATT TTA TTG CTT TTT TCT TTG TAT CTT ATC CCT TAT TGG CAA GGC GCT     642
Ile Leu Leu Leu Phe Ser Leu Tyr Leu Ile Pro Tyr Trp Gln Gly Ala
    170                 175                 180
```

```
AAT CTT TTT GTG GTG CCG AGT TTT AAA GAA TTT GTG TTA GCG ATT TGG      690
Asn Leu Phe Val Val Pro Ser Phe Lys Glu Phe Val Leu Ala Ile Trp
185                 190                 195                 200

CTA ACC TTA CCG GTG CTT GTG TTT GCA TTC GAC CAT AGC CCC ATC ATT      738
Leu Thr Leu Pro Val Leu Val Phe Ala Phe Asp His Ser Pro Ile Ile
                205                 210                 215

TCA ACC TTC ACT CAA AAT GTG GGA AAA GAA TAC GGC GTT TTC AAA GAA      786
Ser Thr Phe Thr Gln Asn Val Gly Lys Glu Tyr Gly Val Phe Lys Glu
            220                 225                 230

TAC AAA CTC AAT CAA ATT GAA TTA GGG ACA TCG CTG ATG CTT TTA GGG      834
Tyr Lys Leu Asn Gln Ile Glu Leu Gly Thr Ser Leu Met Leu Leu Gly
        235                 240                 245

TTT GTG ATG TTT TTT GTG TTT TCG TGC GTC ATG TGC TTG AAT GCT GAT      882
Phe Val Met Phe Phe Val Phe Ser Cys Val Met Cys Leu Asn Ala Asp
    250                 255                 260

GAT TTT GTG AAA GCA AGG GAA CAA AAT ATC CCC ATT TTA AGC TAT TTG      930
Asp Phe Val Lys Ala Arg Glu Gln Asn Ile Pro Ile Leu Ser Tyr Leu
265                 270                 275                 280

GCT AAC ACT TTA AAC AAC CCT TTA ATC AAT TAT GCG GGG CCT GTG GTG      978
Ala Asn Thr Leu Asn Asn Pro Leu Ile Asn Tyr Ala Gly Pro Val Val
                285                 290                 295

GCT TTT TTA GCG ATT TTT TCA TCT TTT TTT GGG CAT TAT TAT GGG GCT     1026
Ala Phe Leu Ala Ile Phe Ser Ser Phe Phe Gly His Tyr Tyr Gly Ala
            300                 305                 310

AAG GAG GGT TTA GAA GGC ATT ATT ATT CAA AGC TTA AAA TTG AAA AAA     1074
Lys Glu Gly Leu Glu Gly Ile Ile Ile Gln Ser Leu Lys Leu Lys Lys
        315                 320                 325

GCT TCT AAA CCC TTG AGC GTT AGC GTA ACG ATT TTT TTA TGG CTG ACT     1122
Ala Ser Lys Pro Leu Ser Val Ser Val Thr Ile Phe Leu Trp Leu Thr
    330                 335                 340

ATC ACG CTT GTG GCT TAT ATT AAC CCC AAT ATC TTG GAT TTT ATT GAA     1170
Ile Thr Leu Val Ala Tyr Ile Asn Pro Asn Ile Leu Asp Phe Ile Glu
345                 350                 355                 360

AAT TTA GGC GGC CCC ATT ATC GCG CTC ATT CTG TTT GTG ATG CCC ATG     1218
Asn Leu Gly Gly Pro Ile Ile Ala Leu Ile Leu Phe Val Met Pro Met
                365                 370                 375

ATA GCT TTT TAT AGT GTT TCT AGT TTG AAG CGT TTT AGA AAT TTC AAA     1266
Ile Ala Phe Tyr Ser Val Ser Ser Leu Lys Arg Phe Arg Asn Phe Lys
            380                 385                 390

GTG GAT ATT TTT GTG TTT GTC TTT GGG AGC TTG ACG GCT TTG AGC GTG     1314
Val Asp Ile Phe Val Phe Val Phe Gly Ser Leu Thr Ala Leu Ser Val
        395                 400                 405

TTT TTA GGA CTA TTT TAATGGCTAG TTTTTCTATT TTATCTATTT TTAAAATCGG C   1370
Phe Leu Gly Leu Phe
```

410

GTGGGGCCTA GC 1382

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
Met Ala Gln Glu Lys Ala Val Pro Arg Asp Pro Lys Lys Leu Asn Ala
 1               5                  10                  15
Phe Asp Leu Arg Trp Met Val Ser Leu Phe Gly Thr Ala Val Gly Ala
            20                  25                  30
Gly Ile Leu Phe Leu Pro Ile Arg Ala Gly Gly His Gly Val Trp Ala
        35                  40                  45
Ile Val Val Met Ser Ala Ile Ile Phe Pro Leu Thr Tyr Leu Gly His
    50                  55                  60
Arg Ala Leu Ala Tyr Phe Ile Gly Ser Lys Asp Lys Glu Asp Ile Thr
65                  70                  75                  80
Met Val Val Arg Ser His Phe Gly Ala Gln Trp Gly Phe Leu Ile Thr
                85                  90                  95
Leu Leu Tyr Phe Leu Ala Ile Tyr Pro Ile Cys Leu Val Tyr Gly Val
            100                 105                 110
Gly Ile Thr Asn Val Phe Asp His Phe Phe Thr Asn Gln Leu His Leu
        115                 120                 125
Ala Pro Phe His Arg Gly Leu Leu Ala Val Ala Leu Val Ser Leu Met
    130                 135                 140
Met Leu Val Met Val Phe Asn Ala Thr Ile Val Thr Arg Ile Cys Asn
145                 150                 155                 160
Ala Leu Val Tyr Pro Leu Cys Leu Ile Leu Leu Leu Phe Ser Leu Tyr
                165                 170                 175
Leu Ile Pro Tyr Trp Gln Gly Ala Asn Leu Phe Val Val Pro Ser Phe
            180                 185                 190
Lys Glu Phe Val Leu Ala Ile Trp Leu Thr Leu Pro Val Leu Val Phe
        195                 200                 205
Ala Phe Asp His Ser Pro Ile Ile Ser Thr Phe Thr Gln Asn Val Gly
    210                 215                 220
Lys Glu Tyr Gly Val Phe Lys Glu Tyr Lys Leu Asn Gln Ile Glu Leu
225                 230                 235                 240
Gly Thr Ser Leu Met Leu Leu Gly Phe Val Met Phe Phe Val Phe Ser
                245                 250                 255
Cys Val Met Cys Leu Asn Ala Asp Asp Phe Val Lys Ala Arg Glu Gln
            260                 265                 270
Asn Ile Pro Ile Leu Ser Tyr Leu Ala Asn Thr Leu Asn Asn Pro Leu
        275                 280                 285
Ile Asn Tyr Ala Gly Pro Val Val Ala Phe Leu Ala Ile Phe Ser Ser
    290                 295                 300
Phe Phe Gly His Tyr Tyr Gly Ala Lys Glu Gly Leu Glu Gly Ile Ile
305                 310                 315                 320
Ile Gln Ser Leu Lys Leu Lys Lys Ala Ser Lys Pro Leu Ser Val Ser
```

```
                325                 330                 335
Val Thr Ile Phe Leu Trp Leu Thr Ile Thr Leu Val Ala Tyr Ile Asn
            340                 345                 350
Pro Asn Ile Leu Asp Phe Ile Glu Asn Leu Gly Gly Pro Ile Ile Ala
        355                 360                 365
Leu Ile Leu Phe Val Met Pro Met Ile Ala Phe Tyr Ser Val Ser Ser
    370                 375                 380
Leu Lys Arg Phe Arg Asn Phe Lys Val Asp Ile Phe Val Phe Val Phe
385                 390                 395                 400
Gly Ser Leu Thr Ala Leu Ser Val Phe Leu Gly Leu Phe
                405                 410
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 63...827
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
TTTGCCACCT TATTGCAAAC CCTAATGCTA ACGCACTACT TTTTTATCTT TAAAGAGAAA     60
GA ATG CTA GAT TTT ATT CAA GAG CTT AGC ACC CCC CAT GTT AGG GAT       107
   Met Leu Asp Phe Ile Gln Glu Leu Ser Thr Pro His Val Arg Asp
    1               5                  10                  15

TTT TTC TTG TTG TTT TTA AGG GTT AGC GGC GTG CTG TCT TTC TTC CCT      155
Phe Phe Leu Leu Phe Leu Arg Val Ser Gly Val Leu Ser Phe Phe Pro
                20                  25                  30

TTT TTT GAA AAC CAT TTA GTG CCT TTG TCG GTG CGT GGG GCT TTG AGT      203
Phe Phe Glu Asn His Leu Val Pro Leu Ser Val Arg Gly Ala Leu Ser
            35                  40                  45

TTG TAT GTG AGC GCG ATT TTT TAC CCC ACT TTA GAA TTT TCA AAC GCC      251
Leu Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala
        50                  55                  60

GCT TAC ACG CCA GAG GGT TTT ATC ATT GCT TGC TTG TGC GAA TTG TTT      299
Ala Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe
    65                  70                  75

TTA GGG GTG TGC GCG TCT GTC TTT TTA CAA ATC GTC TTT GCA AGC TTA      347
Leu Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu
80                  85                  90                  95

GTG TTT GCA ACC GAT AGC ATC AGC TTT TCT ATG GGG CTT ACG ATG GCG      395
Val Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala
```

```
                100                 105                 110

AGC GCG TAT GAT CCT ATT TCA GGA TCG CAA AAA CCC ATT GTG GGG CAA      443
Ser Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln
            115                 120                 125

GCC CTT TTA TTG TTA GCG ATT TTA ATT TTA TTG GAT TTA TCG TTC CAC      491
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His
        130                 135                 140

CAT CAA ATC ATT TTG TTT GTG GAT CAC AGC TTA AAA GCC GTC CCT TTA      539
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu
    145                 150                 155

GGG CAA TTT GTC TTT GAG CCA GCG TTG GCT AAA AAC ATC GTT AAA GCC      587
Gly Gln Phe Val Phe Glu Pro Ala Leu Ala Lys Asn Ile Val Lys Ala
160                 165                 170                 175

TTT TCG CAC CTC TTT GTC ATA GGG TTT TCT ATG GCG TTC CCT ATT TTA      635
Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu
                180                 185                 190

TGC TTG GTG TTA TTG AGC GAT ATT ATT TTT GGC ATG ATC ATG AAA ACC      683
Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr
            195                 200                 205

CAC CCT CAG TTC AAC CTG CTC GCT ATT GGG TTT CCG GTT AAA ATT GCG      731
His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala
        210                 215                 220

ATC GGG TTT GTG GGC ATT ATC TTA ATC GCT TCG GCT ATC ATG GGG CGT      779
Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg
    225                 230                 235

TTT AAA GAA GAA ATC AGC CTG GCC TTT AGC GCC ATT AGC AAA ATC TTT T    828
Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Ala Ile Ser Lys Ile Phe
240                 245                 250                 255

AAAGGATAAA CATGATTAGT TTTAAAGAAG CTCTAAAAAT CCATTCT                  875
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```
Met Leu Asp Phe Ile Gln Glu Leu Ser Thr Pro His Val Arg Asp Phe
 1               5                  10                  15
Phe Leu Leu Phe Leu Arg Val Ser Gly Val Leu Ser Phe Phe Pro Phe
            20                  25                  30
```

```
Phe Glu Asn His Leu Val Pro Leu Ser Val Arg Gly Ala Leu Ser Leu
        35                  40                  45
Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala Ala
    50                  55                  60
Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe Leu
65                  70                  75                  80
Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu Val
                85                  90                  95
Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala Ser
            100                 105                 110
Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln Ala
        115                 120                 125
Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His His
    130                 135                 140
Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu Gly
145                 150                 155                 160
Gln Phe Val Phe Glu Pro Ala Leu Ala Lys Asn Ile Val Lys Ala Phe
                165                 170                 175
Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu Cys
            180                 185                 190
Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr His
        195                 200                 205
Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala Ile
    210                 215                 220
Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg Phe
225                 230                 235                 240
Lys Glu Glu Ile Ser Leu Ala Phe Ser Ala Ile Ser Lys Ile Phe
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 373...1110
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
GAGATATTAA AAAGAGATAT TAAAATGGCT TTTAAGCTTC TATGAAGCCC CCCCCCCTCC     60
TCCTTTTGCC CTTTATTTCG TGGGCAAATC GCCCACAGGA CAAGCGGCCA CACCCACGCT    120
TGGGCGGGTG ATTTTTTCTA CATTTTCTTG AGCTTTTTTG GGGTCATTCA CCCAAGTTTT    180
ATAGAACTCA AAAGGGCATT CCGCCACACC CTTATCCCCA TCGCCACTAG CAAAAACCCC    240
ACTATAACCT CTGTGCAAGA GTTTGAAGAG TTGGTTTTGG CTTTGGTCGT ATTTTCTCGC    300
ATCACGGATT TGTTGCACAG AAAGTTGAGC GTATTGAAGA CCATTTTCTT CTTCCCCGCA    360
TTCGCCCAAA GT ATG CCC GTC AAA ACC AAT AAT GCT AGA ATG CCC AAA ATA    411
             Met Pro Val Lys Thr Asn Asn Ala Arg Met Pro Lys Ile
              1               5                  10

GGA ATA CAC CCC ATC AAA ACC GGT CGC ATT CGC TAC CGC TAC ATA ACA     459
```

```
Gly Ile His Pro Ile Lys Thr Gly Arg Ile Arg Tyr Arg Tyr Ile Thr
    15                  20                  25

TTG ATT GGC CCA CGC CAT AGC TTT TAC TAT TGC AAT TTG TTG CTC CTT      507
Leu Ile Gly Pro Arg His Ser Phe Tyr Tyr Cys Asn Leu Leu Leu Leu
30                  35                  40                  45

AGC CGG ATA CAT GTA ACC TTG ACA GCG CAC AAT GAG TTC TGC CCC ACG      555
Ser Arg Ile His Val Thr Leu Thr Ala His Asn Glu Phe Cys Pro Thr
                50                  55                  60

CAT CGC GCA ATC GCG CCA AAT TTC AGG GTA GTT TCC ATC ATC GCA AAT      603
His Arg Ala Ile Ala Pro Asn Phe Arg Val Val Ser Ile Ile Ala Asn
            65                  70                  75

AAT CAA AGA AAC TTT CAA GCC CTT AGG CCC ATC AAC CAC ATA AGT TTT      651
Asn Gln Arg Asn Phe Gln Ala Leu Arg Pro Ile Asn His Ile Ser Phe
        80                  85                  90

ATC CCC AGG ATA CCA ACA TTC AAT AGG GCA CCA AGG CAA GAT TTT GCG      699
Ile Pro Arg Ile Pro Thr Phe Asn Arg Ala Pro Arg Gln Asp Phe Ala
    95                  100                 105

GTA TTT TTG CAC GAT CTC ACC CTT ATC ATT GAC AAG AAT CAA AGT GTT      747
Val Phe Leu His Asp Leu Thr Leu Ile Ile Asp Lys Asn Gln Ser Val
110                 115                 120                 125

ATA GGG ATT CTT TTT GGC TTG CTC GTG TTT TTC CCC TGT CAA AGA GAA      795
Ile Gly Ile Leu Phe Gly Leu Leu Val Phe Phe Pro Cys Gln Arg Glu
                130                 135                 140

CAC TCC CCA AAC CTT GTT TTT CTT ACA AGC TTC AGC AAA GAT CGC GGT      843
His Ser Pro Asn Leu Val Phe Leu Thr Ser Phe Ser Lys Asp Arg Gly
            145                 150                 155

TTC TTC TCC AGG AAC GCT TGC GGC TGT ATC AAA CAT TTC TTG TCT GTC      891
Phe Phe Ser Arg Asn Ala Cys Gly Cys Ile Lys His Phe Leu Ser Val
        160                 165                 170

ATA CAT AAT CCC ATG CGT GCT GTA TTC AGG GAA AAT AAT CAG ATC CAA      939
Ile His Asn Pro Met Arg Ala Val Phe Arg Glu Asn Asn Gln Ile Gln
    175                 180                 185

CCC AGG CAA ACC CTG TTT GAC CCC ACC AAT CAC CTT AGC GAT ATT GCG      987
Pro Arg Gln Thr Leu Phe Asp Pro Thr Asn His Leu Ser Asp Ile Ala
190                 195                 200                 205

ACA ATT TTC CAA CAC CTC ATT CTT AGT GTG GAG TCT AGG CAT CTT ATA     1035
Thr Ile Phe Gln His Leu Ile Leu Ser Val Glu Ser Arg His Leu Ile
                210                 215                 220

ATT AAC TAC CGC TAC ACC CAC AGT ATC TGG GCT GCT ACT AAT ATC TCC     1083
Ile Asn Tyr Arg Tyr Thr His Ser Ile Trp Ala Ala Thr Asn Ile Ser
            225                 230                 235

ATG TCT CAT ATT ATG TTC CTT GTT TTT TGATGAGAGT TCCTACAAAC CCTCTAC   1137
Met Ser His Ile Met Phe Leu Val Phe
        240                 245
```

TTGAATTTAT AAAATAATTG TGT 1160

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
Met Pro Val Lys Thr Asn Asn Ala Arg Met Pro Lys Ile Gly Ile His
 1               5                  10                  15
Pro Ile Lys Thr Gly Arg Ile Arg Tyr Arg Tyr Ile Thr Leu Ile Gly
            20                  25                  30
Pro Arg His Ser Phe Tyr Tyr Cys Asn Leu Leu Leu Leu Ser Arg Ile
        35                  40                  45
His Val Thr Leu Thr Ala His Asn Glu Phe Cys Pro Thr His Arg Ala
    50                  55                  60
Ile Ala Pro Asn Phe Arg Val Val Ser Ile Ile Ala Asn Asn Gln Arg
65                  70                  75                  80
Asn Phe Gln Ala Leu Arg Pro Ile Asn His Ile Ser Phe Ile Pro Arg
                85                  90                  95
Ile Pro Thr Phe Asn Arg Ala Pro Arg Gln Asp Phe Ala Val Phe Leu
            100                 105                 110
His Asp Leu Thr Leu Ile Ile Asp Lys Asn Gln Ser Val Ile Gly Ile
        115                 120                 125
Leu Phe Gly Leu Leu Val Phe Phe Pro Cys Gln Arg Glu His Ser Pro
    130                 135                 140
Asn Leu Val Phe Leu Thr Ser Phe Ser Lys Asp Arg Gly Phe Phe Ser
145                 150                 155                 160
Arg Asn Ala Cys Gly Cys Ile Lys His Phe Leu Ser Val Ile His Asn
                165                 170                 175
Pro Met Arg Ala Val Phe Arg Glu Asn Asn Gln Ile Gln Pro Arg Gln
            180                 185                 190
Thr Leu Phe Asp Pro Thr Asn His Leu Ser Asp Ile Ala Thr Ile Phe
        195                 200                 205
Gln His Leu Ile Leu Ser Val Glu Ser Arg His Leu Ile Ile Asn Tyr
    210                 215                 220
Arg Tyr Thr His Ser Ile Trp Ala Ala Thr Asn Ile Ser Met Ser His
225                 230                 235                 240
Ile Met Phe Leu Val Phe
                245
```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 79...1611
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```
GGCTTTATAA AAAATGTTAG AAACCCTTAC AAAACAAGCT AATATATTCT ATTCAATTTG      60
CCTCAAGGAC AAACAAAC ATG AAA AAA CTT CTT TAT ACC ATA CTC GCG CTT      111
                    Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu
                     1               5                  10

CTT TTA ATC GGC CTT TTA ACA ATC TAT CTC ATC CTT TTT ACA GAA TGG      159
Leu Leu Ile Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp
            15                  20                  25

GGG AAT AAG ATC ATC GCT TCG TAT ATA GAG AAA AAA ATC AAC CCG AAC      207
Gly Asn Lys Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn
        30                  35                  40

GAG CAC TAC TTG AGC GTT AAA ACC TTT AAA TTG AGA TTC AAC TCT TTG      255
Glu His Tyr Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu
    45                  50                  55

GAT TTT AAA GCT CAA GCC AAC GAT GAT TCC ACG CTC ATT CTT AAG GGG      303
Asp Phe Lys Ala Gln Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly
60                  65                  70                  75

GAT TTT TCA CTT TTA AAG CAA AGC GTA AAT TTG AAT TAC CAT ATA GAT      351
Asp Phe Ser Leu Leu Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp
                80                  85                  90

ATT AAA GAT TTA CGC TCT TTC AAA GAA TGG ATA CCC TAC CCT TTA AGG      399
Ile Lys Asp Leu Arg Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg
            95                  100                 105

GGG GCT GTT ATC ACT TCT GGG AAT ATT AAA GGG CAT AGA AAA GCC CTT      447
Gly Ala Val Ile Thr Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu
        110                 115                 120

ATG ATT CAA GGC GTC TCT AAT GTG GCT CAA TCC CAC ACT GCC TAC AAT      495
Met Ile Gln Gly Val Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn
    125                 130                 135

GCC CTT TTA GAT GAT TTC AAG CTT TCT CGC TTA AAT TTG AAC GCA CAA      543
Ala Leu Leu Asp Asp Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln
140                 145                 150                 155

GAC GCC AAT TTA GAA GAT TTG CTT TAT TTA ATC AAT CGC CCC GCT TAT      591
Asp Ala Asn Leu Glu Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr
                160                 165                 170

GCG AAC GCA AAA GTG TCC TTA CAG GCG GAT TTT AAC TCT CTA AAG CCT      639
Ala Asn Ala Lys Val Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro
            175                 180                 185
```

```
TTA GAG GGG CAT TTG ATC CTA ACA GCT AAT AAC GCT TTA ATC AAT AAC      687
Leu Glu Gly His Leu Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn
        190                 195                 200

GCC CTA ATC AAT CAA ATT TTT CAT TTA AAC CTT AAA GAC ACG CTT GTT      735
Ala Leu Ile Asn Gln Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val
    205                 210                 215

TTC AGC CTC TCG CAT TCA AGC GAC TTT AAA GGA AAC AAA GCC ATC AGC      783
Phe Ser Leu Ser His Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser
220                 225                 230                 235

GAT ACC ACC CTG ACT AGC CCT TTA GCC AAT TTC AAA GCC CTA AAA AGC      831
Asp Thr Thr Leu Thr Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser
                240                 245                 250

GAA TAC CTT TTC TCT ATT TTA AAA CTC AAC GCC CCC TAC ACT TTA GAA      879
Glu Tyr Leu Phe Ser Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu
            255                 260                 265

ATC CCC AAT CTA GCC AAA CTC TAT AAC ATT ACC AAC CAC CCC TTA AAA      927
Ile Pro Asn Leu Ala Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys
        270                 275                 280

GGG AGC TTG ACT TTA AAA GGC GCT ATA GAA CAA AGC CCC AAA CTT TTA      975
Gly Ser Leu Thr Leu Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu
    285                 290                 295

AAA GTC AGC GGC CAT TCA AAT TTA CTA GAC GGC GCG CTG GAT TTC ACG     1023
Lys Val Ser Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr
300                 305                 310                 315

CTT TTA AAT AAA GAT TTG AAA GGG CGT TTT TCC AAT ATT TCC ACT TTA     1071
Leu Leu Asn Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu
                320                 325                 330

AAA GCT TTA GAT TTA TTC CAT TAC CCT AAG TTT TTC CAA TCC GTT GCA     1119
Lys Ala Leu Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala
            335                 340                 345

GAC GCT AAT TTG GAT TAT GAT CTT ATC GCT AAG CAA GGC GTA TTG AAA     1167
Asp Ala Asn Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys
        350                 355                 360

GCC CGC CTA AAA AAC GCA AGA TTC CTC AAA AAT GCA TTC AGC GAT TTT     1215
Ala Arg Leu Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe
    365                 370                 375

CTC TAC TCC ATT TCT AAA TTT GAT ATT ACA AAA GAA ATT TAT AAC GAT     1263
Leu Tyr Ser Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp
380                 385                 390                 395

GCC AAT CTG GTA AGC CAA ATC AAC CAG CAA CGC CTG CTC TCT GAT CTG     1311
Ala Asn Leu Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu
                400                 405                 410

AGT TTA AAA AGC CCC AAA ACC CAA TTG AAA ATC CAT AAC GGT TTG TTG     1359
Ser Leu Lys Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu
```

```
            415                 420                 425

GAT TTA AAC ACC AAA CAA ATG AAC ATG CTC ATG GAT GCG GAA ATT TTA    1407
Asp Leu Asn Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu
        430                 435                 440

AAA TTC ATT TTT AAA ATG AAA CTT CAA GGC AAC ATG CAC CAG CCA AAA    1455
Lys Phe Ile Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys
    445                 450                 455

TTT TCT CTC ATT TTA AAC GAA AAA GCC ATT CAG CAA AAC TTG CAA CAA    1503
Phe Ser Leu Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln
460                 465                 470                 475

GGC TTG AAA GAA ATC TTA AAA AAC GAC ACC CTT AAA AAA GGT TTA GAT    1551
Gly Leu Lys Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp
                480                 485                 490

CAT TTG CTT AAA GAT GAT AAG CTC AAA GAA AAG CTT GAA AAA GGG CTT    1599
His Leu Leu Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu
            495                 500                 505

AAG GGG CTT TTT TAAAATTTTA AAGGATAGAA ATGGCGCACA TTTTAGTTAG CGGGG  1656
Lys Gly Leu Phe
        510

CGACT                                                              1661
```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu
 1               5                  10                  15
Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile
            20                  25                  30
Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser
        35                  40                  45
Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln
    50                  55                  60
Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu
65                  70                  75                  80
Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp Leu Arg
                85                  90                  95
Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val Ile Thr
            100                 105                 110
Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln Gly Val
        115                 120                 125
Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu Asp Asp
```

```
    130                 135                 140
Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn Leu Glu
145                 150                 155                 160
Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val
                165                 170                 175
Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu
            180                 185                 190
Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln
        195                 200                 205
Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val Phe Ser Leu Ser His
    210                 215                 220
Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr
225                 230                 235                 240
Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser Glu Tyr Leu Phe Ser
                245                 250                 255
Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala
            260                 265                 270
Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu
        275                 280                 285
Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His
    290                 295                 300
Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn Lys Asp
305                 310                 315                 320
Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu
                325                 330                 335
Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn Leu Asp
            340                 345                 350
Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu Lys Asn
        355                 360                 365
Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser
    370                 375                 380
Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser
385                 390                 395                 400
Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys Ser Pro
                405                 410                 415
Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys
            420                 425                 430
Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys
        435                 440                 445
Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu Ile Leu
    450                 455                 460
Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile
465                 470                 475                 480
Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp
                485                 490                 495
Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe
            500                 505                 510
```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 53...352
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
CTAATTCTGT CTATTACACC AACAATCAAT CTCAAAACAA AGGACATGAAAG ATG AAA     58
                                                          Met Lys
                                                           1

ACA AAA CAT AAA GGA ATA AGA ATG TTT AAG CAA ATT CGT AGA ATG ATG     106
Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg Met Met
          5                  10                  15

AGT TTG GCA ATA TTA ATG CCT AGT TTT TTA TTG GCG GCA CCA GAT TAC     154
Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro Asp Tyr
     20                  25                  30

AAA CAA AAA TTC ACT CAA ATA TTG GAT TTC ATA AGC AAT GAC TTT ATC     202
Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp Phe Ile
35                   40                  45                  50

AAG GCT ATT GGT GGT CTA ATC ATT GTT GGG ACT TGC ATT TAC GCC TAT     250
Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr Ala Tyr
                55                  60                  65

AAA AAT TGG GAC AGG CTT GGA GAA ATT GGT TGG AAA TGC GTT GGG ATT     298
Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val Gly Ile
           70                  75                  80

ATC ATT ATA ACC GCT GCT ATT TCT AAT GCT AAA ACT TTA AGT CAA TGG     346
Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser Gln Trp
      85                  90                  95

TTA TTT TAGATGGCAT TGCATATTGT TTGTGTTGAA AGTATCAACA TTAGA           397
Leu Phe
    100
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
Met Lys Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg
 1               5                  10                  15
Met Met Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro
            20                  25                  30
```

```
Asp Tyr Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp
         35                  40                  45
Phe Ile Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr
     50                  55                  60
Ala Tyr Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val
65                  70                  75                  80
Gly Ile Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser
                85                  90                  95
Gln Trp Leu Phe
            100
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...318
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
CTTGCCAATC CCTTCAATAT CCACCGAATT GATGCCATGC TCAATTAAAA A ATG ATC      57
                                                          Met Ile
                                                           1

CAA AGC GAC GCT GTC TTT AAG ATA AAT TTC TGT CTT GCC CTT CTT GTA      105
Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu Leu Val
          5                  10                  15

TTT GTA AAG AGG GGC TTG AGC GAT ATA AAC ATG CCC TTG TTC AAT CAG      153
Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe Asn Gln
     20                  25                  30

CGG GCG CAA ATA ACG ATA GAA AAA AGT CAT CAG CAA GGT TTG GAT ATG      201
Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu Asp Met
35                  40                  45                  50

GCT CCC ATC CAC ATC AGC ATC GGT CAT GAT AAT GAT TTT ATG ATA GCG      249
Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met Ile Ala
                55                  60                  65

CAA TCT TTC TAT ATC AAA ACT CTC TTG AAT GCC GCA CCC AAA AGC CGT      297
Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys Ser Arg
            70                  75                  80

GAT CAT GTT TTT AAT TTC TTC TGATTTTAGG ATTTTTGATA AATGGCTTTT TTCC    352
Asp His Val Phe Asn Phe Phe
         85
```

ACATTTAAAA TCTTA 367

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
Met Ile Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu
 1               5                  10                  15
Leu Val Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe
            20                  25                  30
Asn Gln Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu
        35                  40                  45
Asp Met Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met
    50                  55                  60
Ile Ala Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys
65                  70                  75                  80
Ser Arg Asp His Val Phe Asn Phe Phe
                85
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 54...344
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
TAAAAAGCAC TTTAGAGAGA TTTACGAAAG TGTTTTGAAG CGAAGAATGT CTG ATG      56
                                                          Met
                                                           1

ATT ATC TTT GGA AAA GAT TAC CTA TCT ACA GAC TTG CAA AAT AGC GCT     104
Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser Ala
          5                  10                  15

AAA GAT ATT CTT CTC ATC GCT TCG CAA ATT CTC AAA GAA AGA CTT TTT     152
Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu Phe
        20                  25                  30
```

```
GCC CAC AAA AAT GAG ATT TTC TTT TGC CCT AGA AAT AGC TAC ATT CAA      200
Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile Gln
    35                  40                  45

GCG TTT AGA ATC TAT CAA GAA AGA AAG ATT ACC ATA AGT TTT CAC GGT      248
Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His Gly
50                  55                  60                  65

GGA ATA AAT AAT AAT ATC TGC CTT CTC GCC TTG AAA GGC ATC CAC AGT      296
Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His Ser
                70                  75                  80

GTC TAT TTT GAG CTC ATC AAA ATT CTT GAA GCC GTA TTT TTC CAC TTC T    345
Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His Phe
            85                  90                  95

GATCGCAAGC ATCTTTTTTG GGCATTATAA GGTGTGATAA T                        386
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
Met Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser
 1               5                  10                  15
Ala Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu
            20                  25                  30
Phe Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile
        35                  40                  45
Gln Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His
    50                  55                  60
Gly Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His
65                  70                  75                  80
Ser Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His
                85                  90                  95
Phe
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 55...516
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
GCGGTTTGGA TCTTCATTAA AAATTCGTTG CTCACCCCTG GGTTATAAGC TTGA GCT      57
                                                             Ala
                                                              1

TCA GAA GTG GCC CCC TCA GAG GTT TTG TTG GAT TCT TCT TGC TTG TCT      105
Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu Ser
             5                  10                  15

TTT TCT TTG ACT ATA TCC TTA GTT GTT ACT TGT TTA GGA GCG CTT TTT      153
Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu Phe
        20                  25                  30

TCT TTA GCT TCC TCT TTA GCT TCT TCT TTT TTG GGC TCT TCT TTA GGC      201
Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu Gly
    35                  40                  45

TCT TCT TTT TTA ACC TCT TCA ACT TTA GGC TCA GGC TTA GGC TCG GGT      249
Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser Gly
50                  55                  60                  65

TTT GGT TCA GGT TTG GGT TCA GGC TTA GGT TTT GGT TTT GGC TTT GGC      297
Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe Gly
                70                  75                  80

TTG GGT TTA GGC TTA GGT TTA GGC TTT GTA ACC TCC TTT TTG GGT TCT      345
Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly Ser
            85                  90                  95

TCT TTT TTT GGC TCT TCT TTC TTG GGT TTT TCT TTA GGC TCT TCT TTG      393
Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser Leu
        100                 105                 110

GGT TTA GCC GAC TCA GCA TTA GTC TTT GTA TTG GAA TTA GTG TTG ATG      441
Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu Met
    115                 120                 125

CTG GCT AAA CTC ATG GTA ACC TTA GTG GTC CCG GCT TGC GCT AAA GGC      489
Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys Gly
130                 135                 140                 145

TCT GGG GCG TCT TCG CGC AGT AAA AAA TAGCCAAACC CTATAGCGTA TAGGGCA    543
Ser Gly Ala Ser Ser Arg Ser Lys Lys
                150

AAAGAGATTA AAAAGCTAAC ACTCGT                                        569
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
Ala Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu
 1               5                  10                  15
Ser Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu
            20                  25                  30
Phe Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu
        35                  40                  45
Gly Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser
    50                  55                  60
Gly Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe
65                  70                  75                  80
Gly Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly
                85                  90                  95
Ser Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser
            100                 105                 110
Leu Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu
        115                 120                 125
Met Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys
    130                 135                 140
Gly Ser Gly Ala Ser Ser Arg Ser Lys Lys
145                 150
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 77...310
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
CCCCACAAAT CCTAGCGATA GTGAAATGCC CTAATTCATG GACAAAGATT AAAAACGCCA    60
GCATCAAAAC CGCTAC AAT GAA CAT CAT ACC CCT GCA GGC TCT TTG GTG TTA   112
                  Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu
                   1               5                  10

GGA TCT TTT ATC ATC GGC TCT TTT AAA GGC GTG GGT GCT ATA GGG GGC     160
Gly Ser Phe Ile Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly
        15                  20                  25

GTG GGT GCT GTG GTT TTT GGG ATT TCT TTA TTT TCT TTT GGG GGT TTT     208
```

```
Val Gly Ala Val Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe
    30                  35                  40

TGC CAC AAC TCT GTC AAA GCC GCC GCT TTT TTA GGA TCC ATT TTG GCT     256
Cys His Asn Ser Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala
45                  50                  55                  60

AAA ATT TTA CCG AGT TCT TGG GGT TTT AGC GCC ATT AAA ATT TCT AAT     304
Lys Ile Leu Pro Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn
                65                  70                  75

GCG TTT TGAGTGGGTA AATTTTCTAA AATCAGAGCC GATTTAGAAT CTTTCATTT      359
Ala Phe
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu Gly Ser Phe Ile
 1               5                  10                  15
Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly Val Gly Ala Val
            20                  25                  30
Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe Cys His Asn Ser
        35                  40                  45
Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala Lys Ile Leu Pro
    50                  55                  60
Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn Ala Phe
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...998
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGGTTTTGTG AATGACGACT AAAAGAGTGA ATACTGCCAC AAACAAGATA ATG ACA 56
Met Thr
1

TTA AAT ACT TTC TTG GAT ACA TGT TTT CTT TTA TTC ATC AGT ATT CTT 104
Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser Ile Leu
5 10 15

TTT TAT TTA AGT ATA CCA ATT TAT CCT AAC AAA GTG GTG GTT GTC CCG 152
Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val Val Pro
20 25 30

CAA GGT TCG CTC AAA AAA GTG TTT TTT TCT TTA AAA GAG CAA GGC GTG 200
Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln Gly Val
35 40 45 50

GAT ATG AAC GCT TTG GAT TTG CTT TTT TTA CGC CTG ATG GGC ATG CCT 248
Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly Met Pro
55 60 65

AAA AAA GGT TAT ATT GAT ATG GGC GAT GGG GCT TTA AGG AAG GGG GAT 296
Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys Gly Asp
70 75 80

TTT TTA GTC CGT TTG ATT AAG GCA AAA GCG GCA CAA AAA AGT GCG ACT 344
Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser Ala Thr
85 90 95

CTA ATC CCT GGG GAA AGC CGC TAT TTT TTC ACG CAA ATT TTG AGC GAG 392
Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu Ser Glu
100 105 110

ACT TAC CAA CTA GAA ACA AGC GAT CTC AAT CAG GCT TAT GAA AGC ATC 440
Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu Ser Ile
115 120 125 130

GCT CCA CGA TTG AAT GGC GAA GTG ATA GAA GAT GGG GTG ATA TGG CCA 488
Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile Trp Pro
135 140 145

GAC ACT TAT CAT TTG CCT TTA GGG GAG GAC GCT TTT AAA ATC ATG CAA 536
Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile Met Gln
150 155 160

ACT TTG ATT GGT CAA TCC ATG AAA AAA CAC GAA GCC TTA AGC AAA CAA 584
Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser Lys Gln
165 170 175

TGG CTT GGA TAC TAC CAT AAA GAA GAG TGG TTT GAA AAA ATC ATT CTC 632
Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile Ile Leu
180 185 190

GCT TCT ATT GTG CAA AAA GAA GCC GCT AAT GTT GAA GAA ATG CCC TTG 680
Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met Pro Leu
195 200 205 210

ATT GCG AGC GTG ATT TTT AAC CGC TTG AAA AAA GGC ATG CCT TTA CAA 728
Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro Leu Gln

```
                215                 220                 225

ATG GAT GGG GCT TTG AAT TAT CAG GAA TTT TCA CAC GCT AAA GTA ACC     776
Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys Val Thr
            230                 235                 240

AAA GAG CGC ATT AAA ACC GAT AAC ACC CCC TAC AAT ACC TAT AAA TTT     824
Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr Lys Phe
        245                 250                 255

AAG GGT TTG CCT AAA AAT CCT GTA GGG AGC GTG AGC CTA GAA GCG ATT     872
Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu Ala Ile
    260                 265                 270

AGA GCC GTG ATC TTC CCT AAA AAA ACG GAT TTC TTG TAT TTT GTG AAA     920
Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe Val Lys
275                 280                 285                 290

ATG CCG GAT AAA AAA CAT GCT TTC AGC GCG ACT TAT AAA GAG CAT TTA     968
Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu His Leu
                295                 300                 305

AAA AAC ATT AAT CTT TCT AAT AAT CAT TTT TAAGATTAAG GTAAATGGGG CGT  1021
Lys Asn Ile Asn Leu Ser Asn Asn His Phe
            310                 315

TTTTTCTTTT GAATTGAGTA AAAAGTGTTT                                   1051
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
Met Thr Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser
 1               5                  10                  15
Ile Leu Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val
            20                  25                  30
Val Pro Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln
        35                  40                  45
Gly Val Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly
    50                  55                  60
Met Pro Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys
65                  70                  75                  80
Gly Asp Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser
                85                  90                  95
Ala Thr Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu
            100                 105                 110
Ser Glu Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu
        115                 120                 125
Ser Ile Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile
```

```
    130                 135                 140
Trp Pro Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile
145                 150                 155                 160
Met Gln Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser
                165                 170                 175
Lys Gln Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile
            180                 185                 190
Ile Leu Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met
        195                 200                 205
Pro Leu Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro
    210                 215                 220
Leu Gln Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys
225                 230                 235                 240
Val Thr Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr
                245                 250                 255
Lys Phe Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu
            260                 265                 270
Ala Ile Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe
        275                 280                 285
Val Lys Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu
    290                 295                 300
His Leu Lys Asn Ile Asn Leu Ser Asn Asn His Phe
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...584
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
GAAAGTTCGG GGGCGGATTC TATGATTAAT GGCTATGGTT ATACCAAAGA ATG AGT      56
                                                        Met Ser
                                                          1

CAA AAA ATC CTA ATT CTA GGT ATT GGC AAT ATC CTT TTT GGC GAT GAA     104
Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly Asp Glu
          5                  10                  15

GGG ATT GGG GTG CAT TTA GCC CAC TAC CTC AAA AAA AAT TTT TCT TTT     152
Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe Ser Phe
     20                  25                  30

TTC CCT AGC GTG GAT ATT ATA GAT GGG GGG ACA ATG GCC CAG CAG CTC     200
Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln Gln Leu
35                  40                  45                  50
```

```
ATT CCT TTA ATC ACT TCG TAT GAA AAG GTT TTG ATT TTG GAT TGC GTG      248
Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val
                55                  60                  65

AGC GCT GAA GGC GTT GAG ATA GGA TCA GTC TAT GCT TTT GAT TTT AAG      296
Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys
            70                  75                  80

GAC GCT CCT AAA GAA ATC ACA TGG GCT GGG AGC GCT CAT GAA GTG GAA      344
Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu
        85                  90                  95

ATG CTA CAC ACT TTA AGG CTC ACG GAG TTT TTA GGG GAT TTG CCT AAA      392
Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys
    100                 105                 110

ACT TTT ATC GTG GGG CTT GTG CCT TTT GTG ATA GGG AGC GAG ACC ACT      440
Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr
115                 120                 125                 130

TTC AAG CTT TCA AGC AAA ATT TTA AAC GCT TTA GAA ACC GCC TTA AAA      488
Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala Leu Lys
                135                 140                 145

GCC ATA GAA ACC CAA CTC AAC GCA TGG GGG GTT AAA ATG CAA CGC ACC      536
Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln Arg Thr
            150                 155                 160

GAT CAT ATC GCT TTA GAA TGT ATC GCT GAA CTT TCT TAT AAG GGT TTT T    585
Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys Gly Phe
        165                 170                 175

GAATTGGTTT TTGTTTTTCT TTTTAAATGC GTTAATGAAG AAACAAGCCT GA           637
```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly
 1               5                  10                  15
Asp Glu Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe
            20                  25                  30
Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln
        35                  40                  45
Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp
    50                  55                  60
Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp
65                  70                  75                  80
Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu
```

```
                85                  90                  95
Val Glu Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu
            100                 105                 110
Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu
        115                 120                 125
Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala
    130                 135                 140
Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln
145                 150                 155                 160
Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys
                165                 170                 175
Gly Phe
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...161
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
GCATTGCTAA TTTGGGAATA CTTGTTTATG CCAGTGAAAT AGGAGCGGCT ATG ATG      56
                                                          Met Met
                                                            1

TGG CGT AGT CTC ARG GTG GCT TTT ACG ATC ACT GAT ATT AGT AAA ACC     104
Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser Lys Thr
 5                  10                  15

TTT CAA TCC CAG CCT AAG CAC CAT CAA ATC GGC ACT TTA GAA TTG AAT     152
Phe Gln Ser Gln Pro Lys His His Gln Ile Gly Thr Leu Glu Leu Asn
    20                  25                  30

TTC GCC TTT TGATTTAATA TCAGTTTAAT ATTTTTCTTC CTATATGATA TTTATATGA   210
Phe Ala Phe
35

TATT                                                               214
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
Met Met Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser
 1               5                  10                  15
Lys Thr Phe Gln Ser Gln Pro Lys His His Gln Ile Gly Thr Leu Glu
            20                  25                  30
Leu Asn Phe Ala Phe
        35
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1523
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
CTGTATTCGC TTCTGTGGAT TACTACCCTC AAAGAAAAGA AAGCCACAGA ATG AAC      56
                                                        Met Asn
                                                          1

ACC ACC ATC TTA GAA GCT TAT GCG GCT GAG CCA AGC AGG CAA ACC CTC     104
Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln Thr Leu
  5                  10                  15

TCT AAA GTC AGC AAC CGA TTC AAA GAG CAT GGC GCT AAA TTT GAT CTT     152
Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe Asp Leu
20                  25                  30

CGT GTG ATG GCA ACG CAT GGA GGC ACC ATT AGT TGG AAA GCT AAA GAA     200
Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala Lys Glu
35                  40                  45                  50

CTC GCT AGG ACT ATT GTG AGC GGC CCT ATT GGA GGC GTG ATT GGA TCT     248
Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile Gly Ser
                55                  60                  65

AAA TTG CTA GGC GAA ACG CTT GGT TAT GAC AAT ATT GCA TGC AGT GAT     296
Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys Ser Asp
            70                  75                  80

ATT GGK GGC ACG AGC TTT GAT ATG GCG CTT ATC GTT AAG AGC AAT TTT     344
Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser Asn Phe
        85                  90                  95
```

```
AAC ATC GCT TCT GAC CCT GAT ATG GCA CGC CTT GTT TTA TCT CTA CCG      392
Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser Leu Pro
    100                 105                 110

CTT GTG GCT ATG GAT TCT GTT GGC GCA GGT GCT GGG AGT TTT GTG CGC      440
Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe Val Arg
115                 120                 125                 130

ATT GAT CCA CAC AGC CGA TCT GTC AAA CTA GGG CCT GAC AGC GCG GGG      488
Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser Ala Gly
                135                 140                 145

TAT AGA GTT GGC ACT TGT TGG AAA GAC AGC GGG TTA GAC ACG GTT TCA      536
Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr Val Ser
            150                 155                 160

GTA ACC GAT TGC CAT ATT GTT TTA GGC TAT TTG AAC CCG GAT AAT TTC      584
Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp Asn Phe
        165                 170                 175

TTA GGC GGT TTG ATC AAA TTA GAT GTG GAT AGG GCT AAA AAA CAC ATT      632
Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys His Ile
    180                 185                 190

AAA GAA CAA ATC GCT GAT CCG CTA GGC ATT AGC GTA GAA GAT GCG GCT      680
Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp Ala Ala
195                 200                 205                 210

GCT GGT GTG ATT GAA TTG CTT GAT TTG GAG CTT AAA GAA TAC TTG CGA      728
Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr Leu Arg
                215                 220                 225

TCC AAC ATT AGC GCT AAA GGG TAT AGC CCA TCT GAT TTT GTG TGC TTT      776
Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val Cys Phe
            230                 235                 240

TCA TAT GGT GGC GCA GGA CCT GTG CAT ACC TAT GGC TAT ACA GAA GGA      824
Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr Glu Gly
        245                 250                 255

TTA GGG TTT AAG GAT GTG GTA GTG CCT GCG TGG GCG GCT GGA TTT AGC      872
Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly Phe Ser
    260                 265                 270

GCT TTT GGT TGT GCT TGC GCT GAT TTT GAA TAC AGA TAC GAC AAG AGC      920
Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp Lys Ser
275                 280                 285                 290

GTG GAT ATT GCC ATT CCG CAG TAT TCT TCA GAC AAG TCA AAA ATA GAC      968
Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys Ile Asp
                295                 300                 305

GCA TGC AAA ATC ATT CAA GAC GCA TGG GAT GAA TTG ACT TTG AAA GTG     1016
Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu Lys Val
            310                 315                 320

ATT GAA GAG TTC AAG ATC AAT GGA TTT TCT CAA AAA GAT GTG ATC TTA     1064
Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val Ile Leu
```

```
          325                 330                 335

AGA CCT GGA TAC AGG ATG CAG TAT ATG GGG CAA TTG AAT GAT TTA GAG    1112
Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp Leu Glu
    340                 345                 350

ATC ACT TCT CCT GTG TCA AAA GCT GCA AGC GTG GCT GAT TGG GAA GAG    1160
Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp Glu Glu
355                 360                 365                 370

ATT GTC AAA GAA TAT GAA AAA ACC TAC GCT CGC GTT TAT TCT GAA TCA    1208
Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser Glu Ser
                375                 380                 385

GCG TGT TCT CCA GAG CTT GGT TTT AGC GTG ACT GGC GTG ATC ATG CGT    1256
Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile Met Arg
            390                 395                 400

GGT GTT GTG GCT ACG CAA AAA CCT GTG ATT CCG GTT GAA AAA GAG CAT    1304
Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys Glu His
        405                 410                 415

GGT GCT ACG CCC CCA AAA GAA GCC AAA ATA GGC GTT AGA AAA TTC TAT    1352
Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys Phe Tyr
    420                 425                 430

CGG CAT AAA AAA TGG GTG GAT GCA GAT GTG TGG CAA ATG GAA AAA TTA    1400
Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu Lys Leu
435                 440                 445                 450

CTG CCT GGA AAT GAA GTC ATA GGA CCT GCG ATC GTG GAA TCA GAT GCG    1448
Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser Asp Ala
                455                 460                 465

ACC ACT TTC GTG ATA CCC AAA GGC TTT GCG ACA AGA CTA GAC AAA CAC    1496
Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp Lys His
            470                 475                 480

CGA TTG TTC CAC TTG AAA GAA ATT AAA TAAAGGAGTT CAAAATGGCA AATTTAT  1550
Arg Leu Phe His Leu Lys Glu Ile Lys
        485                 490

TGAAAAACGG CAAAACTTTA AAACAA                                       1576
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Asn Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln

```
 1               5                  10                  15
Thr Leu Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe
            20                  25                  30
Asp Leu Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala
        35                  40                  45
Lys Glu Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile
    50                  55                  60
Gly Ser Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys
65                  70                  75                  80
Ser Asp Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser
                85                  90                  95
Asn Phe Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser
            100                 105                 110
Leu Pro Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe
        115                 120                 125
Val Arg Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser
    130                 135                 140
Ala Gly Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr
145                 150                 155                 160
Val Ser Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp
                165                 170                 175
Asn Phe Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys
            180                 185                 190
His Ile Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp
        195                 200                 205
Ala Ala Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr
    210                 215                 220
Leu Arg Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val
225                 230                 235                 240
Cys Phe Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr
                245                 250                 255
Glu Gly Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly
            260                 265                 270
Phe Ser Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp
        275                 280                 285
Lys Ser Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys
    290                 295                 300
Ile Asp Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu
305                 310                 315                 320
Lys Val Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val
                325                 330                 335
Ile Leu Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp
            340                 345                 350
Leu Glu Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp
        355                 360                 365
Glu Glu Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser
    370                 375                 380
Glu Ser Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile
385                 390                 395                 400
Met Arg Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys
                405                 410                 415
Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys
            420                 425                 430
Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu
        435                 440                 445
Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser
    450                 455                 460
Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp
```

```
465                 470                 475                 480
Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
                485                 490
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...261
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
GTAAGCTAGA GTTTATGCAA AGGGAGATGA GTAGCCTAGA AGCTAAGCAT T ATG ATT      57
                                                          Met Ile
                                                           1

CAG TTA AAA TCA AAT TTG GAT TGG TAC GCA GAT TAT TTG AAT TTT TTA      105
Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn Phe Leu
 5                   10                  15

GAT CGC TTT GGG GAA AAA ATG GAA GAA TCC AAA GAG CGA AAA CAA CTC      153
Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys Gln Leu
    20                  25                  30

CTG ATC GCT TCC CTT GCA CCT CTT GCG GGC TTT GCT GCA AGA ATA TCG      201
Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg Ile Ser
35                  40                  45                  50

CCG GGA TTA TTG AGC TTA TTG GGT TTG ATG CTG GCA ATG GGG TGT GCA      249
Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly Cys Ala
                55                  60                  65

AAT TTT TGG ATT TAGAAACCAA TCTGTGCAAG ATTTATGAAT CGCGCCCGTT AA      303
Asn Phe Trp Ile
            70
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
Met Ile Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn
 1               5                  10                  15
Phe Leu Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys
            20                  25                  30
Gln Leu Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg
        35                  40                  45
Ile Ser Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly
    50                  55                  60
Cys Ala Asn Phe Trp Ile
65                  70
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...773
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
TGGCTTAATT GTTAAGCCGG CTAGAAAAAG AGCGTTATTT GCGCCATATC  ATG CTA      56
                                                        Met Leu
                                                         1

GAA GAT GTG GGC GAA GAG GGT CAA TTG AAG CTT TTA AAA TCT AGC GTT      104
Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser Ser Val
          5                  10                  15

TTA GTC ATT GGG GCT GGG GGT CTT GGA TCG GCG GTT TTG ATG TAT TTG      152
Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met Tyr Leu
    20                  25                  30

TGT GCC GCT GGG ATA GGA AAA ATC GGT ATT GTA GAT TTT GAT GTA GTA      200
Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp Val Val
35                  40                  45                  50

GAT ATG AGT AAT TTG CAA CGC CAA ATC ATC CAT TCA CAG GAT TTT TTA      248
Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp Phe Leu
                55                  60                  65

AAC CAA TCT AAA GCC TCT AGC GCG AAA GCG CGC TTA AAA CAA CTC AAT      296
Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln Leu Asn
            70                  75                  80

GCG GGT ATT GAA ATA GAG GCT TTT GAA GAA CGC TTT AAG GCT CAT AAC      344
Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala His Asn
        85                  90                  95
```

```
GCT CTT TCT CTC ATA GAG CCT TAT GAT TTT ATC ATA GAC GCC ACG GAC      392
Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala Thr Asp
    100                 105                 110

AAT TTT AAC GCT AAA TTT TTG ATC AAT GAC GCT TGC GTG TTA GCC CAA      440
Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu Ala Gln
115                 120                 125                 130

AAA CCC TAT TCG CAT GCC GGG GTT TTA GAA TAC AGG GGG CAA AGC ATG      488
Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln Ser Met
                135                 140                 145

AGC GTT TTA CCC CAT AGC GCA TGC TTA GCG TGC GTT TTT GAT AAG CCC      536
Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp Lys Pro
            150                 155                 160

CCT AAA AAG GGA TTA AAT CCC ATT TCA GGG CTT TTT GGG GTC TTA CCC      584
Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val Leu Pro
        165                 170                 175

GGA GTT TTA GGG TGT ATC CAA GCG AGC GAA TGC CTT AAA TAT TTT TTA      632
Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr Phe Leu
    180                 185                 190

GGG TTT GAA ACT TTA CTT ATA AAT ACT TTA CTT ATA GCC GAT ATT AAA      680
Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp Ile Lys
195                 200                 205                 210

ACG ATG GAT TTT AAA AAA ATT CAA GCA CCC AAA AAC CCT GAA TGT AGG      728
Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu Cys Arg
                215                 220                 225

GTT TGT GGC ACG CAT AAA ATC ACG CAT TTA CAG GAT TAT GAA ATT TAGAT    778
Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu Ile
            230                 235                 240

TAAGGGGTAA GTTTTGGATT TATCAACCAT ATTAGGCTTG GTATTGGC                 826
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
Met Leu Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser
 1               5                  10                  15
Ser Val Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met
            20                  25                  30
Tyr Leu Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp
        35                  40                  45
Val Val Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp
```

```
    50                  55                  60
Phe Leu Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln
65                  70                  75                  80
Leu Asn Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala
                85                  90                  95
His Asn Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala
            100                 105                 110
Thr Asp Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu
        115                 120                 125
Ala Gln Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln
    130                 135                 140
Ser Met Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp
145                 150                 155                 160
Lys Pro Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val
                165                 170                 175
Leu Pro Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr
            180                 185                 190
Phe Leu Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp
        195                 200                 205
Ile Lys Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu
    210                 215                 220
Cys Arg Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu
225                 230                 235                 240
Ile
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...494
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
AAAATTCATT CTATTTTAGA TAATGAGTTC AATCCCCACA AACAGCAAGA ATG AAT      56
                                                          Met Asn
                                                            1

CGC ATG AAT AAA AAT TAT CTT TTA ATC TTT TTG TTG TTA GCG AGT CTT     104
Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu
          5                  10                  15

GTT GCT AGA GAG AAG GAC GCT TCT TCA AAC CTT TTT GAT TTG ATT GAT     152
Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp
     20                  25                  30

AAG GGG ATC AAC AGA GAA CAA GAA TTA AAA GAG CAG GAG CAA AAA ACG     200
```

```
Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln Lys Thr
35                  40                  45                  50

CGC TTA AAA CTG GCT CAA AGC CCT TTA GTA GCG TTA GAG ATT GTC CCC      248
Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile Val Pro
                55                  60                  65

CAA GAA ACG CCC TAT TTA GAA TGG CAA GGG GCT AGG GAG TCG TAT TAT      296
Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser Tyr Tyr
            70                  75                  80

TTA AAG GTG AGC GCT GTA GTG GAG AGC GTG GTT ATC TTA AAA ATT GAC      344
Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys Ile Asp
        85                  90                  95

ATC AAT CAA GGG CGT TCT TGC TCG CTC TAC CCC ACG CCT AAA AGC GTT      392
Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys Ser Val
    100                 105                 110

TCT TTA GTG AGG AAT CAA AGC GTA GCC TAT GAA ATT TTA TGC GAA AAC      440
Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys Glu Asn
115                 120                 125                 130

CAA CCC CTA TGG ATA GAA GTA AGC ACC AAT TTA GGC AAA CGC ACC TTT      488
Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg Thr Phe
                135                 140                 145

CAG TTT TAACCTGCAA CCAACATTAA AGAATGCCTT TAGCATTTTA AAACCCCTTT AT    546
Gln Phe

C                                                                    547
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```
Met Asn Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala
 1               5                  10                  15
Ser Leu Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu
            20                  25                  30
Ile Asp Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln
        35                  40                  45
Lys Thr Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile
    50                  55                  60
Val Pro Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser
65                  70                  75                  80
Tyr Tyr Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys
                85                  90                  95
Ile Asp Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys
```

```
            100                 105                 110
Ser Val Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys
        115                 120                 125
Glu Asn Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg
    130                 135                 140
Thr Phe Gln Phe
145
```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1631
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
CCTTTCTTTA TTCTCATTGC ATCTTGTGGG ATCATTTTTT TTTTTTATTA ATG CTA      56
                                                        Met Leu
                                                          1

GCT TCC ATC ATC TCA ATT TTA AGG GTT TTT GTT TTG TTA TTC AAC ACG     104
Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe Asn Thr
        5                   10                  15

CCG TTA TTC ATC TTT GCT TTT TTG CCT GTT GGT TTT TTA GGG TAT TTT     152
Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly Tyr Phe
    20                  25                  30

ATC TTG CAA GCT TAT GCT AAA AAT CCC CTG TTC CCT AAA CTA TGG CTA     200
Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu Trp Leu
35                  40                  45                  50

GTA TTG GCT AGT TTG TTT TTT TAT GCT TTT TGG AAT GTG AAG TAT TTG     248
Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys Tyr Leu
                55                  60                  65

CCC TTA TTG GTT GGC TCT ATT GTT TTT AAT TAT TTT GTG GCT TTG AAA     296
Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala Leu Lys
            70                  75                  80

ATC CAT CAA ACC CAG CCA AAT GCA TAT AAA AGA TTA TGG CTT ATT TTG     344
Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu Ile Leu
        85                  90                  95

GGC TTG ATC GCT AAT GTT TCA CTT TTA GGA TTT TTC AAA TAC ACT GAT     392
Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr Thr Asp
    100                 105                 110
```

```
TTT TTC TTA ACC AAT TTC AAT CTA ATA TGG AAG AGC CAT TTT GAA ACC      440
Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe Glu Thr
115                 120                 125                 130

TTG CAT TTA ATC TTG CCT TTA GCG ATC AGC TTT TTC ACT TTG CAA CAA      488
Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu Gln Gln
                135                 140                 145

ATC GCT TAC TTG ATG GAC ACT TAT AAG CAA AAT CAA ATC ATG CAG CCC      536
Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met Gln Pro
            150                 155                 160

AAA ATG AGA GAG AGA GTG AGT GAA AAC GCT CCT ATT TTA TTA AAT CCT      584
Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu Asn Pro
        165                 170                 175

CCC ACT TCA TTT TTT TCA CTT TCG CAT TTT TTA GAT TAC GCT TTA TTT      632
Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala Leu Phe
    180                 185                 190

GTG AGT TTC TTC CCT CAA CTC ATT GCA GGG CCT ATT GTG CAT CAT AGC      680
Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His His Ser
195                 200                 205                 210

GAG ATG ATG CCT CAA TTT AAA GAT AAA AAC AAT CAA TAT TTG AAT TAC      728
Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu Asn Tyr
                215                 220                 225

AGA AAT ATC GCT TTA GGC TTG TTT ATC TTT TCT ATC GGT TTG TTT AAA      776
Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu Phe Lys
            230                 235                 240

AAG GTC GTG ATT GCA GAT AAT ACC GCT CAT TTT GCT GAT TTT GGA TTT      824
Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe Gly Phe
        245                 250                 255

GAT AAG GCG ACT AGC TTA AGT TTT ATT CAA GCA TGG ATG ACT TCT TTA      872
Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr Ser Leu
    260                 265                 270

TCT TAT TCG TTC CAG CTG TAT TTT GAT TTT AGC GGT TAT TGC GAT ATG      920
Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys Asp Met
275                 280                 285                 290

GCT ATA GGC ATT GGC CTC TTT TTT AAC ATC AAA CTC CCT ATC AAT TTT      968
Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile Asn Phe
                295                 300                 305

AAT AGC CCC TAT AAG GCT TTG AAT ATC CAA GAT TTT TGG AGG AGG TGG     1016
Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg Arg Trp
            310                 315                 320

CAT ATC ACT TTG AGC CGC TTC TTA AAA GAG TAT TTG TAT ATC CCT TTA     1064
His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile Pro Leu
        325                 330                 335

GGG GGT AAT AGG GTG AAA GAA TTA ATC GTG TAT AGG AAT TTA ATT TTA     1112
Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu Ile Leu
```

```
    340                 345                 350

GTG TTT TTG ATT GGG GGG TTT TGG CAT GGG GCT GGT TGG ACT TTT ATC    1160
Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr Phe Ile
355                 360                 365                 370

ATT TGG GGG CTA TTG CAT GGG ATT GCT TTG AGC GTT CAT AGA GCG TAT    1208
Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg Ala Tyr
                375                 380                 385

TCT CAT GCC ACT AGA AAA TTC CAT TTC ACT ATG CCA AAG ATT TTA GCA    1256
Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile Leu Ala
            390                 395                 400

TGG CTC ATC ACT TTT AAT TTT ATC AAT CTC GCA TGG GTG TTT TTT AGA    1304
Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe Phe Arg
        405                 410                 415

GCC AAA AAT TTA GAA AGC GCT TTG AAG GTT TTA AAG GGG ATG GTT GGT    1352
Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met Val Gly
    420                 425                 430

TTG AAT GGT GTT TCG CTT TGT CAT CTT TCA AAA GAG GCA TCA GAG TTT    1400
Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser Glu Phe
435                 440                 445                 450

TTA AAT CGT GTC AAT GAT AAC ATG ATC ATG CAC ACC ATA ATG TAT GCA    1448
Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met Tyr Ala
                455                 460                 465

TCC CCC ACA TTT AAA ATG TGT GTT TTG ATG ATA ATC ATC TCT TTT TGT    1496
Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser Phe Cys
            470                 475                 480

TTA AAA AAT AGT TCC CAT TTA TAC CAA TCC AAT CAA ATG GAT TGG ATT    1544
Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp Trp Ile
        485                 490                 495

AAA ACA ACA AGC GCT TGT TTG TTG CTC TCT ATA GGT TTT TTA TTT ATT    1592
Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu Phe Ile
    500                 505                 510

TTT GCC AGT TCT CAA TCG GTA TTT TTG TAT TTT AAT TTT TAGGACACTG CT  1643
Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe
515                 520                 525

ATGGAATTTT ATAAAAAACA AACTTTAATC ATTGTTTCTT T                      1684
```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 527 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```
Met Leu Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe
 1               5                  10                  15
Asn Thr Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly
            20                  25                  30
Tyr Phe Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu
        35                  40                  45
Trp Leu Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys
    50                  55                  60
Tyr Leu Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala
65                  70                  75                  80
Leu Lys Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu
                85                  90                  95
Ile Leu Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr
            100                 105                 110
Thr Asp Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe
        115                 120                 125
Glu Thr Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu
    130                 135                 140
Gln Gln Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met
145                 150                 155                 160
Gln Pro Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu
                165                 170                 175
Asn Pro Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala
            180                 185                 190
Leu Phe Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His
        195                 200                 205
His Ser Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu
    210                 215                 220
Asn Tyr Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu
225                 230                 235                 240
Phe Lys Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe
                245                 250                 255
Gly Phe Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr
            260                 265                 270
Ser Leu Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys
        275                 280                 285
Asp Met Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile
    290                 295                 300
Asn Phe Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg
305                 310                 315                 320
Arg Trp His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile
                325                 330                 335
Pro Leu Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu
            340                 345                 350
Ile Leu Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr
        355                 360                 365
Phe Ile Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg
    370                 375                 380
Ala Tyr Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile
385                 390                 395                 400
Leu Ala Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe
                405                 410                 415
Phe Arg Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met
            420                 425                 430
Val Gly Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser
        435                 440                 445
```

```
Glu Phe Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met
    450                 455                 460
Tyr Ala Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser
465                 470                 475                 480
Phe Cys Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp
                485                 490                 495
Trp Ile Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu
            500                 505                 510
Phe Ile Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe
        515                 520                 525
```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3973 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...3920
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
AAAGTCGCAC CCTTTGTGCA AAAATCGTTT TACAAGAAGA AAGGAAAAAA ATG GAA      56
                                                        Met Glu
                                                          1

ATA CAA CAA ACA CAC CGC AAA ATC AAT CGC CCT TTG GTT TCT CTC GCT     104
Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser Leu Ala
          5                  10                  15

TTA GTA GGA GCG TTA GTC AGC ATC ACA CCG CAA CAA AGT CAT GCC GCC     152
Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His Ala Ala
     20                  25                  30

TTT TTC ACA ACC GTG ATC ATT CCA GCC ATT GTT GGG GGG ATT GCT ACA     200
Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile Ala Thr
35                  40                  45                  50

GGC GCT GCT GTA GGA ACG GTC TCA GGG CTT CTT GGC TGG GGG CTA AAA     248
Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly Leu Lys
                55                  60                  65

CAA GCC GAA GAA GCC AAT AAA ACC CCA GAT AAA CCC GAT AAA GTT TGG     296
Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys Val Trp
            70                  75                  80

CGC ATT CAA GCA GGA AAA GGC TTT AAT GAA TTC CCT AAC AAG GAA TAC     344
Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys Glu Tyr
        85                  90                  95
```

```
GAC TTA TAC AGA TCC CTA CTA TCT AGT AAG ATT GAT GGA GGC TGG GAT      392
Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly Trp Asp
    100                 105                 110

TGG GGG AAT GCC GCT ACG CAT TAT TGG GTC AAA GGC GGG CAA TGG AAC      440
Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln Trp Asn
115                 120                 125                 130

AAG CTT GAA GTG GAT ATG AAA GAC GCT GTA GGG ACT TAT AAT CTC TCA      488
Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn Leu Ser
                135                 140                 145

GGG CTA AGA AAC TTT ACT GGT GGG GAT TTA GAT GTC AAT ATG CAA AAA      536
Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met Gln Lys
            150                 155                 160

GCC ACT TTG CGC TTG GGC CAA TTC AAT GGC AAT TCT TTC ACA AGC TAT      584
Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr
        165                 170                 175

AAG GAT AGC GCT GAT CGC ACC ACG AGA GTG GAT TTC AAC GCT AAA AAT      632
Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn
    180                 185                 190

ATC TTA ATT GAT AAT TTT TTA GAA ATC AAT AAT CGT GTG GGT TCT GGA      680
Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly
195                 200                 205                 210

GCC GGG AGG AAA GCC AGC TCT ACG GTT TTA ACT TTG CAA GCT TCA GAA      728
Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu
                215                 220                 225

GGG ATT ACT AGC AGT AAA AAT GCG GAA ATT TCT CTT TAT GAT GGC GCC      776
Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala
            230                 235                 240

ACG CTC AAT TTG GCT TCA AAC AGC GTT AAA TTA ATG GGT AAT GTG TGG      824
Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp
        245                 250                 255

ATG GGC CGT TTG CAA TAT GTG GGA GCG TAT TTG GCC CCT TCA TAC AGC      872
Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser
    260                 265                 270

ACG ATA AAC ACT TCA AAA GTG ACA GGG GAA GTG AAT TTT AAC CAT CTC      920
Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu
275                 280                 285                 290

ACT GTG GGC GAT CAC AAC GCC GCT CAA GCA GGC ATT ATC GCT AGT AAC      968
Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn
                295                 300                 305

AAG ACT CAT ATT GGC ACA CTG GAT TTG TGG CAA AGC GCG GGA CTA AAC     1016
Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn
            310                 315                 320

ATT ATC GCC CCT CCA GAA GGC GGT TAT AAG GAT AAA CCT AAG GAT AAA     1064
Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys
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        325                 330                 335

CCT AGT AAC ACC ACG CAA AAT AAT GCT AAC AAC AAC CAA CAA AAC AGC    1112
Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser
    340                 345                 350

GCT CAA AAC AAT AGT AAC ACT CAG GTT ATT AAC CCA CCC AAT AGC GCG    1160
Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala
355                 360                 365                 370

CAA AAA ACA GAA ATT CAA CCC ACG CAA GTC ATT GAT GGG CCT TTT GCT    1208
Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala
                375                 380                 385

GGT GGC AAA GAC ACG GTT GTC AAT ATT GAT CGC ATC AAC ACT AAC GCT    1256
Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr Asn Ala
            390                 395                 400

GAT GGC ACG ATT AAA GTG GGA GGG TAT AAA GCT TCT CTT ACC ACC AAT    1304
Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr Thr Asn
        405                 410                 415

GCG GCT CAT TTG CAT ATC GGC AAA GGC GGT ATC AAT CTG TCC AAT CAA    1352
Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser Asn Gln
    420                 425                 430

GCG AGC GGG CGC ACC CTT TTA GTG GAA AAT CTA ACC GGG AAT ATC ACC    1400
Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr
435                 440                 445                 450

GTT GAT GGG CCT TTA AGA GTG AAT AAT CAA GTG GGT GGT TAT GCT TTG    1448
Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu
                455                 460                 465

GCA GGA TCA AGC GCG AAT TTT GAG TTT AAG GCT GGT ACG GAT ACC AAA    1496
Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp Thr Lys
            470                 475                 480

AAC GGC ACA GCC ACT TTT AAT AAC GAT ATT AGT TTG GGA AGA TTT GTG    1544
Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg Phe Val
        485                 490                 495

AAT TTA AAA GTG GAT GCT CAT ACA GCT AAT TTT AAA GGT ATT GAT ACT    1592
Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile Asp Thr
    500                 505                 510

GGT AAT GGT GGT TTC AAC ACC TTA GAT TTT AGT GGC GTT ACA GGT AAG    1640
Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr Gly Lys
515                 520                 525                 530

GTC AAT ATC AAC AAG CTC ATT ACG GCT TCC ACT AAT GTG GCC GTT AAA    1688
Val Asn Ile Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala Val Lys
                535                 540                 545

AAC TTC AAC ATT AAT GAA TTG GTT GTT AAG ACC AAT GGG GTG AGT GTG    1736
Asn Phe Asn Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val Ser Val
            550                 555                 560
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GGG GAA TAC ACT CAT TTT AGC GAA GAT ATA GGC AGT CAA TCG CGC ATC 1784
Gly Glu Tyr Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser Arg Ile
565 570 575

AAT ACC GTG CGT TTG GAA ACT GGC ACT AGG TCA ATC TTT TCT GGG GGT 1832
Asn Thr Val Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser Gly Gly
580 585 590

GTC AAA TTT AAA AGC GGT GAA AAA CTG GTT ATA GAT GAG TTT TAC TAT 1880
Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe Tyr Tyr
595 600 605 610

AGC CCT TGG AAT TAT TTT GAC GCT AGG AAT ATT AAA AAT GTT GAA ATC 1928
Ser Pro Trp Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val Glu Ile
615 620 625

ACC AGA AAA TTC GCT TCT TCA ACC CCA GAA AAC CCT TGG GGC ACA TCA 1976
Thr Arg Lys Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly Thr Ser
630 635 640

AAG CTT ATG TTT AAT AAT CTA ACC CTG GGT CAA AAT GCG GTC ATG GAC 2024
Lys Leu Met Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val Met Asp
645 650 655

TAT AGT CAA TTT TCA AAT TTA ACC ATT CAG GGG GAT TTC ATC AAC AAT 2072
Tyr Ser Gln Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile Asn Asn
660 665 670

CAA GGC ACT ATC AAT TAT TTG GTC CGA GGC GGG CAA GTA GCC ACC TTG 2120
Gln Gly Thr Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala Thr Leu
675 680 685 690

AAT GTA GGC AAT GCG GCA GCT ATG TTC TTT AGT AAT AAT GTG GAT AGC 2168
Asn Val Gly Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val Asp Ser
695 700 705

GCG ACT GGG TTT TAC CAA CCG CTC ATG AAG ATT AAC AGC GCT CAA GAT 2216
Ala Thr Gly Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala Gln Asp
710 715 720

CTC ATT AAA AAT AAA GAA CAT GTC TTA TTG AAA GCG AAA ATC ATC GGT 2264
Leu Ile Lys Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly
725 730 735

TAT GGC AAT GTT TCT TTA GGC ACT AAC AGC ATT AGT AAT GTT AAT CTA 2312
Tyr Gly Asn Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val Asn Leu
740 745 750

ATA GAG CAA TTC AAA GAG CGC CTA GCC CTT TAC AAC AAC AAT AAC CGC 2360
Ile Glu Gln Phe Lys Glu Arg Leu Ala Leu Tyr Asn Asn Asn Asn Arg
755 760 765 770

ATG GAT ATT TGT GTG GTG CGA AAT ACT GAT GAC ATT AAA GCA TGC GGG 2408
Met Asp Ile Cys Val Val Arg Asn Thr Asp Asp Ile Lys Ala Cys Gly
775 780 785

ACG GCT ATC GGC AAT CAA AGC ATG GTG AAT AAC CCC GAC AAT TAC AAG 2456
Thr Ala Ile Gly Asn Gln Ser Met Val Asn Asn Pro Asp Asn Tyr Lys

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                790                 795                 800

TAT CTT ATC GGT AAA GCA TGG AAG AAC ATA GGG ATC AGC AAA ACA GCT    2504
Tyr Leu Ile Gly Lys Ala Trp Lys Asn Ile Gly Ile Ser Lys Thr Ala
        805                 810                 815

AAT GGC TCT AAA ATT TCG GTG TAT TAT TTA GGC AAT TCT ACG CCT ACT    2552
Asn Gly Ser Lys Ile Ser Val Tyr Tyr Leu Gly Asn Ser Thr Pro Thr
    820                 825                 830

GAG AAA GGT GGC AAT ACC ACA AAT TTA CCT ACA AAC ACC ACT AGC AAT    2600
Glu Lys Gly Gly Asn Thr Thr Asn Leu Pro Thr Asn Thr Thr Ser Asn
835                 840                 845                 850

GTG CGT TCT GCC AAC AAC GCC CTT GCG CAA AAC GCT CCT TTC GCT CAA    2648
Val Arg Ser Ala Asn Asn Ala Leu Ala Gln Asn Ala Pro Phe Ala Gln
                855                 860                 865

CCT AGC GCC ACT CCT AAT TTA GTC GCT ATC AAT CAG CAT GAT TTT GGC    2696
Pro Ser Ala Thr Pro Asn Leu Val Ala Ile Asn Gln His Asp Phe Gly
            870                 875                 880

ACC ATT GAA AGC GTG TTT GAA TTG GCT AAC CGC TCT AAA GAT ATT GAC    2744
Thr Ile Glu Ser Val Phe Glu Leu Ala Asn Arg Ser Lys Asp Ile Asp
        885                 890                 895

ACG CTT TAT GCT AAC TCA GGC GCG CAA GGC AGG GAT CTC TTA CAA ACC    2792
Thr Leu Tyr Ala Asn Ser Gly Ala Gln Gly Arg Asp Leu Leu Gln Thr
    900                 905                 910

TTA TTG ATT GAT AGC CAT GAT GCG GGT TAT GCC AGA CAA ATG ATT GAT    2840
Leu Leu Ile Asp Ser His Asp Ala Gly Tyr Ala Arg Gln Met Ile Asp
915                 920                 925                 930

AAC ACA AGC ACC GGT GAA ATC ACC AAG CAA TTG AAT GCG GCC ACT ACC    2888
Asn Thr Ser Thr Gly Glu Ile Thr Lys Gln Leu Asn Ala Ala Thr Thr
                935                 940                 945

ACT TTA AAC AAC ATA GCC AGT TTA GAG CAT AAG ACA AGC AGC TTA CAA    2936
Thr Leu Asn Asn Ile Ala Ser Leu Glu His Lys Thr Ser Ser Leu Gln
            950                 955                 960

ACT TTG AGC TTG AGT AAT GCG ATG ATC TTA AAT TCT CGT TTA GTC AAT    2984
Thr Leu Ser Leu Ser Asn Ala Met Ile Leu Asn Ser Arg Leu Val Asn
        965                 970                 975

CTC TCC AGA AGG CAC ACC AAT AAT ATT GAC TCA TTC GCC CAA CGC TTA    3032
Leu Ser Arg Arg His Thr Asn Asn Ile Asp Ser Phe Ala Gln Arg Leu
    980                 985                 990

CAA GCT TTA AAA GAC CAA AAA TTC GCT TCT TTA GAA AGC GCG GCG GAA    3080
Gln Ala Leu Lys Asp Gln Lys Phe Ala Ser Leu Glu Ser Ala Ala Glu
995                1000                1005                1010

GTG TTG TAT CAA TTT GCC CCT AAA TAT GAA AAA CCT ACC AAT GTT TGG    3128
Val Leu Tyr Gln Phe Ala Pro Lys Tyr Glu Lys Pro Thr Asn Val Trp
               1015                1020                1025
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GCT AAC GCT ATT GGG GGA ACG AGC TTG AAT AAT GGC GGC AAC GCT TCA    3176
Ala Asn Ala Ile Gly Gly Thr Ser Leu Asn Asn Gly Gly Asn Ala Ser
          1030                1035                1040

TTG TAT GGC ACA AGT GCG GGC GTA GAT GCC TAC CTT AAT GGG GAA GTG    3224
Leu Tyr Gly Thr Ser Ala Gly Val Asp Ala Tyr Leu Asn Gly Glu Val
      1045                1050                1055

GAA GCC ATT GTG GGC GGT TTT GGA AGC TAT GGT TAT AGC TCT TTT AAT    3272
Glu Ala Ile Val Gly Gly Phe Gly Ser Tyr Gly Tyr Ser Ser Phe Asn
  1060                1065                1070

AAT CAA GCG AAC TCT CTT AAC TCT GGA GCC AAT AAC ACT AAT TTT GGC    3320
Asn Gln Ala Asn Ser Leu Asn Ser Gly Ala Asn Asn Thr Asn Phe Gly
1075                1080                1085                1090

GTG TAT AGC CGT ATC TTT GCT AAC CAG CAT GAA TTT GAT TTT GAA GCT    3368
Val Tyr Ser Arg Ile Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
              1095                1100                1105

CAA GGG GCG CTA GGG AGT GAT CAA TCA AGC TTG AAT TTC AAA AGC GCT    3416
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Ala
          1110                1115                1120

CTA TTG CGA GAT TTG AAT CAA AGC TAT AAT TAC TTA GCC TAT AGC GCT    3464
Leu Leu Arg Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
      1125                1130                1135

GCA ACA AGA GCG AGC TAT GGT TAT GAC TTT GCA TTT TTT AGG AAC GCT    3512
Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
  1140                1145                1150

TTG GTG TTA AAA CCA AGC GTG GGC GTG AGC TAT AAC CAT TTA GGT TCA    3560
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
1155                1160                1165                1170

ACC AAC TTT AAA AGC AAT AGC AAT CAA GTG GCT TTG AAA AAT GGC TCT    3608
Thr Asn Phe Lys Ser Asn Ser Asn Gln Val Ala Leu Lys Asn Gly Ser
              1175                1180                1185

AGC AGT CAG CAT TTA TTC AAC GCT AGC GCT AAT GTG GAA GCG CGC TAT    3656
Ser Ser Gln His Leu Phe Asn Ala Ser Ala Asn Val Glu Ala Arg Tyr
          1190                1195                1200

TAT TAT GGG GAC ACT TCA TAC TTC TAT ATG AAC GCT GGA GTT TTA CAA    3704
Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val Leu Gln
      1205                1210                1215

GAA TTT GCT AAC TTT GGT TCT AGC AAT GCG GTA TCT TTA AAC ACC TTT    3752
Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn Thr Phe
  1220                1225                1230

AAA GTG AAT GCC GCA CAC AAT CCT TTA AGT ACC CAT GCC AGA GTG ATG    3800
Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg Val Met
1235                1240                1245                1250

ATG GGT GGG GAA TTA AAA TTA GCT AAA GAA GTG TTT TTG AAT TTG GGC    3848
Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn Leu Gly
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                1255                1260                1265

TTT GTT TAT TTG CAC AAT TTG ATT TCC AAT ATA GGC CAT TTC GCT TCC     3896
Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe Ala Ser
            1270                1275                1280

AAT TTA GGA ATG AGG TAT AGT TTC TAAATACCGC TCTTAAACCC ATGCTCAAAG    3950
Asn Leu Gly Met Arg Tyr Ser Phe
        1285                1290

CATGGGTTTG AAATCTTACA AAA                                          3973
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(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

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Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
 1               5                  10                  15
Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His
            20                  25                  30
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
        35                  40                  45
Ala Thr Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly
    50                  55                  60
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65                  70                  75                  80
Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
                85                  90                  95
Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
            100                 105                 110
Trp Asp Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln
        115                 120                 125
Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn
    130                 135                 140
Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145                 150                 155                 160
Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
                165                 170                 175
Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
            180                 185                 190
Lys Asn Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly
        195                 200                 205
Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
    210                 215                 220
Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
225                 230                 235                 240
Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn
                245                 250                 255
Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
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            260                 265                 270
Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
        275                 280                 285
His Leu Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala
    290                 295                 300
Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
305                 310                 315                 320
Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys
                325                 330                 335
Asp Lys Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln
            340                 345                 350
Asn Ser Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn
        355                 360                 365
Ser Ala Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro
    370                 375                 380
Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr
385                 390                 395                 400
Asn Ala Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr
                405                 410                 415
Thr Asn Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser
            420                 425                 430
Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn
        435                 440                 445
Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr
    450                 455                 460
Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp
465                 470                 475                 480
Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg
                485                 490                 495
Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile
            500                 505                 510
Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr
        515                 520                 525
Gly Lys Val Asn Ile Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala
    530                 535                 540
Val Lys Asn Phe Asn Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val
545                 550                 555                 560
Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser
                565                 570                 575
Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser
            580                 585                 590
Gly Gly Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe
        595                 600                 605
Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val
    610                 615                 620
Glu Ile Thr Arg Lys Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly
625                 630                 635                 640
Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val
                645                 650                 655
Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile
            660                 665                 670
Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala
        675                 680                 685
Thr Leu Asn Val Gly Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val
    690                 695                 700
Asp Ser Ala Thr Gly Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala
705                 710                 715                 720
Gln Asp Leu Ile Lys Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile
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                725                 730                 735
Ile Gly Tyr Gly Asn Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val
            740                 745                 750
Asn Leu Ile Glu Gln Phe Lys Glu Arg Leu Ala Leu Tyr Asn Asn Asn
        755                 760                 765
Asn Arg Met Asp Ile Cys Val Val Arg Asn Thr Asp Asp Ile Lys Ala
    770                 775                 780
Cys Gly Thr Ala Ile Gly Asn Gln Ser Met Val Asn Asn Pro Asp Asn
785                 790                 795                 800
Tyr Lys Tyr Leu Ile Gly Lys Ala Trp Lys Asn Ile Gly Ile Ser Lys
                805                 810                 815
Thr Ala Asn Gly Ser Lys Ile Ser Val Tyr Tyr Leu Gly Asn Ser Thr
            820                 825                 830
Pro Thr Glu Lys Gly Gly Asn Thr Thr Asn Leu Pro Thr Asn Thr Thr
        835                 840                 845
Ser Asn Val Arg Ser Ala Asn Asn Ala Leu Ala Gln Asn Ala Pro Phe
    850                 855                 860
Ala Gln Pro Ser Ala Thr Pro Asn Leu Val Ala Ile Asn Gln His Asp
865                 870                 875                 880
Phe Gly Thr Ile Glu Ser Val Phe Glu Leu Ala Asn Arg Ser Lys Asp
                885                 890                 895
Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln Gly Arg Asp Leu Leu
            900                 905                 910
Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly Tyr Ala Arg Gln Met
        915                 920                 925
Ile Asp Asn Thr Ser Thr Gly Glu Ile Thr Lys Gln Leu Asn Ala Ala
    930                 935                 940
Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu His Lys Thr Ser Ser
945                 950                 955                 960
Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile Leu Asn Ser Arg Leu
                965                 970                 975
Val Asn Leu Ser Arg Arg His Thr Asn Asn Ile Asp Ser Phe Ala Gln
            980                 985                 990
Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala Ser Leu Glu Ser Ala
        995                1000                1005
Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr Glu Lys Pro Thr Asn
   1010                1015                1020
Val Trp Ala Asn Ala Ile Gly Gly Thr Ser Leu Asn Asn Gly Gly Asn
025                1030                1035                1040
Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp Ala Tyr Leu Asn Gly
               1045                1050                1055
Glu Val Glu Ala Ile Val Gly Gly Phe Gly Ser Tyr Gly Tyr Ser Ser
           1060                1065                1070
Phe Asn Asn Gln Ala Asn Ser Leu Asn Ser Gly Ala Asn Asn Thr Asn
       1075                1080                1085
Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn Gln His Glu Phe Asp Phe
   1090                1095                1100
Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys
105                1110                1115                1120
Ser Ala Leu Leu Arg Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr
               1125                1130                1135
Ser Ala Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg
           1140                1145                1150
Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu
       1155                1160                1165
Gly Ser Thr Asn Phe Lys Ser Asn Ser Asn Gln Val Ala Leu Lys Asn
   1170                1175                1180
Gly Ser Ser Ser Gln His Leu Phe Asn Ala Ser Ala Asn Val Glu Ala
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185                 1190                1195                1200
Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val
                1205                1210                1215
Leu Gln Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn
            1220                1225                1230
Thr Phe Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg
        1235                1240                1245
Val Met Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn
    1250                1255                1260
Leu Gly Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe
265                 1270                1275                1280
Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
                1285                1290
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 55...1284
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

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TTAGTAGAAA TTGAAGCGAT AGCCATTAAG TAATTTATTA AAGGGACTAT CAGC ATG      57
                                                            Met
                                                             1

AAA AAA GAG GTC GTG GTC ATA GGC GGT GGG ATT GTA GGG CTT TCT TGT     105
Lys Lys Glu Val Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser Cys
          5                  10                  15

GCG TAT TCT ATG CAC AAG TTA GGG CAT AAG GTC TGC GTG ATA GAA AAA     153
Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu Lys
      20                  25                  30

AAC GAT GGC GCA AAC GGC ACT TCT TTT GGG AAT GCT GGG CTT ATT TCT     201
Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile Ser
  35                  40                  45

GCG TTT AAA AAA GCC CCA CTC TCA TGC CCT GGT GTG GTG TTA GAC ACC     249
Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp Thr
50                  55                  60                  65

CTG AAG CTC ATG CTC AAA AAC CAA GCC CCT TTA AAA TTC CAT TTC GGG     297
Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe Gly
                70                  75                  80

CTT AAT TTA AAG CTC TAT CAA TGG ATT TTA AAA TTT GTA AAA AGC GCG     345
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Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser Ala
            85                  90                  95

AAC GCC AAA TCC ACG CAC CGC ACC ATG GCG TTG TTT GAA CGC TAC GGG      393
Asn Ala Lys Ser Thr His Arg Thr Met Ala Leu Phe Glu Arg Tyr Gly
        100                 105                 110

TGG CTG AGT ATT GAT ATG TAT CAT CAA ATG CTA AAA GAC GGC ATG GAC      441
Trp Leu Ser Ile Asp Met Tyr His Gln Met Leu Lys Asp Gly Met Asp
    115                 120                 125

TTT TGG TAT AAA GAA GAT GGG CTT TTA ATG ATC TAC ACT CTA GAA GAA      489
Phe Trp Tyr Lys Glu Asp Gly Leu Leu Met Ile Tyr Thr Leu Glu Glu
130                 135                 140                 145

AGT TTT GAA AAA AAG CTT AAA ACT TGC GAT AAC AGC GGC GCT TAT AAA      537
Ser Phe Glu Lys Lys Leu Lys Thr Cys Asp Asn Ser Gly Ala Tyr Lys
                150                 155                 160

ATC CTT AGC GCT AAA GAG ACC AAA GAA TAC ATG CCC GTT GTT AAT GAC      585
Ile Leu Ser Ala Lys Glu Thr Lys Glu Tyr Met Pro Val Val Asn Asp
            165                 170                 175

AAT ATC TGC GGG AGC GTG CTT TTA ACC GAA AAC GCG CAT GTG GAT CCG      633
Asn Ile Cys Gly Ser Val Leu Leu Thr Glu Asn Ala His Val Asp Pro
        180                 185                 190

GGC GAA GTG ATG CAC TCT TTG CAA GAA TAT TTA CAA AAT GTT GGC GTG      681
Gly Glu Val Met His Ser Leu Gln Glu Tyr Leu Gln Asn Val Gly Val
    195                 200                 205

GAG TTC CTT TAT AAT GAA GAA GTG ATC GAT TTT GAG TTT AAA AAT AAC      729
Glu Phe Leu Tyr Asn Glu Glu Val Ile Asp Phe Glu Phe Lys Asn Asn
210                 215                 220                 225

CTC ATT GAG GGC GTT ATC ACG CAC AAG GAA AAA ATC CAA GCA GAA ACA      777
Leu Ile Glu Gly Val Ile Thr His Lys Glu Lys Ile Gln Ala Glu Thr
                230                 235                 240

ATC ATT CTA GCC ACT GGG GCT AAC CCC ACT CTC ATT AAA AAA ACC AAG      825
Ile Ile Leu Ala Thr Gly Ala Asn Pro Thr Leu Ile Lys Lys Thr Lys
            245                 250                 255

AAC GAT TTT TTA ATG ATG GGG GCT AAA GGA TAT AGC ATC ACC TTT AAA      873
Asn Asp Phe Leu Met Met Gly Ala Lys Gly Tyr Ser Ile Thr Phe Lys
        260                 265                 270

ATG CCT GAA GAA TTA AAA CCC AAA ACC TCT TCT TTA TTT GCG GAT ATT      921
Met Pro Glu Glu Leu Lys Pro Lys Thr Ser Ser Leu Phe Ala Asp Ile
    275                 280                 285

TTC ATG GCG ATG ACC CCA CGA AGA GAC ACT GTA AGG ATC ACT TCT AAA      969
Phe Met Ala Met Thr Pro Arg Arg Asp Thr Val Arg Ile Thr Ser Lys
290                 295                 300                 305

TTA GAA TTA AAC ACC AAC AAC GCT CTC ATT GAT AAA GAG CAA ATC GCT     1017
Leu Glu Leu Asn Thr Asn Asn Ala Leu Ile Asp Lys Glu Gln Ile Ala
                310                 315                 320
```

```
AAC ATG AAA AAG AAT TTA GCC GCT TTC ACG CAG CCT TTT GAA ATG AAA    1065
Asn Met Lys Lys Asn Leu Ala Ala Phe Thr Gln Pro Phe Glu Met Lys
            325                 330                 335

GAC GCC ATA GAG TGG TGC GGT TTC AGA CCC TTA ACC CCT AAT GAT ATT    1113
Asp Ala Ile Glu Trp Cys Gly Phe Arg Pro Leu Thr Pro Asn Asp Ile
        340                 345                 350

CCT TAT TTG GGC TAT GAC AAA CGC TAT AAA AAC TTA ATC CAT GCG ACA    1161
Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala Thr
    355                 360                 365

GGG CTA GGG TGG CTT GGC ATC ACT TTT GGC CCA GCC ATT GGT AAA ATC    1209
Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys Ile
370                 375                 380                 385

ATC GCC AAT TTG AGC CAA GAC GGA GCG AAT GAA AAA AAT GCC GAT ATT    1257
Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp Ile
                390                 395                 400

ATG CTT TTT TCT GCA TTT TTT AGG GAT TAAGGAATTT CTTTTTTAAA CCCTAGT  1311
Met Leu Phe Ser Ala Phe Phe Arg Asp
            405                 410

TTATTAAGGA GTTTTTATGG AAAC                                        1335
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
Met Lys Lys Glu Val Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser
 1               5                  10                  15
Cys Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu
            20                  25                  30
Lys Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile
        35                  40                  45
Ser Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp
    50                  55                  60
Thr Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe
65                  70                  75                  80
Gly Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser
                85                  90                  95
Ala Asn Ala Lys Ser Thr His Arg Thr Met Ala Leu Phe Glu Arg Tyr
            100                 105                 110
Gly Trp Leu Ser Ile Asp Met Tyr His Gln Met Leu Lys Asp Gly Met
        115                 120                 125
Asp Phe Trp Tyr Lys Glu Asp Gly Leu Leu Met Ile Tyr Thr Leu Glu
    130                 135                 140
Glu Ser Phe Glu Lys Lys Leu Lys Thr Cys Asp Asn Ser Gly Ala Tyr
```

```
145                 150                 155                 160
Lys Ile Leu Ser Ala Lys Glu Thr Lys Glu Tyr Met Pro Val Val Asn
                165                 170                 175
Asp Asn Ile Cys Gly Ser Val Leu Leu Thr Glu Asn Ala His Val Asp
            180                 185                 190
Pro Gly Glu Val Met His Ser Leu Gln Glu Tyr Leu Gln Asn Val Gly
        195                 200                 205
Val Glu Phe Leu Tyr Asn Glu Glu Val Ile Asp Phe Glu Phe Lys Asn
    210                 215                 220
Asn Leu Ile Glu Gly Val Ile Thr His Lys Glu Lys Ile Gln Ala Glu
225                 230                 235                 240
Thr Ile Ile Leu Ala Thr Gly Ala Asn Pro Thr Leu Ile Lys Lys Thr
                245                 250                 255
Lys Asn Asp Phe Leu Met Met Gly Ala Lys Gly Tyr Ser Ile Thr Phe
            260                 265                 270
Lys Met Pro Glu Glu Leu Lys Pro Lys Thr Ser Ser Leu Phe Ala Asp
        275                 280                 285
Ile Phe Met Ala Met Thr Pro Arg Arg Asp Thr Val Arg Ile Thr Ser
    290                 295                 300
Lys Leu Glu Leu Asn Thr Asn Asn Ala Leu Ile Asp Lys Glu Gln Ile
305                 310                 315                 320
Ala Asn Met Lys Lys Asn Leu Ala Ala Phe Thr Gln Pro Phe Glu Met
                325                 330                 335
Lys Asp Ala Ile Glu Trp Cys Gly Phe Arg Pro Leu Thr Pro Asn Asp
            340                 345                 350
Ile Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala
        355                 360                 365
Thr Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys
    370                 375                 380
Ile Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp
385                 390                 395                 400
Ile Met Leu Phe Ser Ala Phe Phe Arg Asp
                405                 410
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1526
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
AAAAACGCTA TAAGATAGTC AAATACATTC AATAAATGCA AGGGGAAATC ATG GAA      56
                                                        Met Glu
                                                          1

CAT AAA GAA ATC GTT ATA GGG GTT GAT CTA GGC TCT AGA AAG ATT TGC     104
```

```
His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys Ile Cys
          5                  10                  15

GCG ATA GTG GCT GAA TTT AAA GAA GGG ATT TTG CGC ATC ATT GGC ACG      152
Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile Gly Thr
    20                  25                  30

GCC CAT CAA GAC TCC AAA GAA ATC AAT TCA AAA GCC ATT AAA AGA GGG      200
Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys Arg Gly
35                  40                  45                  50

CGT ATC AAT AGC CTT GCT CAC GCT TCC AAC GCC ATT AAA GAA GTG ATT      248
Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu Val Ile
                55                  60                  65

AAT AGC GCT AAA AAA ATG GCA GGT TTG AAC GCT GAT GAA GAC AGA AAT      296
Asn Ser Ala Lys Lys Met Ala Gly Leu Asn Ala Asp Glu Asp Arg Asn
            70                  75                  80

AAC CCC ATG CCC CAT TTT GGG GAA TAC CAC CCT AAA ACT AAG GCG ATT      344
Asn Pro Met Pro His Phe Gly Glu Tyr His Pro Lys Thr Lys Ala Ile
        85                  90                  95

GTT TCT TTT TCT GGG GCT TAT ACT GAA AGC ATT AGA GAT GTT ACC GGT      392
Val Ser Phe Ser Gly Ala Tyr Thr Glu Ser Ile Arg Asp Val Thr Gly
    100                 105                 110

GTA GCG AGC ACC AAA GAT AAT GTG GTA ACC ATT GAT GAA ATC AAT CGC      440
Val Ala Ser Thr Lys Asp Asn Val Val Thr Ile Asp Glu Ile Asn Arg
115                 120                 125                 130

GCT ATC AAT AGT GCA TGC GCT AAA GCA GGC TTA GAT AAC GAC AAA CAT      488
Ala Ile Asn Ser Ala Cys Ala Lys Ala Gly Leu Asp Asn Asp Lys His
                135                 140                 145

ATT TTG CAT GCT CTC CCC TAT CGC TTC ACT TTA GAC AAA CAA GAA GTG      536
Ile Leu His Ala Leu Pro Tyr Arg Phe Thr Leu Asp Lys Gln Glu Val
            150                 155                 160

AAT GAC CCT TTA GGG ATG AGC GGG ACT CGC TTG GAA GTC TTT ATC CAC      584
Asn Asp Pro Leu Gly Met Ser Gly Thr Arg Leu Glu Val Phe Ile His
        165                 170                 175

ATT GTC TAT ACA GAA AAA AAC AAC ATT GAA AAT TTA GAA AAA ATC ATG      632
Ile Val Tyr Thr Glu Lys Asn Asn Ile Glu Asn Leu Glu Lys Ile Met
    180                 185                 190

ATC CAA TCT GGG GTA GAG ATT GAA AAC ATC GTG ATC AAT TCT TAT GCA      680
Ile Gln Ser Gly Val Glu Ile Glu Asn Ile Val Ile Asn Ser Tyr Ala
195                 200                 205                 210

GCC TCG ATT GCC ACC TTA TCT AAT GAT GAA AGG GAA TTG GGC GTG GCT      728
Ala Ser Ile Ala Thr Leu Ser Asn Asp Glu Arg Glu Leu Gly Val Ala
                215                 220                 225

TGC GTG GAT ATG GGC GGA GAG ACA TGC AAC CTT ACG ATT TAT AGC GGC      776
Cys Val Asp Met Gly Gly Glu Thr Cys Asn Leu Thr Ile Tyr Ser Gly
            230                 235                 240
```

```
AAT TCC ATA CGC TAT AAC AAA TAT TTG CCC GTA GGC TCT CAC CAT TTA      824
Asn Ser Ile Arg Tyr Asn Lys Tyr Leu Pro Val Gly Ser His His Leu
        245                 250                 255

ACC ACG GAT TTA TCG CAC ATG CTC AAC ACC CCA TTC CCT TAC GCT GAA      872
Thr Thr Asp Leu Ser His Met Leu Asn Thr Pro Phe Pro Tyr Ala Glu
    260                 265                 270

GAA GTT AAG ATC AAA TAC GGG GAT CTT TCT TTT GAA GGC GGC GAA GAA      920
Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly Glu Glu
275                 280                 285                 290

ACG CCC TCT CAA AAT GTC CAA ATC CCT ACC ACC GGC TCG GAT GGC CAT      968
Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp Gly His
                295                 300                 305

GAA AGC CAT ATT GTG CCG CTT AGT GAA ATC CAA ACT ATC ATG AGA GAA     1016
Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met Arg Glu
            310                 315                 320

AGG GCT TTA GAA ACT TTT AAA ATC ATC CAC AGG AGC ATT CAA GAT AGC     1064
Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln Asp Ser
        325                 330                 335

GGC TTA GAA GAG CAT TTG GGC GGA GGC GTT GTG TTA ACC GGT GGG ATG     1112
Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly Gly Met
    340                 345                 350

GCT TTA ATG AAA GGG ATC AAA GAA TTA GCC AGA ACC CAT TTC ACT AAT     1160
Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe Thr Asn
355                 360                 365                 370

TAC CCG GTG CGT TTG GCA GCC CCT GTG GAA AAA TAC AAT ATC ATG GGC     1208
Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile Met Gly
                375                 380                 385

ATG TTT GAA GAT TTG AAA GAC CCT CGC TTT TCA GTC GTA GTT GGC TTG     1256
Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val Gly Leu
            390                 395                 400

ATT TTA TAC AAA GCA GGG GGG CAT ACC AAT TAT GAA AGA GAC TCT AAA     1304
Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp Ser Lys
        405                 410                 415

GGG GTT ATC CGC TAC CAT GAA AGC GAT GAT TAC ACA AGA ACA GCC CAT     1352
Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr Ala His
    420                 425                 430

CAA TCA AGC CCT ACC CCC CAT ATC CAT TCA TCG CCC ACA GAA AGG AAT     1400
Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu Arg Asn
435                 440                 445                 450

TTG AGC GAT TTA AAA GCC CCT AGT GCT CCT TTA AAC ACC GCT AAA AAC     1448
Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala Lys Asn
                455                 460                 465

GAT GAC TTT TTA CCT ATA AAA CCC ACC GAA CAA AAA GGT TTT TTT AAA     1496
Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys
```

```
            470                 475                 480

AGT TTC CTT GAT AAG ATT TCT AAA TTC TTT TAAGATACAG CCATTTCTTT ATG  1549
Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe
        485                 490

CGATAAAAAC GCCTTGATGG TTATCAAAAG                                  1579
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
Met Glu His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys
 1               5                  10                  15
Ile Cys Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile
            20                  25                  30
Gly Thr Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys
        35                  40                  45
Arg Gly Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu
    50                  55                  60
Val Ile Asn Ser Ala Lys Lys Met Ala Gly Leu Asn Ala Asp Glu Asp
65                  70                  75                  80
Arg Asn Asn Pro Met Pro His Phe Gly Glu Tyr His Pro Lys Thr Lys
                85                  90                  95
Ala Ile Val Ser Phe Ser Gly Ala Tyr Thr Glu Ser Ile Arg Asp Val
            100                 105                 110
Thr Gly Val Ala Ser Thr Lys Asp Asn Val Val Thr Ile Asp Glu Ile
        115                 120                 125
Asn Arg Ala Ile Asn Ser Ala Cys Ala Lys Ala Gly Leu Asp Asn Asp
    130                 135                 140
Lys His Ile Leu His Ala Leu Pro Tyr Arg Phe Thr Leu Asp Lys Gln
145                 150                 155                 160
Glu Val Asn Asp Pro Leu Gly Met Ser Gly Thr Arg Leu Glu Val Phe
                165                 170                 175
Ile His Ile Val Tyr Thr Glu Lys Asn Asn Ile Glu Asn Leu Glu Lys
            180                 185                 190
Ile Met Ile Gln Ser Gly Val Glu Ile Glu Asn Ile Val Ile Asn Ser
        195                 200                 205
Tyr Ala Ala Ser Ile Ala Thr Leu Ser Asn Asp Glu Arg Glu Leu Gly
    210                 215                 220
Val Ala Cys Val Asp Met Gly Gly Glu Thr Cys Asn Leu Thr Ile Tyr
225                 230                 235                 240
Ser Gly Asn Ser Ile Arg Tyr Asn Lys Tyr Leu Pro Val Gly Ser His
                245                 250                 255
His Leu Thr Thr Asp Leu Ser His Met Leu Asn Thr Pro Phe Pro Tyr
            260                 265                 270
Ala Glu Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly
        275                 280                 285
Glu Glu Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp
```

```
    290                 295                 300
Gly His Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met
305                 310                 315                 320
Arg Glu Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln
                325                 330                 335
Asp Ser Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly
            340                 345                 350
Gly Met Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe
        355                 360                 365
Thr Asn Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile
    370                 375                 380
Met Gly Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val
385                 390                 395                 400
Gly Leu Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp
                405                 410                 415
Ser Lys Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr
            420                 425                 430
Ala His Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu
        435                 440                 445
Arg Asn Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala
    450                 455                 460
Lys Asn Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe
465                 470                 475                 480
Phe Lys Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe
                485                 490
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1934
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
AGCGCTTGAA ATTTTTAGCC ATTTATGACA CGAATTTAGA CGAATTTTAC ATG ATA      56
                                                          Met Ile
                                                            1

AGA GTG GCA GGG CTT AAA CAA CTC TAT GAG CAT AAA ATC GCC TCT AAA     104
Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala Ser Lys
  5                  10                  15

GGC ATT GAT GGC GCA AGC CCT GAA GAA CAA TTA GAA AAA ATC AAG CAT     152
Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile Lys His
 20                  25                  30

TAT TTA GCG CAT GAA ATT GAA GAA AGG GAG TTA GAA TTC CAA AAA ATC     200
```

```
Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln Lys Ile
35                  40                  45                  50

CAA GCC CTA CTC TTT AAA AAA GGG CTT TGT ATC ACC CCC TAT AAT GAA      248
Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr Asn Glu
                55                  60                  65

TTG AAT TTA GAG CAA AAA GCG AAG GCT AAA ACC TAT TTT AAA GAG CAG      296
Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys Glu Gln
            70                  75                  80

CTT TAC GCG TTA GTT TTG CCT TTT AAA TTG GAT TCT TCA CAC ACT TTC      344
Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His Thr Phe
        85                  90                  95

CCG CCT TTA GCG AAT TTG ACT TTC GCG CTT TTT GCC CGC ATC AAA GAC      392
Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile Lys Asp
    100                 105                 110

AAA GAA ACC CAA ATT ATC TCC TAT GCG CTC ATC AAA CTC CCC TCT TTT      440
Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro Ser Phe
115                 120                 125                 130

ATC TTC CGT TTT GTA GAG CTA GAA AAA GGC TTG TTT GTG TTA GCT GAA      488
Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu Ala Glu
                135                 140                 145

GAA ATC GTG GAA GCG CAT TTA GAA GAA TTG TTT TTA GAG CAT GAG ATT      536
Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His Glu Ile
            150                 155                 160

TTA GAT TGC ATG GCG TTT AGG GTA ACT TGC GAT GCG GAT ATT GCT ATC      584
Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile Ala Ile
        165                 170                 175

ACT GAA GAT GAA GCG CAT GAT TAT GCA GAT TTG ATG AGT AAG AGT TTG      632
Thr Glu Asp Glu Ala His Asp Tyr Ala Asp Leu Met Ser Lys Ser Leu
    180                 185                 190

AGG AAA CGC AAT CAA GGC GAA ATC GTG CGC TTG CAA ACC CAA AAA GGG      680
Arg Lys Arg Asn Gln Gly Glu Ile Val Arg Leu Gln Thr Gln Lys Gly
195                 200                 205                 210

AGT CAA GAG CTT TTA AAA ACC CTC TTA GCG TCT TTA AGG AGT TTT CAA      728
Ser Gln Glu Leu Leu Lys Thr Leu Leu Ala Ser Leu Arg Ser Phe Gln
                215                 220                 225

ACC CAC TCT TAC AAA AAG CAC AAA CTC ACC GGC ATG CAT ATC TAT AAA      776
Thr His Ser Tyr Lys Lys His Lys Leu Thr Gly Met His Ile Tyr Lys
            230                 235                 240

AGC GCG ATC ATG CTC AAT TTA GGG GAT TTG TGG GAA TTA GTC AAT CAT      824
Ser Ala Ile Met Leu Asn Leu Gly Asp Leu Trp Glu Leu Val Asn His
        245                 250                 255

AGC GAT TTT AAA GCG CTC AAA TCG CCC AAT TTC ACA CCC AAA ATC CAC      872
Ser Asp Phe Lys Ala Leu Lys Ser Pro Asn Phe Thr Pro Lys Ile His
    260                 265                 270
```

```
CCT CAT TTC AAT GAA AAC GAT CTT TTC AAA TCT ATA GAA AAA CAG GAT      920
Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys Gln Asp
275                 280                 285                 290

CTG TTG CTG TTT CAT CCT TAT GAA AGT TTT GAG CCT GTG ATT GAT TTA      968
Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile Asp Leu
                295                 300                 305

ATA GAG CAA GCC GCT AGC GAT CCA GCC ACC CTT TCT ATC AAA ATG ACG     1016
Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys Met Thr
            310                 315                 320

CTT TAT CGT GTG GGC AAG CAT TCC CCC ATT GTC AAA GCT TTG ATT GAA     1064
Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu Ile Glu
        325                 330                 335

GCG GCG AGC AAG ATT CAA GTG AGC GTT TTA GTG GAA TTA AAA GCG CGC     1112
Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys Ala Arg
    340                 345                 350

TTT GAT GAA GAG AGC AAT CTG CAC TGG GCA AAA GCT TTA GAA AGG GCG     1160
Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu Arg Ala
355                 360                 365                 370

GGC GCG TTA GTC GTT TAT GGC GTT TTC AAA CTC AAA GTG CAT GCT AAA     1208
Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His Ala Lys
                375                 380                 385

ATG CTA TTG ATC ACT AAA AAA ACA GAC AAC CAA TTA CGC CAT TTC ACC     1256
Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His Phe Thr
            390                 395                 400

CAT TTA AGC ACG GGC AAT TAC AAC CCT TTG AGC GCT AAA GTC TAT ACC     1304
His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val Tyr Thr
        405                 410                 415

GAT GTG AGT TTT TTT AGC GCT AAA AAT GAA ATC GCT AAC GAC ATT ATC     1352
Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp Ile Ile
    420                 425                 430

AAG CTT TTC CAT TCC TTG CTC ACT AGC AGC GCG ACT AAT AGC GCA TTA     1400
Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser Ala Leu
435                 440                 445                 450

GAA ACG CTT TTT ATG GCA CCC AAA CAA ATC AAG CCT AAA ATC ATT GAA     1448
Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile Ile Glu
                455                 460                 465

CTC ATT CAA AAT GAA ATG AAT CAC CAA CAA GAA GGC TAT ATC ATT TTA     1496
Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile Ile Leu
            470                 475                 480

AAA GCC AAC GCC CTA GTG GAT AGC GAA ATC ATT GAA TGG CTC TAT CAA     1544
Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu Tyr Gln
        485                 490                 495

GCC TCT CAA AAA GGG GTT AAA ATT GAT CTC ATT ATT AGA GGG ATT TGC     1592
Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly Ile Cys
```

```
    500                 505                 510

TGT TTA AAG CCC CAA GTC AAG GGC TTG AGC GAA AAT ATC AGG GTG TAT    1640
Cys Leu Lys Pro Gln Val Lys Gly Leu Ser Glu Asn Ile Arg Val Tyr
515                 520                 525                 530

TCT ATC GTG GGG AAA TAT TTA GAA CAT GCA CGC ATT TAT TAT TTT AAA    1688
Ser Ile Val Gly Lys Tyr Leu Glu His Ala Arg Ile Tyr Tyr Phe Lys
                535                 540                 545

CAT GAA AAT ATT TAT TTT TCT AGC GCG GAT TTA ATG CCC AGG AAT TTA    1736
His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg Asn Leu
            550                 555                 560

GAA AGG CGC GTG GAA TTG CTC ATT CCA GCC ACA AAC CCA AAG ATC GCT    1784
Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys Ile Ala
        565                 570                 575

CAT AAA TTG TTG CAT ATT TTA GAA ATC CAA CTC AAA GAC ACC TTA AAA    1832
His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr Leu Lys
    580                 585                 590

CGC TAC GAG TTA AAT TCT AAA GGC CGT TAC ATT AAA GTT TCA AAC CCT    1880
Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser Asn Pro
595                 600                 605                 610

AAC GAT CCT TTA AAT TCG CAG GAT TAT TTT GAA AAA CAA GCC CTT AAA    1928
Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala Leu Lys
                615                 620                 625

ACC TTT TAAGGGTTAT CGTTCAAATC ATAAAAGATA AGGATTTAAA TGCTTTATTC AT  1986
Thr Phe

T                                                                  1987
```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 628 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
Met Ile Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala
 1               5                  10                  15
Ser Lys Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile
            20                  25                  30
Lys His Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln
        35                  40                  45
Lys Ile Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr
    50                  55                  60
Asn Glu Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys
```

65 70 75 80
Glu Gln Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His
85 90 95
Thr Phe Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile
100 105 110
Lys Asp Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro
115 120 125
Ser Phe Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu
130 135 140
Ala Glu Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His
145 150 155 160
Glu Ile Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile
165 170 175
Ala Ile Thr Glu Asp Glu Ala His Asp Tyr Ala Asp Leu Met Ser Lys
180 185 190
Ser Leu Arg Lys Arg Asn Gln Gly Glu Ile Val Arg Leu Gln Thr Gln
195 200 205
Lys Gly Ser Gln Glu Leu Leu Lys Thr Leu Leu Ala Ser Leu Arg Ser
210 215 220
Phe Gln Thr His Ser Tyr Lys Lys His Lys Leu Thr Gly Met His Ile
225 230 235 240
Tyr Lys Ser Ala Ile Met Leu Asn Leu Gly Asp Leu Trp Glu Leu Val
245 250 255
Asn His Ser Asp Phe Lys Ala Leu Lys Ser Pro Asn Phe Thr Pro Lys
260 265 270
Ile His Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys
275 280 285
Gln Asp Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile
290 295 300
Asp Leu Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys
305 310 315 320
Met Thr Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu
325 330 335
Ile Glu Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys
340 345 350
Ala Arg Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu
355 360 365
Arg Ala Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His
370 375 380
Ala Lys Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His
385 390 395 400
Phe Thr His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val
405 410 415
Tyr Thr Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp
420 425 430
Ile Ile Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser
435 440 445
Ala Leu Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile
450 455 460
Ile Glu Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile
465 470 475 480
Ile Leu Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu
485 490 495
Tyr Gln Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly
500 505 510
Ile Cys Cys Leu Lys Pro Gln Val Lys Gly Leu Ser Glu Asn Ile Arg
515 520 525
Val Tyr Ser Ile Val Gly Lys Tyr Leu Glu His Ala Arg Ile Tyr Tyr

```
    530                 535                 540
Phe Lys His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg
545                 550                 555                 560
Asn Leu Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys
                565                 570                 575
Ile Ala His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr
            580                 585                 590
Leu Lys Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser
        595                 600                 605
Asn Pro Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala
    610                 615                 620
Leu Lys Thr Phe
625
```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 616 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...563
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
TATAATATAG ATTTTATTTT AGCTAAAAAT GGCATGGGTT TTAGCAAGGA ATG GGC      56
                                                          Met Gly
                                                            1

TTG AAA AAT CTC TCA ACA CTT CTG GTG TTT TTA TTC TTT TGT TTA GGG     104
Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly
          5                  10                  15

TGT GTG AGC AAT TTT AAT GAA GAC ACT TAC ACG CTA GAC TTA GTT TTA     152
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu
     20                  25                  30

GAA AAA AAG ATC CAA GCC AGC AGG AAA GGT GAA ATC ACC CAA GAT AAT     200
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn
35                  40                  45                  50

GTG CCT ATC ATC ACG GCT ATC GCT ACG CAT TTA AAC GAT GTG GAT AGC     248
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser
                55                  60                  65

GGC ACT TAC TAT GAC CAT GAG TAT TTT TTA GTG GAG ATT TTC ACG CAA     296
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln
            70                  75                  80

AAT AAC GAC TGG ATA GAT GAT GGC TAT ATT TCT TAT GAA CTT TTT GGC     344
```

```
Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu Phe Gly
        85                  90                  95

ACA AAA CCT ATA GGC TCA GAG CCT TTA TGG GTG CGA GAA ATC ACA AAA     392
Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile Thr Lys
    100                 105                 110

GAT GAA TTT GAT GGC ATT TTA GAA ACC ACG AAC AGG TGG AGC AGA GCT     440
Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser Arg Ala
115                 120                 125                 130

TTT TTG CTC GCT TTT AAC AAA TTG GAT TAT TTA GCG GTT CAA GAA GCC     488
Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln Glu Ala
                135                 140                 145

AAA CTA GAG CTT GAT GCC TAT AGT TTG GGC AAG ATT GTT TTT AAT TTC     536
Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe Asn Phe
            150                 155                 160

GCT TAT CAA GTC CCC CTA CCT CAA TTT TAATGCGCTT AGATTACGCC TTATTCA   590
Ala Tyr Gln Val Pro Leu Pro Gln Phe
    165                 170

GTCAGCATTT AGTAAATAGC AGAGAA                                       616
```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
Met Gly Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys
 1               5                  10                  15
Leu Gly Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu
            20                  25                  30
Val Leu Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln
        35                  40                  45
Asp Asn Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val
    50                  55                  60
Asp Ser Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe
65                  70                  75                  80
Thr Gln Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu
                85                  90                  95
Phe Gly Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile
            100                 105                 110
Thr Lys Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser
        115                 120                 125
Arg Ala Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln
    130                 135                 140
Glu Ala Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe
145                 150                 155                 160
```

Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe
165 170

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 966...2291
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ATTGTGAATT AGGAGTGAGC GTGAATAGTA ATGGCAATAA AGACAAACAA CAGCAGAATG 60
TAAGCAGTGG GATTTCTCAA ATCTCATTAA AAAAGGTGGC AACTTTTGAT GAAAATGGGG 120
CGAGTTTTGA GAATTTAAAT TCTATCAACT TTATTTATGG GGCTAATGGG AGCGGTAAGA 180
CAACCACTTC TAGTTTTTTA AAAAATCTAG CTGAAAATGG GATTGAAGAC AAGTTTGCTA 240
ATAGTAAAAT AGCATGGTAT AACAATGAGA GTTTAAAGAT TGAAGTTTAT AACAAGCAAT 300
TTAAAGAAGA GCAATTGAGA AACTCTCAAG TTAAAGGCAT TTTTACGCTC GGTAAAAAAA 360
CGAACGAGAA TTTAGAAAAA ATTGAAAGCA AGAAAGAATC AATAAACAAA GAGAATGAAA 420
AGAAAATAAA AAATGAAGCA AGCTTGCAAG TTTTAACACA AAAAAAGGAA AAGGAAGAAA 480
AGGATTTTGC TGATAGGTGT TGGGAAAAAC TTTATAAGAA AAATGAAGAG GATTTTAAAG 540
AAACGCTAGA AGGCTTTAAG CGTAAAGAGA AGTTTAAAGA AAAAATCCTT AAGGAATTTG 600
AAAACGATAA ATACAATCAA AGCGAAATAG TAGGGTTAGA AAAATTAAAG GAAAAAATTG 660
AGATTGTTTT TGGTGAAAAC CAAACAGAAT TGGCACTATT GGAATGCAAT TTAACAGATT 720
TTGATTTTAT TGAAAATCAT TCTATTTGGG AACAAAAAAT TGTAGGGAGT GGTGATGCAG 780
CCATTGCAGA TTTAATAAAA AGATTAAGCA ATGAAGATTG GGTAGCTCAA GGTAGAGAAT 840
ATATAAAAGA TAATAGTATA TGCCCTTTCT GTCAAAAAGA AACCATTACC GAAGAATTTA 900
AAAAACAACT AGAATCTTAT TTTGATACAA GTTATCAAGA ATCTATTGAA ACGATCAAGG 960
AAAAG ATG GAA GAC TAC GCA AGC AGA ACC GCT GGA GCA CTG GAG CGA CTT 1010
Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu
1 5 10 15

GAT AAG ATT GTT GAA ACA GAA CAG AAG AAT CAA CAA ACT AAA TTG GAC 1058
Asp Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp
20 25 30

ACA GAA AAT TTG AAA ATA ATT ATT GAA ACT TTG AGA AGT AAA ATC AAT 1106
Thr Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn
35 40 45

GGG AAT CAG CAA AAG ATG CTT GAT AAA AGT AAA GAA ATG AGC AGA AAT 1154
Gly Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn
50 55 60

TTT AAG CTT GAT AGC ACT AAA AAC GAG ATA GAC GCA ATT AAA GAT TTG 1202
Phe Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu
65 70 75

```
ATT AAA AAG GCT AAT GAG CAA ATA GCC AAT TAT AAT GAG ATG ATA AAG    1250
Ile Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys
80                  85                  90                  95

GAT ATT GAA AAA CAG AAA AAG AGT TGT AAG GAA CAA ACT TGG AAA TTT    1298
Asp Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe
                100                 105                 110

CTA GTC AAT GAA TTT AAA AGT GAT ATA CAA GAA TAT AAT AAA AAG TAT    1346
Leu Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr
            115                 120                 125

TGC GGT TTG GAG AAA GGA ATA AAC AAT TTA GAG AAA GCA ATT AGT GAA    1394
Cys Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu
        130                 135                 140

AAT CAA GAA GAG GTA AAG AAA TTA GAA AAT GAA ATT AAG GAA TTA GAA    1442
Asn Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu
    145                 150                 155

AAA ACT ATG GTA AGC ATA AAG CCC ATT GTC AAT GAA ATC AAT ACG CTT    1490
Lys Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu
160                 165                 170                 175

TTA AAA GGG TAT GGA TTC GCG AAT TTT AGT TTG GCA TGC ACT GAA GAT    1538
Leu Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp
                180                 185                 190

GAA AAA TTT TAT CGT ATT CAA AGA GAA GAT GGT CAA TTA GTA GGA GAA    1586
Glu Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu
            195                 200                 205

ACA CTG AGC GAG GGT GAA GTT ACT TTC ATC ACT TTC TTA TAT TAT TAT    1634
Thr Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr
        210                 215                 220

CAT TTA GCA AAA GGC TCT TTA GAA GAG AAC GAT ATA TCA AAA AAT AAG    1682
His Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys
    225                 230                 235

GTT TTA GTG ATT GAT GAC CCC ATT TCA AGT TTG GAT AGC AAT ATA TTG    1730
Val Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu
240                 245                 250                 255

TTT ATA GTG AGT GTT TTA GTT AAA GAT CTT ATG AAA GAA GCC ATG GAA    1778
Phe Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu
                260                 265                 270

GAA AAA ACA AAC ATC AAG CAA GTT ATT ATA CTA ACC CAC AAC ACA TAT    1826
Glu Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr
            275                 280                 285

TTT TAC AAG GAA ATT ACA TTA GAA TGT GAT TTA AAA CGC TAT CAA GGG    1874
Phe Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly
        290                 295                 300

AAA TAT TCT TTT TGG ATA ATT AAA AAG GAT AAT AAT GTT TCA AAA ATT    1922
Lys Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile
```

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    305                 310                 315

AAA GAT TAT AAA GAA AAT CCC ATT AAA AAT TCC TAT GAA TTG CTA TGG    1970
Lys Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp
320                 325                 330                 335

CAA GAA GTA AAA CAA GCA AAA GAA AAT AAT GCT TCT TGG GTA TCT TTA    2018
Gln Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu
                340                 345                 350

CAA AAT GTT ATG CGA AGA ATT ATT GAG TAT TAC TTT AGG ATT TTA GGC    2066
Gln Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly
            355                 360                 365

GGT TTT AAA CAT AAT GAT AGC TTG AGT GAA TGT TTT GAA AAT ATT GAA    2114
Gly Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu
        370                 375                 380

GAA AAA CGA GTG TGT AAT TCT TTC ATT TCA TGG TTT AAT GAT GGC TCT    2162
Glu Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser
    385                 390                 395

CAT GGG ATT TCA GAT GAT TTG TTT ATG CAA AGT CAA GAT ACA AGT ATT    2210
His Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile
400                 405                 410                 415

GAG ACA TAT TTA AAA GTT TTT GAA AAA ATA TTT AAA GAA ACC GGT CAT    2258
Glu Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His
                420                 425                 430

GAA GCT CAT TAT AAA ATG ATG ATG AGA ATG AAG TAATTGAATT AAAAACAAGG  2311
Glu Ala His Tyr Lys Met Met Met Arg Met Lys
            435                 440

AATAACATGC GAATCGTATT TATGGGAACG                                   2341
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu Asp
 1               5                  10                  15
Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp Thr
            20                  25                  30
Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn Gly
        35                  40                  45
Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe
    50                  55                  60
Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile
```

```
65                  70                  75                  80
Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp
                85                  90                  95
Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu
            100                 105                 110
Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys
        115                 120                 125
Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu Asn
    130                 135                 140
Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu Lys
145                 150                 155                 160
Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu Leu
                165                 170                 175
Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp Glu
            180                 185                 190
Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu Thr
        195                 200                 205
Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr His
    210                 215                 220
Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys Val
225                 230                 235                 240
Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu Phe
                245                 250                 255
Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu Glu
            260                 265                 270
Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr Phe
        275                 280                 285
Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly Lys
    290                 295                 300
Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile Lys
305                 310                 315                 320
Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp Gln
                325                 330                 335
Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu Gln
            340                 345                 350
Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly Gly
        355                 360                 365
Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu Glu
    370                 375                 380
Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser His
385                 390                 395                 400
Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile Glu
                405                 410                 415
Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His Glu
            420                 425                 430
Ala His Tyr Lys Met Met Met Arg Met Lys
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...3740
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
TTATGTGGGC TACAACATAG GCTTTTGATT AAACAAAATA AGGGAAAAAT ATG ATA      56
                                                          Met Ile
                                                            1

AAA AAA GCT AGA AAA TTC ATA CCA TTC TTT TTA ATT GGC TCC CTC TTA     104
Lys Lys Ala Arg Lys Phe Ile Pro Phe Phe Leu Ile Gly Ser Leu Leu
          5                  10                  15

GCT GAA GAC AAT GGC TGG TAT ATG TCT GTA GGC TAT CAA ATC GGT GGC     152
Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile Gly Gly
     20                  25                  30

ACG CAA CAA TTC ATC AAT AAC AAA CAA CTT TTA GAA AAT CAA AAT ATC     200
Thr Gln Gln Phe Ile Asn Asn Lys Gln Leu Leu Glu Asn Gln Asn Ile
35                  40                  45                  50

ATC AAC AGC GTA ACC CAA AGC GCG ATC AAC ATT GCA GGG CCT ACT ACC     248
Ile Asn Ser Val Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro Thr Thr
                55                  60                  65

GGC CTT ATC ACT TTA AGC TCT CAA ACC GTC ATT GAC GCT TTA GGC TAT     296
Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu Gly Tyr
            70                  75                  80

GGC GTG AGT AAC ACT GTT GGC AAC CAA TTA GAG GGC ATT TCT AAT ATC     344
Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser Asn Ile
        85                  90                  95

TTG AAT CAA ATT GGC AAA AGA AAA GAC TTT TAT TCT AGC CGT CAA ATC     392
Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg Gln Ile
    100                 105                 110

TCT AGC ATT TCC CAA CAA ATC ATA GGG CTT AAA GGA AGC TCT GAT CCC     440
Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser Asp Pro
115                 120                 125                 130

TTA AAA GCC CAT TCT TCA CAG ATC ACA GCC AAA CTC CTT TCC AAC ACC     488
Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser Asn Thr
                135                 140                 145

CAA AGC GCG TTT GAT CAG GGC ATC GCG CTA AGC ACT AAC ATC ATT AGC     536
Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile Ile Ser
            150                 155                 160

TCT ATC AAT AGC CTA AAC CCT AGC AAC AAC ACC CAA GAG GTT AAA AAA     584
Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val Lys Lys
        165                 170                 175

CAG CTC CAA AAC ACC GCG CAA TCC ATG ACA GAA TTG TTG CAA CAA ATT     632
Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Gln Ile
```

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    180                 185                 190

GAA CAC AGC ATC ACT AAA ACC ACT AGC ACC ACT TAC GCG CAA TCC TTA      680
Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln Ser Leu
195                 200                 205                 210

CTC TCC AAT CTA ACC GAT GCG GTG AAT GCC TCT AGC AAT AAT ACC GCT      728
Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn Thr Ala
                215                 220                 225

TAT GTG AGC GCT CTT GTT AAC GCT TTA AAC ACT TTA GGG GTA GGG GTT      776
Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val Gly Val
            230                 235                 240

TTC CCC ACC ACA ACC ACA ACG CAT GTG GTG TTA AAC CCA CCG GGA CAA      824
Phe Pro Thr Thr Thr Thr Thr His Val Val Leu Asn Pro Pro Gly Gln
        245                 250                 255

GTC GTA TTC TAT CCA ACC AAT TCC ATT TTA GGC TCT ACT TCT TCA AAC      872
Val Val Phe Tyr Pro Thr Asn Ser Ile Leu Gly Ser Thr Ser Ser Asn
    260                 265                 270

AGC AAT AAC CAA CAA CAA TAC AAC AAC ACC CTT TTA ATG AAC ACC TTA      920
Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn Thr Leu
275                 280                 285                 290

CAA GGG ACA TTA AGC GCT AAT ACT CAA AAT AAC CCC AAT GGT TGC GCC      968
Gln Gly Thr Leu Ser Ala Asn Thr Gln Asn Asn Pro Asn Gly Cys Ala
                295                 300                 305

AAT CAA GTC CAG TGT TTG GAG CAA TTC ATC CAA AAT TTA GCC CCT TTA     1016
Asn Gln Val Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Ala Pro Leu
            310                 315                 320

GCC GCA ACC CCC ACT TCA AAC AAC CAG GCC AAC CAG CAA GTC CAA GCC     1064
Ala Ala Thr Pro Thr Ser Asn Asn Gln Ala Asn Gln Gln Val Gln Ala
        325                 330                 335

ATC GCT CAA AAG CTT CAA AGC GTT GCT ATC AAC ACT TTA GAC AAC AAT     1112
Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Thr Leu Asp Asn Asn
    340                 345                 350

GCG ATC AAC AAC ACC ACC TAT AAT TTA AAC AAT TTG CAC AAC GCT TTG     1160
Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn Ala Leu
355                 360                 365                 370

AAT TTC CAA GCC TAT GAA AGC ACG ATA GAA CAA TAC AAT AAC GCT TTA     1208
Asn Phe Gln Ala Tyr Glu Ser Thr Ile Glu Gln Tyr Asn Asn Ala Leu
                375                 380                 385

AAA CAA ATT TCT TGG ATC AGT TTT ACT GAG CCT AAA AAC TTA CTC AAA     1256
Lys Gln Ile Ser Trp Ile Ser Phe Thr Glu Pro Lys Asn Leu Leu Lys
            390                 395                 400

AAC ACT TCC AAT AAC TAC CAA ATC GGC ACC GTT ACC AAC GCT CAA GGG     1304
Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Ala Gln Gly
        405                 410                 415
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CAA AAT ATC AGC GCC TAT GAT TGC ATG ACT GCT ACC GGA AGC CTT TCT    1352
Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser Leu Ser
    420                 425                 430

AGC AAT GCT TCT AGC GGG ATT TCA TGC TCA GCC ACA AGC TCC ACA AGT    1400
Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser Thr Ser
435                 440                 445                 450

TCC ACA AAT AGC TTT GAC AAT TCT TTA GTC GCT ACC TCC AAA GTC CAA    1448
Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys Val Gln
                455                 460                 465

ACC ATC AAC GGC AAA GAG CAG ATC GGC GTG AAT TCT TTT AAC CTT GTC    1496
Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn Leu Val
            470                 475                 480

TCT CAA GTG TGG AGC GTT TAT AAT TCT TTA AAA ACT TCA GAA GAA AAT    1544
Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu Glu Asn
        485                 490                 495

TTG CAA AAA AAC GCC AAT ATT TTA TGC GCT AAT GGG ACG CAA TCT GGG    1592
Leu Gln Lys Asn Ala Asn Ile Leu Cys Ala Asn Gly Thr Gln Ser Gly
    500                 505                 510

ACA AGC TCA TGC AAT AGC TCT TCA GGG GGT TTG AGC ATC AGC GGG AAC    1640
Thr Ser Ser Cys Asn Ser Ser Ser Gly Gly Leu Ser Ile Ser Gly Asn
515                 520                 525                 530

GCC CAA TTG CAA AAT ATT TTA AGC CCT ACT AGT GGG ACT ACC ACT AAT    1688
Ala Gln Leu Gln Asn Ile Leu Ser Pro Thr Ser Gly Thr Thr Thr Asn
                535                 540                 545

ACT CAA GCT AAA AGC AAC GCT CCC AAA CTA AAA GCG ATG GTG GTG GTG    1736
Thr Gln Ala Lys Ser Asn Ala Pro Lys Leu Lys Ala Met Val Val Val
            550                 555                 560

AAT AAT GAA GAA GAA GCT AAA ACG GCC AAT TTA GCC CAA AGC AGC GGG    1784
Asn Asn Glu Glu Glu Ala Lys Thr Ala Asn Leu Ala Gln Ser Ser Gly
        565                 570                 575

ACA ACC ACA CAA TCT CCT AAC AGC ACG GTG ATG GGA GCT TTA AAC ACC    1832
Thr Thr Thr Gln Ser Pro Asn Ser Thr Val Met Gly Ala Leu Asn Thr
    580                 585                 590

GTG TTG CAA AAT GTC AGC AAT TTC CAA CAA AGC ATT CAA AAC GCT TTT    1880
Val Leu Gln Asn Val Ser Asn Phe Gln Gln Ser Ile Gln Asn Ala Phe
595                 600                 605                 610

CAA AAC CAA GAA AGT AAT ATC CAA GCT TGG GCG AAT GCG ATT TAT AAC    1928
Gln Asn Gln Glu Ser Asn Ile Gln Ala Trp Ala Asn Ala Ile Tyr Asn
                615                 620                 625

ACT AAT GGG AGT CAG TCG CAA GAG ATG ACA CCT AAC AAT AAC CAA GAT    1976
Thr Asn Gly Ser Gln Ser Gln Glu Met Thr Pro Asn Asn Asn Gln Asp
            630                 635                 640

TTA CGC ATC CAA TTG AGG GCG AAT TTT TAC CAG CTC ATC AAT ACC ATT    2024
Leu Arg Ile Gln Leu Arg Ala Asn Phe Tyr Gln Leu Ile Asn Thr Ile
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        645                 650                 655

AAC CAG CAA GTG CCT ACA GAC ATG AAT GCT TTA ATT AAT CAA AGC CAA    2072
Asn Gln Gln Val Pro Thr Asp Met Asn Ala Leu Ile Asn Gln Ser Gln
    660                 665                 670

CAA ACC CAA CAA ACA AGC GGA TCA GCA AGC AAT AAT AAC GCA TGC GCG    2120
Gln Thr Gln Gln Thr Ser Gly Ser Ala Ser Asn Asn Asn Ala Cys Ala
675                 680                 685                 690

AGT GGA ATG AGT GGG AGT AAT GGT AAC TGG TGC TAT CAG CAA TGG TCC    2168
Ser Gly Met Ser Gly Ser Asn Gly Asn Trp Cys Tyr Gln Gln Trp Ser
                695                 700                 705

GAT TCT AAG GCT TAT TAC AGC GGG TTG CAA AGC GCT TTA GGG TAT CAA    2216
Asp Ser Lys Ala Tyr Tyr Ser Gly Leu Gln Ser Ala Leu Gly Tyr Gln
            710                 715                 720

ACG CAA GCG ACA ACT CAA AGC GGG AGC AAT GGT GGG AAC AGC ATC ACC    2264
Thr Gln Ala Thr Thr Gln Ser Gly Ser Asn Gly Gly Asn Ser Ile Thr
        725                 730                 735

TAC AAT GTC CAA CAA ATC ACG CTC ACT AGT AAT GGT TTG CTC AAC CAA    2312
Tyr Asn Val Gln Gln Ile Thr Leu Thr Ser Asn Gly Leu Leu Asn Gln
    740                 745                 750

ATC ATC ACA AAT CTT AAG AGC GTT AAT GGA GGC AAT GGC GCG AGT GGT    2360
Ile Ile Thr Asn Leu Lys Ser Val Asn Gly Gly Asn Gly Ala Ser Gly
755                 760                 765                 770

ACA GGC AGT GGG AAT GGC ACC AGT CAA ATC AAC ACA GCC TAC CAG ATG    2408
Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn Thr Ala Tyr Gln Met
                775                 780                 785

CTC ACA GAC GCC AGC GAT GGG AAA TTA GGG ACT TAT AGT AGT AGT AGT    2456
Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr Tyr Ser Ser Ser Ser
            790                 795                 800

GGC AGT AAT AAC GGC TAT ACG CCA TGC AAT AGC ACC AAT GGG AGC AAT    2504
Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser Thr Asn Gly Ser Asn
        805                 810                 815

AAA ACG AGT GGG AAC AAT TGT TAT GAA CCC AAC AAA CAA CAA AAC GCC    2552
Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn Lys Gln Gln Asn Ala
    820                 825                 830

ACC ACC GCA ACC GCC ACA ACC GAC AGC AAT TTA CAA AAA GTC TAT AAT    2600
Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu Gln Lys Val Tyr Asn
835                 840                 845                 850

GAC GCC CAA AAA ATA GCC AAC ATT ATC GCC AGC TCT GGG AAC AAT AAA    2648
Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser Ser Gly Asn Asn Lys
                855                 860                 865

GGC GTT GAA AAC GGC TTA AAA CAA TTC TTT GAA GCG TTA AAA AAT AAT    2696
Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu Ala Leu Lys Asn Asn
            870                 875                 880
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AGC AGC AGT CTC AGT AAT TTA TGT GGT AAT GGT AGT AGC GGT AGT AGT    2744
Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly Ser Ser
        885                 890                 895

GGC ACT ACT TGC TCC GGT TGG CTT ATC AAC CTT TTA GGG GCA ATC CCC    2792
Gly Thr Thr Cys Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala Ile Pro
    900                 905                 910

ACC AAT GGA GTG AGC GAT ACG AAT AAT TTA ATT AAT CTG CTC ACT GAA    2840
Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu Thr Glu
915                 920                 925                 930

TTC ATT AAA ACC GCC GGG TTT ATC CAA AAT AAT GAT AGT AGT GTA TCT    2888
Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser Val Ser
                935                 940                 945

ACT AGT CTT ACA AGC GCT TTT CAA GCC ATT ACG AGC GCT ATT TCT CAA    2936
Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln
            950                 955                 960

GGG TTT CAA GCC TTA CAA AAC GAT ATT AGC CCT AAT GCG ATT TTA ACC    2984
Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr
        965                 970                 975

TTG CTC CAA GAG ATT ACT TCT AAC ACC ACC ACC ATT CAG TCA TTC TCG    3032
Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser
    980                 985                 990

CAA ACC TTA CGG CAG CTT TTA GGG GAT AAA ACA TTC TTT ATG GCG CAA    3080
Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr Phe Phe Met Ala Gln
995                1000                1005                1010

CAA AAG CTC ATT GAT GCG ATG ATT AAC GCC AGA AAT CAG GTT CAA AAC    3128
Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg Asn Gln Val Gln Asn
               1015                1020                1025

GCG CAA AAT CAA GCC AAT AAC TAC GGC TCT CAA CCC GTT TTA AGC CAG    3176
Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln Pro Val Leu Ser Gln
           1030                1035                1040

TAT GCG GCC GCT AAA AGC ACC CAA CAT GGC ATG AGC AAT GGT TTA GGG    3224
Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met Ser Asn Gly Leu Gly
       1045                1050                1055

GTT GGT TTG GGC TAT AAA TAC TTC TTT GGT AAA GCG AGA AAA TTA GGC    3272
Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys Leu Gly
   1060                1065                1070

CTT AGG CAT TAT TTT TTC TTT GAT TAC GGC TTT AGT GAA ATA GGC CTA    3320
Leu Arg His Tyr Phe Phe Phe Asp Tyr Gly Phe Ser Glu Ile Gly Leu
1075                1080                1085                1090

GCC AAT CAA AGC GTG AAA GCG AAT ATC TTT GCT TAT GGG GTA GGC ACG    3368
Ala Asn Gln Ser Val Lys Ala Asn Ile Phe Ala Tyr Gly Val Gly Thr
               1095                1100                1105

GAT TTT TTA TGG AAC TTA TTC AGG AGG ACT TAC AAC ACT AAA GCG TTG    3416
Asp Phe Leu Trp Asn Leu Phe Arg Arg Thr Tyr Asn Thr Lys Ala Leu
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            1110                1115                1120

AAT TTT GGG CTA TTT GCT GGG GTC CAA CTG GGC GGC GCA ACC TGG CTT    3464
Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr Trp Leu
        1125                1130                1135

AGC TCC TTA AGG CAA CAA ATC ATT GAC AAC TGG GGG AGT GCT AAT GAC    3512
Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala Asn Asp
    1140                1145                1150

ATC CAT TCA ACG AAT TTT CAA GTG GCG CTG AAT TTT GGG GTG CGC ACC    3560
Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val Arg Thr
1155                1160                1165                1170

AAC TTC GCG GAG TTT AAG CGT TTT GCT AAG AAA TTC CAC AAT CAA GGG    3608
Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn Gln Gly
                1175                1180                1185

GTC ATC AGC CAA AAG AGC GTG GAA TTT GGG ATC AAA GTG CCT CTC ATC    3656
Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro Leu Ile
            1190                1195                1200

AAT CAA GCG TAT TTG AAT AGC GCT GGA GCT GAT GTG AGT TAC AGG AGG    3704
Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr Arg Arg
        1205                1210                1215

CTT TAT ACT TTT TAT ATC AAT TAC ATC ATG GGG TTT TAAAAAAGGG TGTGTC  3756
Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe
    1220                1225                1230

ATGGAAATCT TACAATTCAT CGGCTATGGG AATATGG                           3793
```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1230 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
Met Ile Lys Lys Ala Arg Lys Phe Ile Pro Phe Phe Leu Ile Gly Ser
 1               5                  10                  15
Leu Leu Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile
            20                  25                  30
Gly Gly Thr Gln Gln Phe Ile Asn Asn Lys Gln Leu Leu Glu Asn Gln
        35                  40                  45
Asn Ile Ile Asn Ser Val Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro
    50                  55                  60
Thr Thr Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu
65                  70                  75                  80
Gly Tyr Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser
                85                  90                  95
Asn Ile Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg
```

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                100                 105                 110
Gln Ile Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser
            115                 120                 125
Asp Pro Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser
    130                 135                 140
Asn Thr Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile
145                 150                 155                 160
Ile Ser Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val
                165                 170                 175
Lys Lys Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln
            180                 185                 190
Gln Ile Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln
        195                 200                 205
Ser Leu Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn
    210                 215                 220
Thr Ala Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val
225                 230                 235                 240
Gly Val Phe Pro Thr Thr Thr Thr Thr His Val Val Leu Asn Pro Pro
                245                 250                 255
Gly Gln Val Val Phe Tyr Pro Thr Asn Ser Ile Leu Gly Ser Thr Ser
            260                 265                 270
Ser Asn Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn
        275                 280                 285
Thr Leu Gln Gly Thr Leu Ser Ala Asn Thr Gln Asn Asn Pro Asn Gly
    290                 295                 300
Cys Ala Asn Gln Val Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Ala
305                 310                 315                 320
Pro Leu Ala Ala Thr Pro Thr Ser Asn Asn Gln Ala Asn Gln Gln Val
                325                 330                 335
Gln Ala Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Thr Leu Asp
            340                 345                 350
Asn Asn Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn
        355                 360                 365
Ala Leu Asn Phe Gln Ala Tyr Glu Ser Thr Ile Glu Gln Tyr Asn Asn
    370                 375                 380
Ala Leu Lys Gln Ile Ser Trp Ile Ser Phe Thr Glu Pro Lys Asn Leu
385                 390                 395                 400
Leu Lys Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Ala
                405                 410                 415
Gln Gly Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser
            420                 425                 430
Leu Ser Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser
        435                 440                 445
Thr Ser Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys
    450                 455                 460
Val Gln Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn
465                 470                 475                 480
Leu Val Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu
                485                 490                 495
Glu Asn Leu Gln Lys Asn Ala Asn Ile Leu Cys Ala Asn Gly Thr Gln
            500                 505                 510
Ser Gly Thr Ser Ser Cys Asn Ser Ser Ser Gly Gly Leu Ser Ile Ser
        515                 520                 525
Gly Asn Ala Gln Leu Gln Asn Ile Leu Ser Pro Thr Ser Gly Thr Thr
    530                 535                 540
Thr Asn Thr Gln Ala Lys Ser Asn Ala Pro Lys Leu Lys Ala Met Val
545                 550                 555                 560
Val Val Asn Asn Glu Glu Glu Ala Lys Thr Ala Asn Leu Ala Gln Ser
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                565                 570                 575
Ser Gly Thr Thr Thr Gln Ser Pro Asn Ser Thr Val Met Gly Ala Leu
            580                 585                 590
Asn Thr Val Leu Gln Asn Val Ser Asn Phe Gln Gln Ser Ile Gln Asn
        595                 600                 605
Ala Phe Gln Asn Gln Glu Ser Asn Ile Gln Ala Trp Ala Asn Ala Ile
    610                 615                 620
Tyr Asn Thr Asn Gly Ser Gln Ser Gln Glu Met Thr Pro Asn Asn Asn
625                 630                 635                 640
Gln Asp Leu Arg Ile Gln Leu Arg Ala Asn Phe Tyr Gln Leu Ile Asn
                645                 650                 655
Thr Ile Asn Gln Gln Val Pro Thr Asp Met Asn Ala Leu Ile Asn Gln
            660                 665                 670
Ser Gln Gln Thr Gln Gln Thr Ser Gly Ser Ala Ser Asn Asn Asn Ala
        675                 680                 685
Cys Ala Ser Gly Met Ser Gly Ser Asn Gly Asn Trp Cys Tyr Gln Gln
    690                 695                 700
Trp Ser Asp Ser Lys Ala Tyr Tyr Ser Gly Leu Gln Ser Ala Leu Gly
705                 710                 715                 720
Tyr Gln Thr Gln Ala Thr Thr Gln Ser Gly Ser Asn Gly Gly Asn Ser
                725                 730                 735
Ile Thr Tyr Asn Val Gln Gln Ile Thr Leu Thr Ser Asn Gly Leu Leu
            740                 745                 750
Asn Gln Ile Ile Thr Asn Leu Lys Ser Val Asn Gly Gly Asn Gly Ala
        755                 760                 765
Ser Gly Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn Thr Ala Tyr
    770                 775                 780
Gln Met Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr Tyr Ser Ser
785                 790                 795                 800
Ser Ser Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser Thr Asn Gly
                805                 810                 815
Ser Asn Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn Lys Gln Gln
            820                 825                 830
Asn Ala Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu Gln Lys Val
        835                 840                 845
Tyr Asn Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser Ser Gly Asn
    850                 855                 860
Asn Lys Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu Ala Leu Lys
865                 870                 875                 880
Asn Asn Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly
                885                 890                 895
Ser Ser Gly Thr Thr Cys Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala
            900                 905                 910
Ile Pro Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu
        915                 920                 925
Thr Glu Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser
    930                 935                 940
Val Ser Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile
945                 950                 955                 960
Ser Gln Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile
                965                 970                 975
Leu Thr Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser
            980                 985                 990
Phe Ser Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr Phe Phe Met
        995                1000                1005
Ala Gln Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg Asn Gln Val
   1010                1015                1020
Gln Asn Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln Pro Val Leu
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025                 1030                1035                1040
Ser Gln Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met Ser Asn Gly
                1045                1050                1055
Leu Gly Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys
            1060                1065                1070
Leu Gly Leu Arg His Tyr Phe Phe Phe Asp Tyr Gly Phe Ser Glu Ile
        1075                1080                1085
Gly Leu Ala Asn Gln Ser Val Lys Ala Asn Ile Phe Ala Tyr Gly Val
    1090                1095                1100
Gly Thr Asp Phe Leu Trp Asn Leu Phe Arg Arg Thr Tyr Asn Thr Lys
105                 1110                1115                1120
Ala Leu Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr
                1125                1130                1135
Trp Leu Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala
            1140                1145                1150
Asn Asp Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val
        1155                1160                1165
Arg Thr Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn
    1170                1175                1180
Gln Gly Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro
185                 1190                1195                1200
Leu Ile Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr
                1205                1210                1215
Arg Arg Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe
            1220                1225                1230
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 48...1226
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
TAAGGATAAA ATCAAGCGAT TAGCCCGAAT TTTAAGAGAG TATTAAG ATG AAT AAA      56
                                                    Met Asn Lys
                                                     1

AAA GCG TAT TTT GGG GAG TTT GGA GGG AGT TTT GTT TCG GAG TTG TTA      104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu
     5                  10                  15

GTG CCT GCA TTA AGA GAA TTA GAA CAG GCG TTT GAT GCG TGT TTG AAA      152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys
20                  25                  30                  35

GAT GAA AAA TTC CAA AAA GAA TAT TTT CGT CTT TTA AAG GAT TTT GTG      200
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Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val
                  40                  45                  50

GGC CGT CCT AGC CCT TTA ACC TTG TGT CAA AAT ATC GTT TCT AAC CCT      248
Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro
            55                  60                  65

AAA GTC AAG CTT TAT TTA AAA CGA GAG GAT TTA ATC CAT GGC GGG GCG      296
Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His Gly Gly Ala
        70                  75                  80

CAT AAG ACT AAT CAA GCC TTA GGG CAA GCC CTT TTA GCG AAA AAA ATG      344
His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala Lys Lys Met
    85                  90                  95

GGT AAA ACA AGG ATC ATC GCT GAA ACA GGC GCC GGT CAG CAT GGC GTG      392
Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Val
100                 105                 110                 115

GCG ACG GCT ATC GCT TGC GCA TTA TTG AAC TTA AAA TGC GTG GTT TTT      440
Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys Val Val Phe
                120                 125                 130

ATG GGA TCT AAA GAC ATC AAG CGC CAG GAA ATG AAT GTT TTT AGA ATG      488
Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val Phe Arg Met
            135                 140                 145

CAC TTA TTA GGC GCT GAA GTG AGA GAG GTT AAT TCA GGG AGC GCG ACG      536
His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly Ser Ala Thr
        150                 155                 160

CTT AAA GAC GCT GTG AAT GAA GCC TTA AGA GAT TGG GCG AGC AGT TAC      584
Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala Ser Ser Tyr
    165                 170                 175

AAG GAC ACG CAT TAT TTG CTA GGC ACA GCC GCC GGG CCA CAC CCT TAC      632
Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro His Pro Tyr
180                 185                 190                 195

CCC ACA ATG GTT AAA ACC TTT CAA AAA ATG ATA GGC GAT GAG GTT AAA      680
Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp Glu Val Lys
                200                 205                 210

AGC CAG ATT TTA GAA AAA GAA AAC CGC TTG CCT GAT TAT GTG ATC GCA      728
Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr Val Ile Ala
            215                 220                 225

TGC GTT GGA GGG GGG TCT AAC GCT ATA GGG ATA TTC AGC GCA TTT TTA      776
Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser Ala Phe Leu
        230                 235                 240

AAC GAC AAA GAA GTT AAA CTC ATA GGC GTA GAG CCG GCG GGT TTA GGG      824
Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala Gly Leu Gly
    245                 250                 255

CTA GAA ACC AAT AAG CAT GGG GCG ACT TTG AAT AAG GGG CGT GTG GGG      872
Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly Arg Val Gly
260                 265                 270                 275
```

```
ATT TTG CAT GGG AAT AAA ACC TAT CTT TTA CAA GAT GAT GAA GGC CAG      920
Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln
                280                 285                 290

ATT GCA GAA AGC CAT AGC ATT AGC GCC GGG CTT GAT TAT CCA GGA GTG      968
Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val
            295                 300                 305

GGG CCA GAA CAC AGC TAT TTA AAA GAA AGT GGG CGT GCG GTT TAT GAA     1016
Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu
        310                 315                 320

AGC GCA AGC GAT GCT GAA GCG CTA GAA GCC TTC AAG TTG TTG TGC CAA     1064
Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln
    325                 330                 335

AAA GAA GGC ATT ATC CCA GCG CTA GAA AGC TCA CAC GCC TTA GCG TAT     1112
Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr
340                 345                 350                 355

GCC TTA AAG CTC GCT CAA AAA TGC GAA GAA GAA AGC ATC ATC GTA GTG     1160
Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val
                360                 365                 370

AAT TTA AGC GGC AGA GGG GAT AAG GAT TTA AGC ACC GTT TAT AAC GCT     1208
Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala
            375                 380                 385

TTA AAA GGA GGT TTA AAA TGAGGTATCA AAACATGTTT GAAACCTTAA AAA        1259
Leu Lys Gly Gly Leu Lys
        390
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser
 1               5                  10                  15
Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala
            20                  25                  30
Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys
        35                  40                  45
Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val
    50                  55                  60
Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His
65                  70                  75                  80
Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala
                85                  90                  95
```

```
Lys Lys Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln
            100                 105                 110
His Gly Val Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys
        115                 120                 125
Val Val Phe Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val
    130                 135                 140
Phe Arg Met His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly
145                 150                 155                 160
Ser Ala Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala
                165                 170                 175
Ser Ser Tyr Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro
            180                 185                 190
His Pro Tyr Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp
        195                 200                 205
Glu Val Lys Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr
    210                 215                 220
Val Ile Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser
225                 230                 235                 240
Ala Phe Leu Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala
                245                 250                 255
Gly Leu Gly Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly
            260                 265                 270
Arg Val Gly Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp
        275                 280                 285
Glu Gly Gln Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr
    290                 295                 300
Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala
305                 310                 315                 320
Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu
                325                 330                 335
Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala
            340                 345                 350
Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile
        355                 360                 365
Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val
    370                 375                 380
Tyr Asn Ala Leu Lys Gly Gly Leu Lys
385                 390
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 197...547
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
TGGTGATGCA AAACCAAAAC AAGCGCATCA TGAATTACAT TCCTATTAAG TTGAATTTAA      60
GTGGGGTGAT CCCCCCTATT TTCGCTTCAG CTTTGCTCGT GTTCCCTTCT ACGATTTTGC     120
AGCAAGCCAC AAGCAACAAA ACCTTGCAAG CGGTTGCGNA TTTTTTAAGC CCGCAAGGTA     180
TGCGTATAAT ATTTTG ATG TTC TTG CTC ATC ATC TTT TTT GCT TAC TTT TAT      232
                  Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr
                   1               5                  10

TCT TCT ATT GTG TTC AAT TCT AAG GAT ATT GCG GAT AAT TTG AGG CGT        280
Ser Ser Ile Val Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg
        15                  20                  25

AAT GGC GGG TAT ATT CCA GGG CTT AGG CCT GGA GAG GGG ACT TCA TCG        328
Asn Gly Gly Tyr Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser
    30                  35                  40

TTT TTA AAT TCT GTA GCG AGT AAG CTC ACT TTG TGG GGT TCA TTG TAT        376
Phe Leu Asn Ser Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr
45                  50                  55                  60

TTA GCG CTC ATT TCT ACC GTG CCT TGG ATT TTG GTT AAG GCT ATG GGC        424
Leu Ala Leu Ile Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly
                65                  70                  75

GTG CCT TTT TAC TTT GGA GGC ACA GCG GTG CTG ATT GTG GTT CAA GTC        472
Val Pro Phe Tyr Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val
            80                  85                  90

GCT ATT GAC ACC ATG AAA AAG ATT GAA GCG CAA ATT TAT ATG AGC AAG        520
Ala Ile Asp Thr Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys
        95                  100                 105

TAT AAA ACT TTA AGC GCG GTA GGC TTT TAATGGCAAT CTCTATTAAA AGCCCAA      574
Tyr Lys Thr Leu Ser Ala Val Gly Phe
    110                 115

AAGAAATCAA AGCTCTAAGA AAAGCCG                                          601
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr Ser Ser Ile Val
 1               5                  10                  15
Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg Asn Gly Gly Tyr
            20                  25                  30
Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser Phe Leu Asn Ser
        35                  40                  45
Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr Leu Ala Leu Ile
    50                  55                  60
```

```
Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly Val Pro Phe Tyr
65                  70                  75                  80
Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val Ala Ile Asp Thr
                85                  90                  95
Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys Tyr Lys Thr Leu
            100                 105                 110
Ser Ala Val Gly Phe
        115
```

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 725 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 64...675
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```
GAAAACAGGA TAACGCATGA AACATGTGAG TAGGGATTTT GATACCGGTT GGGTTGCGTA     60
TCA ATG ACT CTA GGC ATT GAT GAA GCG GGT AGG GGG TGT TTG GCC GGT     108
    Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly
     1               5                  10                  15

TCG CTT TTT GTG GCT GGG GTG GCG TGT AAT GAA AAA ACA GCC TTA GAA     156
Ser Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu
                20                  25                  30

TTT CTA AAA ATG GGT TTA AAA GAC AGC AAG AAG CTC AGC CTA AAA AAG     204
Phe Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys
            35                  40                  45

CGC TTT TTC TTA GAA TAT AAG ATC AAA ACG CAT GGT GAG GTG GGG TTT     252
Arg Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe
        50                  55                  60

TTC GTG GTT AAA AAA AGC GCA AAT GAA ATT GAT AGC TTG GGC TTA GGG     300
Phe Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly
    65                  70                  75

GCG TGT TTG AAA CTC GCT GTG CAA GAA ATT TTA GAA AAT GGT TGC TCT     348
Ala Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser
80                  85                  90                  95

TTA GTT GAT GAA ATA AAA ATA GAC GGC AAC ACG GCG TTT GGC TTG AAC     396
Leu Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn
                100                 105                 110

AAA CGC TAC CCC CAT ATA CAA ACC ATC ATC AAG GGC GAT GAA ACA ATC     444
```

```
Lys Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile
            115                 120                 125

GCT CAA ATC GCT ATG GCG TCT GTT TTG GCG AAA GCT TTT AAG GAC AGA     492
Ala Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg
        130                 135                 140

GAA ATG CTA GAG TTG CAC GCT TTG TTT AAG GAA TAC GGC TGG GAT AAG     540
Glu Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys
    145                 150                 155

AAT TGC GGG TAT GGG ACT AAA CAA CAT ATA GAA GCG ATC ATT AAG CTA     588
Asn Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu
160                 165                 170                 175

GGG GCT ACG CCT TTT CAT CGG CAT AGC TTC ACG CTT AAA AAC CGC ATC     636
Gly Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile
                180                 185                 190

TTA AAT CCC AAA CTC TTA GAG GTG GAA CAA CGC CTT ATT TAAAAGGGCG CT   687
Leu Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile
            195                 200

GAGATGGGTA GCGCTCGCTG AAGAAAGGTC GATGCGTT                          725
```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```
Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly Ser
 1               5                  10                  15
Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu Phe
            20                  25                  30
Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys Arg
        35                  40                  45
Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe Phe
    50                  55                  60
Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly Ala
65                  70                  75                  80
Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser Leu
                85                  90                  95
Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn Lys
            100                 105                 110
Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile Ala
        115                 120                 125
Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg Glu
    130                 135                 140
Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys Asn
145                 150                 155                 160
```

```
Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu Gly
                165                 170                 175
Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile Leu
            180                 185                 190
Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 58...2769
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```
GATTAATCAG TGGAAGAATA CAAAGACACC CTAAACTTAA ACACAACCAC CTTTTCT ATG     60
                                                                Met
                                                                 1

AAG GGG AAT TTG AGC GTT AAT GAG CCT AAA ACT TAC GCC AAA TGG CAA      108
Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp Gln
             5                  10                  15

GAG CAA CAA GCG TTT AAA CGC ATG CAA GCT AGG AAA GAC AAC CAT GGG      156
Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His Gly
        20                  25                  30

GAT TTC ACT TTG CAT GAC GGG CCG CCT TAT GCG AAC GGG CAT TTG CAT      204
Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu His
    35                  40                  45

TTG GGG CAT GCC TTA AAT AAA ATT TTA AAA GAC ATT GTC GTT AAA AGA      252
Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys Arg
50                  55                  60                  65

GAA TAT TTT AAG GGG AAG AAA ATC TAT TAC ACG CCC GGT TGG GAT TGC      300
Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp Cys
                70                  75                  80

CAT GGT TTG CCC ATT GAG CAG CAA ATT TTA GAG CGA TTA GAA AAA GAA      348
His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys Glu
            85                  90                  95

AAA ACA AGC CTA GAA AAC CCC ACG CTG TTT AGA GAA AAG TGC CGA GAT      396
Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg Asp
        100                 105                 110

CAT GCG AAG AAA TTT TTA GAA ATC CAA AAG AAT GAA TTT TTG CAA TTG      444
```

```
His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln Leu
    115                 120                 125

GGT GTT TTG GGG GAT TTT GAA GAT CCT TAT AAA ACC ATG GAT TTT AAA      492
Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe Lys
130                 135                 140                 145

TTT GAA GCG AGC ATT TAT AGA GCC TTA GTG GAA GTG GCT AAA AAA GGG      540
Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys Gly
                150                 155                 160

CTT TTG AAA GAG CGC CAC AAG CCT ATT TAT TGG AGT TAT GCA TGC GAG      588
Leu Leu Lys Glu Arg His Lys Pro Ile Tyr Trp Ser Tyr Ala Cys Glu
            165                 170                 175

AGC GCT TTA GCG GAA GCT GAA GTG GAA TAC AAA ATG AAA AAA TCG CCC      636
Ser Ala Leu Ala Glu Ala Glu Val Glu Tyr Lys Met Lys Lys Ser Pro
        180                 185                 190

TCC ATT TTC GTG GCG TTT GGT TTG AAA AAG GAG AGT TTA GAA AAA TTA      684
Ser Ile Phe Val Ala Phe Gly Leu Lys Lys Glu Ser Leu Glu Lys Leu
    195                 200                 205

AAA GTC AAA AAA GCG AGC TTG GTG ATT TGG ACG ACC ACG CCT TGG ACT      732
Lys Val Lys Lys Ala Ser Leu Val Ile Trp Thr Thr Thr Pro Trp Thr
210                 215                 220                 225

TTG TAT GCG AAT GTA GCG ATC GCT TTG AAA AAA GAC GCT GTT TAT GCG      780
Leu Tyr Ala Asn Val Ala Ile Ala Leu Lys Lys Asp Ala Val Tyr Ala
                230                 235                 240

CTC ACC CAA AAA GGC TAT TTA GTC GCT AAA GCC TTG CAT GAA AAA TTA      828
Leu Thr Gln Lys Gly Tyr Leu Val Ala Lys Ala Leu His Glu Lys Leu
            245                 250                 255

GCC GCT TTA GGG GTG GTG GAT AAT GAG ATC ACA CAT GAA TTC AAT TCC      876
Ala Ala Leu Gly Val Val Asp Asn Glu Ile Thr His Glu Phe Asn Ser
        260                 265                 270

AAT GAT TTA GAA TAT TTA GTG GCT ACA AAC CCG CTC AAT CAA AGG GAT      924
Asn Asp Leu Glu Tyr Leu Val Ala Thr Asn Pro Leu Asn Gln Arg Asp
    275                 280                 285

TCG CTG GTG GCT TTA GGA GAG CAT GTC GGT TTA GAA GAT GGC ACA GGA      972
Ser Leu Val Ala Leu Gly Glu His Val Gly Leu Glu Asp Gly Thr Gly
290                 295                 300                 305

GCC GTG CAT ACC GCA CCT GGG CAT GGT GAA GAG GAC TAT TAT TTA GGC     1020
Ala Val His Thr Ala Pro Gly His Gly Glu Glu Asp Tyr Tyr Leu Gly
                310                 315                 320

TTA AGA TAT AAT TTA GAA GTG TTA ATG TCT GTA GAT GAG AAA GGT TGC     1068
Leu Arg Tyr Asn Leu Glu Val Leu Met Ser Val Asp Glu Lys Gly Cys
            325                 330                 335

TAT GAT GAG GGC ATT ATC CAT AAC CAA CTA TTA GAT GAA AGC TAT CTG     1116
Tyr Asp Glu Gly Ile Ile His Asn Gln Leu Leu Asp Glu Ser Tyr Leu
        340                 345                 350
```

```
GGC GAG CAT GTT TTT AAG GCT CAA AAA CGC ATT ATA GAG CAA TTG GGC     1164
Gly Glu His Val Phe Lys Ala Gln Lys Arg Ile Ile Glu Gln Leu Gly
    355                 360                 365

GAT TCT TTA TTG CTA GAG CAA GAG ATT GAG CAT TCT TAT CCG CAT TGC     1212
Asp Ser Leu Leu Leu Glu Gln Glu Ile Glu His Ser Tyr Pro His Cys
370                 375                 380                 385

TGG AGG ACG CAC AAG CCT GTG ATT TAC AGA GCG ACT ACG CAA TGG TTT     1260
Trp Arg Thr His Lys Pro Val Ile Tyr Arg Ala Thr Thr Gln Trp Phe
                390                 395                 400

ATT TTA ATG GAT GAG CCT TTT ATC CAA AAT GAT GGC TCT CAA AAA ACC     1308
Ile Leu Met Asp Glu Pro Phe Ile Gln Asn Asp Gly Ser Gln Lys Thr
            405                 410                 415

TTA AGA GAA GTG GCT TTA GAT GCG ATT GAA AAG GTG GAA TTT GTG CCA     1356
Leu Arg Glu Val Ala Leu Asp Ala Ile Glu Lys Val Glu Phe Val Pro
        420                 425                 430

AGC AGC GGG AAA AAC CGC CTA AAA ACC ATG ATA GAA AAC CGC CCT GAT     1404
Ser Ser Gly Lys Asn Arg Leu Lys Thr Met Ile Glu Asn Arg Pro Asp
    435                 440                 445

TGG TGC TTG AGC CGG CAA AGA AAA TGG GGC GTG CCA CTG GCC TTT TTC     1452
Trp Cys Leu Ser Arg Gln Arg Lys Trp Gly Val Pro Leu Ala Phe Phe
450                 455                 460                 465

ATA GAC AAA CGC ACG AAT AAG CCT TGT TTT GAA AGC GAA GTT TTA GAG     1500
Ile Asp Lys Arg Thr Asn Lys Pro Cys Phe Glu Ser Glu Val Leu Glu
                470                 475                 480

CAT GTG GCC AAT CTT TTT GAG AAA AAA GGC TGT GAT GTG TGG TGG GAG     1548
His Val Ala Asn Leu Phe Glu Lys Lys Gly Cys Asp Val Trp Trp Glu
            485                 490                 495

TAT AGC GTG AAA GAT TTA TTG CCC CCT AGC TAT CAA GAG GAC GCC AAG     1596
Tyr Ser Val Lys Asp Leu Leu Pro Pro Ser Tyr Gln Glu Asp Ala Lys
        500                 505                 510

CAT TAT GAG AAA ATC ATG CAC ATT TTA GAC GTG TGG TTT GAT AGT GGT     1644
His Tyr Glu Lys Ile Met His Ile Leu Asp Val Trp Phe Asp Ser Gly
    515                 520                 525

AGC ACC TTT AAG GCG GTT TTA GAA GAC TAT CAT GGA GAA AAA GGG CAA     1692
Ser Thr Phe Lys Ala Val Leu Glu Asp Tyr His Gly Glu Lys Gly Gln
530                 535                 540                 545

AGC CCT AGC GAT GTG ATC TTA GAA GGG AGC GAT CAG CAT AGG GGG TGG     1740
Ser Pro Ser Asp Val Ile Leu Glu Gly Ser Asp Gln His Arg Gly Trp
                550                 555                 560

TTT CAA AGC TCG CTT CTA ATC GGT TGT GTT TTA AAC AAC CAA GCC CCT     1788
Phe Gln Ser Ser Leu Leu Ile Gly Cys Val Leu Asn Asn Gln Ala Pro
            565                 570                 575

TTT AAA AAG GTC ATT ACG CAT GGC TTT ATC GTA GAT GAA AAG GGC GAA     1836
Phe Lys Lys Val Ile Thr His Gly Phe Ile Val Asp Glu Lys Gly Glu
```

```
          580                 585                 590

AAA ATG AGT AAA TCT AAG GGC AAT GTG GTG TCT TTG GAC AAG CTG CTC    1884
Lys Met Ser Lys Ser Lys Gly Asn Val Val Ser Leu Asp Lys Leu Leu
    595                 600                 605

AAA ACG CAT GGG AGC GAT GTG GTG CGT TTG TGG GTA GCG TTT AAT GAC    1932
Lys Thr His Gly Ser Asp Val Val Arg Leu Trp Val Ala Phe Asn Asp
610                 615                 620                 625

TAT CAA AAC GAT TTG AGA GTC TCT CAA ACC TTT TTC ACT CAA ACA GAA    1980
Tyr Gln Asn Asp Leu Arg Val Ser Gln Thr Phe Phe Thr Gln Thr Glu
                630                 635                 640

CAA CAT TAT AAA AAA TTC CGC AAC ACC CTG AAA TTC TTA CTC GCT AAT    2028
Gln His Tyr Lys Lys Phe Arg Asn Thr Leu Lys Phe Leu Leu Ala Asn
            645                 650                 655

TTT AGC GAT ATG GAT CTC AAG AAT TTA GAA CGC CCC CAT AAC TTC AGC    2076
Phe Ser Asp Met Asp Leu Lys Asn Leu Glu Arg Pro His Asn Phe Ser
        660                 665                 670

CCT TTA GAT CAT TTT ATG TTA GAG ACT TTA GAA ACC ATA AGC GCT GGA    2124
Pro Leu Asp His Phe Met Leu Glu Thr Leu Glu Thr Ile Ser Ala Gly
    675                 680                 685

GTC AAT AGC GCG TTT GAA GAG CAT GAT TTT GTG AAA GGC TTG AAT ATT    2172
Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn Ile
690                 695                 700                 705

TTA ATG GCG TTT GTT ACC AAT GAA TTG AGC GGG ATT TAT TTA GAC GCT    2220
Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp Ala
                710                 715                 720

TGC AAG GAT AGC TTG TAT TGC GAT AGC AAA AAC AAT GAA AAA CGC CAA    2268
Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg Gln
            725                 730                 735

GCC ATT CAA ATG GTT TTA CTC GCT ACA GCT AGT AAG TTG TGC TAC TTT    2316
Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr Phe
        740                 745                 750

TTA GCC CCG ATT TTA ACG CAC ACG ATT GAA GAA GTT TTA GAG CAT AGC    2364
Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His Ser
    755                 760                 765

CAA GCG CTT CGC ATT TTT TTA CAA GCC AAA GAT GTG TTT GAT TTA AAA    2412
Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu Lys
770                 775                 780                 785

GAC ATT AGC GTT TCA GAA AAA CTC CAC CTC AAA GAG TTT AAA AAA CCA    2460
Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys Pro
                790                 795                 800

GAA AAT TTT GAA GCC GTT TTA GCC TTG CGT TCT GCC TTT AAT GAA GAG    2508
Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu Glu
            805                 810                 815
```

```
TTA GAC CGA TTG AAA AAA GAA GGC GTC ATT AAA AAT TCG TTA GAG TGC     2556
Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu Cys
        820                 825                 830

GCT ATT GAA GTA AAA GAA AAA GCG TTG GAT GAA AAT TTA GTA GAA GAG     2604
Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu Glu
    835                 840                 845

TTG CTG ATG GTA AGC TTT GTG GGG ATT GCA AAA GAA AAA TTG AGT GAA     2652
Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser Glu
850                 855                 860                 865

ACG CCA GCA TTC ACG CTC TTT AAA GCC CCC TTT TAT AAA TGC CCC AGG     2700
Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro Arg
                870                 875                 880

TGT TGG CGT TTT AAA AGC GAG CTA GAA AAC ACC CCT TGC AAG CGT TGC     2748
Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg Cys
            885                 890                 895

GAA CAG GTT TTA AAA GAG CGA TGATAAAAGG ATAGGGCTTT TGAAAACTTT ACAA  2803
Glu Gln Val Leu Lys Glu Arg
        900

ACCCATAGAG TTTTACAA                                                2821
```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```
Met Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp
 1               5                  10                  15
Gln Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His
            20                  25                  30
Gly Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu
        35                  40                  45
His Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys
    50                  55                  60
Arg Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp
65                  70                  75                  80
Cys His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys
                85                  90                  95
Glu Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg
            100                 105                 110
Asp His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln
        115                 120                 125
Leu Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe
    130                 135                 140
Lys Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys
```

```
145                 150                 155                 160
Gly Leu Leu Lys Glu Arg His Lys Pro Ile Tyr Trp Ser Tyr Ala Cys
                165                 170                 175
Glu Ser Ala Leu Ala Glu Ala Glu Val Glu Tyr Lys Met Lys Lys Ser
            180                 185                 190
Pro Ser Ile Phe Val Ala Phe Gly Leu Lys Lys Glu Ser Leu Glu Lys
        195                 200                 205
Leu Lys Val Lys Lys Ala Ser Leu Val Ile Trp Thr Thr Thr Pro Trp
    210                 215                 220
Thr Leu Tyr Ala Asn Val Ala Ile Ala Leu Lys Lys Asp Ala Val Tyr
225                 230                 235                 240
Ala Leu Thr Gln Lys Gly Tyr Leu Val Ala Lys Ala Leu His Glu Lys
                245                 250                 255
Leu Ala Ala Leu Gly Val Val Asp Asn Glu Ile Thr His Glu Phe Asn
            260                 265                 270
Ser Asn Asp Leu Glu Tyr Leu Val Ala Thr Asn Pro Leu Asn Gln Arg
        275                 280                 285
Asp Ser Leu Val Ala Leu Gly Glu His Val Gly Leu Glu Asp Gly Thr
    290                 295                 300
Gly Ala Val His Thr Ala Pro Gly His Gly Glu Glu Asp Tyr Tyr Leu
305                 310                 315                 320
Gly Leu Arg Tyr Asn Leu Glu Val Leu Met Ser Val Asp Glu Lys Gly
                325                 330                 335
Cys Tyr Asp Glu Gly Ile Ile His Asn Gln Leu Leu Asp Glu Ser Tyr
            340                 345                 350
Leu Gly Glu His Val Phe Lys Ala Gln Lys Arg Ile Ile Glu Gln Leu
        355                 360                 365
Gly Asp Ser Leu Leu Leu Glu Gln Glu Ile Glu His Ser Tyr Pro His
    370                 375                 380
Cys Trp Arg Thr His Lys Pro Val Ile Tyr Arg Ala Thr Thr Gln Trp
385                 390                 395                 400
Phe Ile Leu Met Asp Glu Pro Phe Ile Gln Asn Asp Gly Ser Gln Lys
                405                 410                 415
Thr Leu Arg Glu Val Ala Leu Asp Ala Ile Glu Lys Val Glu Phe Val
            420                 425                 430
Pro Ser Ser Gly Lys Asn Arg Leu Lys Thr Met Ile Glu Asn Arg Pro
        435                 440                 445
Asp Trp Cys Leu Ser Arg Gln Arg Lys Trp Gly Val Pro Leu Ala Phe
    450                 455                 460
Phe Ile Asp Lys Arg Thr Asn Lys Pro Cys Phe Glu Ser Glu Val Leu
465                 470                 475                 480
Glu His Val Ala Asn Leu Phe Glu Lys Lys Gly Cys Asp Val Trp Trp
                485                 490                 495
Glu Tyr Ser Val Lys Asp Leu Leu Pro Pro Ser Tyr Gln Glu Asp Ala
            500                 505                 510
Lys His Tyr Glu Lys Ile Met His Ile Leu Asp Val Trp Phe Asp Ser
        515                 520                 525
Gly Ser Thr Phe Lys Ala Val Leu Glu Asp Tyr His Gly Glu Lys Gly
    530                 535                 540
Gln Ser Pro Ser Asp Val Ile Leu Glu Gly Ser Asp Gln His Arg Gly
545                 550                 555                 560
Trp Phe Gln Ser Ser Leu Leu Ile Gly Cys Val Leu Asn Asn Gln Ala
                565                 570                 575
Pro Phe Lys Lys Val Ile Thr His Gly Phe Ile Val Asp Glu Lys Gly
            580                 585                 590
Glu Lys Met Ser Lys Ser Lys Gly Asn Val Val Ser Leu Asp Lys Leu
        595                 600                 605
Leu Lys Thr His Gly Ser Asp Val Val Arg Leu Trp Val Ala Phe Asn
```

```
    610                 615                 620
Asp Tyr Gln Asn Asp Leu Arg Val Ser Gln Thr Phe Phe Thr Gln Thr
625                 630                 635                 640
Glu Gln His Tyr Lys Lys Phe Arg Asn Thr Leu Lys Phe Leu Leu Ala
                645                 650                 655
Asn Phe Ser Asp Met Asp Leu Lys Asn Leu Glu Arg Pro His Asn Phe
            660                 665                 670
Ser Pro Leu Asp His Phe Met Leu Glu Thr Leu Glu Thr Ile Ser Ala
        675                 680                 685
Gly Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn
    690                 695                 700
Ile Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp
705                 710                 715                 720
Ala Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg
                725                 730                 735
Gln Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr
            740                 745                 750
Phe Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His
        755                 760                 765
Ser Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu
    770                 775                 780
Lys Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys
785                 790                 795                 800
Pro Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu
                805                 810                 815
Glu Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu
            820                 825                 830
Cys Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu
        835                 840                 845
Glu Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser
    850                 855                 860
Glu Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro
865                 870                 875                 880
Arg Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg
                885                 890                 895
Cys Glu Gln Val Leu Lys Glu Arg
            900
```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 70...288
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TGTAGAATGA AATCCTAGCC AGTGAGCTAG AATTTAAATT TTTAATCAAA GGAGTCATCA 60

```
TGGCACACC ATG AAG AAC AAC ACG GCG GGC ACC ACC ACC ACC ATC ACC ACA   111
          Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr
           1               5                  10

CAC ACC ACC ACC ACT ATC ATG GCG GTG AAC ACC ACC ATC ACC ACC ACA     159
His Thr Thr Thr Thr Ile Met Ala Val Asn Thr Thr Ile Thr Thr Thr
15                  20                  25                  30

GCT CTC ATC ATG AAG AAG GTT GTT GCA GCA CTA GCG ACA GTC ATC ATC     207
Ala Leu Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile
                35                  40                  45

AAG AAG AAG GTT GCT GCC ACG GGC ATC ACG AGT AAT ATC GGT GTG GCT     255
Lys Lys Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala
            50                  55                  60

AGG GGC AAC TTG ACT AGG GTT GTC TCT GGC TTT TGACTTTAAA ATACAATCAT   308
Arg Gly Asn Leu Thr Arg Val Val Ser Gly Phe
        65                  70

TCCATTCTAA CCCATTCTGA TCAAACCCGT T                                  339
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr His Thr
 1               5                  10                  15
Thr Thr Thr Ile Met Ala Val Asn Thr Thr Ile Thr Thr Thr Ala Leu
            20                  25                  30
Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile Lys Lys
        35                  40                  45
Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala Arg Gly
    50                  55                  60
Asn Leu Thr Arg Val Val Ser Gly Phe
65                  70
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...734
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
GTTTTCTACT TATGATTTTG TGGAAGAATA TTGCAAATTA AAGGAAATGC  ATG CTT      56
                                                        Met Leu
                                                         1

GAA AAA GTG TTT CAA GAA ATT ACC AAT AAA AGA AAG TTT TTT GCA AGT      104
Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe Ala Ser
          5                  10                  15

TCT AGC ACA GGG GAG CAG TTT GAA AAC CAA TTT AGG AAT GAA TTA AAA      152
Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu Leu Lys
     20                  25                  30

AAA CAC TTT AGC GAA ATC AAT GGC GAT TTA ACA GAA GAA TTA AGC CAT      200
Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu Ser His
35                  40                  45                  50

ATT GAA GAA AAG CCT AAT AAA GAA ATC AAA ACC ACT TTT AAC CAA CTC      248
Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn Gln Leu
                55                  60                  65

AAA AAG CAA GTT TTA GAA AAA AAT CAC CCG CAC ACC CTT AAA AAC CCT      296
Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys Asn Pro
           70                  75                  80

TTT TCA AAC CTT ACA AGC CAT TTT TTA TAC CAG CCT TTT GGC TCA CAA      344
Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly Ser Gln
      85                  90                  95

AAT TAC CCT GAT TTT TTG GTT TTT ATT TTT GAC TAT GTG GTG GGG ATT      392
Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val Gly Ile
 100                 105                 110

GAA ATC AAG TTT TCT AAA AAC GAT AAG GGT GAA AAA AAT CTT CAA ACA      440
Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu Gln Thr
115                 120                 125                 130

TCT CGC CCC ATG TGG AAT TCA AAC CTG CCT AAA CCC AAT GCG ATT TAT      488
Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala Ile Tyr
                135                 140                 145

GTG TAT GGA GTC GCT AAT GCA AAC ATC ACT TTT TTT AAA GGC TCA GAT      536
Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly Ser Asp
           150                 155                 160

ATT TTG AGT TAT GAA ACC AGA GAG GTC TTG CTC AAG TAT TTT GAT ATT      584
Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe Asp Ile
      165                 170                 175

TTA GAT AAA GAT GAA AGA AGT TTG AAA AAC GCC TTA AAG GAT TTA GAA      632
Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp Leu Glu
 180                 185                 190
```

```
AAC CCT TTT GGG TTT GCC CCC TAC ATC AGA AAA GCT TAT GAG CAT AAA      680
Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu His Lys
195                 200                 205                 210

AGG AAT TTT CTA ACC ACC ACC AGA TTG AAA GCT TCT TTT CGC CCA ACC      728
Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg Pro Thr
                215                 220                 225

ACA TTT TAAGAGAGCG GAATGTCTTG GAATTTTTGA AAACGCTCAC TCATTAGCGT AT    786
Thr Phe


T                                                                    787
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
Met Leu Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe
 1               5                  10                  15
Ala Ser Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu
            20                  25                  30
Leu Lys Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu
        35                  40                  45
Ser His Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn
    50                  55                  60
Gln Leu Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys
65                  70                  75                  80
Asn Pro Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly
                85                  90                  95
Ser Gln Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val
            100                 105                 110
Gly Ile Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu
        115                 120                 125
Gln Thr Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala
    130                 135                 140
Ile Tyr Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly
145                 150                 155                 160
Ser Asp Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe
                165                 170                 175
Asp Ile Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp
            180                 185                 190
Leu Glu Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu
        195                 200                 205
His Lys Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg
    210                 215                 220
Pro Thr Thr Phe
225
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 53...493
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
CCAAACCCTT TTGAAACACT TGCTCACTAA CCCATTATAA GCCGCAAAAA CC ATG CTC     58
                                                           Met Leu
                                                            1

TCT TTA AAA CAA GAT TCC TTT TTT TTC TTA TGT TTA GGA ATC CTG GGG     106
Ser Leu Lys Gln Asp Ser Phe Phe Phe Leu Cys Leu Gly Ile Leu Gly
          5                  10                  15

TTT TAT TTT TAT AGC CTT TTG AGG GAT TTA ATG CCT TTT TTA CCC CCA     154
Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu Pro Pro
     20                  25                  30

ATG ATT GGG TTT TTA TTC TTG TTT TAT GCG AAA AAA TAC GAT CAT TTT     202
Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp His Phe
35                  40                  45                  50

TTA CCC AGT TTG AGC GTG TTT GGT TGT TTG TTT TGG TTT GAG AGC ATG     250
Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu Ser Met
                55                  60                  65

CAT TTA AAG ACT TTA GGC GTT TTA GCT TTA TTG TTT TTA ATC TAC CAT     298
His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile Tyr His
          70                  75                  80

CAA ATC GCC TAT AAA AAC TCT TTA AAG CTT TTT AAT GAC GGC TTT TTA     346
Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly Phe Leu
     85                  90                  95

TTC AAA ACT TTG CAT GTT TTT TTG GTT TAT TAC CTT TAT TTA TCG CGC     394
Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu Ser Arg
100                 105                 110

TTT TTT TCG ATG TCT TTG AGT TTG AAA ATA CTC GGC TTT CTC GCT CTT     442
Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu Ala Leu
115                 120                 125                 130

TTT GCT TTA ATA GAA AGC GCT TTG TGG GGT TTG TAT GAA AAA TCT TCG     490
Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys Ser Ser
                135                 140                 145
```

CTA TAAGCTTTTG CTCTTTGTTT TTATAGGGTT TTGGGGGTTA CTAGCCT 540
Leu

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
Met Leu Ser Leu Lys Gln Asp Ser Phe Phe Phe Leu Cys Leu Gly Ile
 1               5                  10                  15
Leu Gly Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu
            20                  25                  30
Pro Pro Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp
        35                  40                  45
His Phe Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu
    50                  55                  60
Ser Met His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile
65                  70                  75                  80
Tyr His Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly
                85                  90                  95
Phe Leu Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu
            100                 105                 110
Ser Arg Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu
        115                 120                 125
Ala Leu Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys
    130                 135                 140
Ser Ser Leu
145
```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1835
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CACTAAAGTC AATCCAAGCG CAAGTTGGAT GAAAAAATAA GAAGGAAGTT ATG AAA 56
Met Lys

```
AAG TCA TTC AAA AAA TTA GGC TTT GTC TCT TTA GCG GCT AGT GGC GTG      104
Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser Gly Val
          5                  10                  15

CTT TTA GGG AGC ATG AAC GCT ACC GAT TTA GAA ACC TAC GCA GCA TTG      152
Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala Ala Leu
     20                  25                  30

CAA AAA TCA TCG CAT GTT TTT GGT AAT TAT GCT GAA AAG GAT AAG GAT      200
Gln Lys Ser Ser His Val Phe Gly Asn Tyr Ala Glu Lys Asp Lys Asp
35                   40                  45                  50

AGT AAA TTA ACA AGC GAT TCA CCA ACG CAA CAA CAA GAT CAA AAA GTA      248
Ser Lys Leu Thr Ser Asp Ser Pro Thr Gln Gln Gln Asp Gln Lys Val
                55                  60                  65

GCC CAA AAC ACC GCT TCA AAC GAC AGC CAA GAA GCG ACA ACA CTT GAA      296
Ala Gln Asn Thr Ala Ser Asn Asp Ser Gln Glu Ala Thr Thr Leu Glu
           70                  75                  80

AAC ACC GCT TCT ACT GAC AAC ACA ACC GCC ACA ACT GAT GAA ACT TAT      344
Asn Thr Ala Ser Thr Asp Asn Thr Thr Ala Thr Thr Asp Glu Thr Tyr
      85                  90                  95

ACA AAA AGC ACT GAC ACT ACT GTA GCT GGT GCG GCT CAA AAA GTA GAA      392
Thr Lys Ser Thr Asp Thr Thr Val Ala Gly Ala Ala Gln Lys Val Glu
 100                 105                 110

ACC GAT AAC ACA GCC GTT CAA AGC GCT GAA CAA ACT TTA AAA ACA GAT      440
Thr Asp Asn Thr Ala Val Gln Ser Ala Glu Gln Thr Leu Lys Thr Asp
115                 120                 125                 130

GTA GCT AAA GTT CAA GCT GAT GCT AGT GCT AAA GAT TTT GAT GAA ACC      488
Val Ala Lys Val Gln Ala Asp Ala Ser Ala Lys Asp Phe Asp Glu Thr
                135                 140                 145

ACT TTT CAA GCC GAT CAA GCA GCA GAG CAA ACC GCT GAA AAA GCT TTA      536
Thr Phe Gln Ala Asp Gln Ala Ala Glu Gln Thr Ala Glu Lys Ala Leu
           150                 155                 160

CAA CAG GCT GAG AGC AAA CTC AAC ACC GAT CAA CAG ACT TTA AAC ACA      584
Gln Gln Ala Glu Ser Lys Leu Asn Thr Asp Gln Gln Thr Leu Asn Thr
      165                 170                 175

GCG TTA CAA GAT CAG ACG AAA ACA CCA ACC CCA TCA ACC CCA CCA ACT      632
Ala Leu Gln Asp Gln Thr Lys Thr Pro Thr Pro Ser Thr Pro Pro Thr
 180                 185                 190

AAA GAG GAA CCA AAA CAC ACC GCT TCA AGC GGC ACA CCA CCA GCT CCA      680
Lys Glu Glu Pro Lys His Thr Ala Ser Ser Gly Thr Pro Pro Ala Pro
195                 200                 205                 210

GAA AGC CCA CCA GCT AAA AAA GAT GAA ACA AGT GGC ACA CCA AGT GCT      728
Glu Ser Pro Pro Ala Lys Lys Asp Glu Thr Ser Gly Thr Pro Ser Ala
                215                 220                 225
```

```
AGT GGG AGT TCT GTG GCA AGC CAG CTA ACC AAA GAT ACC ACT ATG GTT      776
Ser Gly Ser Ser Val Ala Ser Gln Leu Thr Lys Asp Thr Thr Met Val
            230                 235                 240

AAT AAT CTT AAG AGT GTG AGC GTG AGC GCG ATG AAC ACC ACT TTA AGT      824
Asn Asn Leu Lys Ser Val Ser Val Ser Ala Met Asn Thr Thr Leu Ser
        245                 250                 255

GGA GTA GAA ACC ATG TCT CAA CAA ACT GCA ACG ATT GGC AAC CTT TTG      872
Gly Val Glu Thr Met Ser Gln Gln Thr Ala Thr Ile Gly Asn Leu Leu
    260                 265                 270

AAT AGT AGC ACC GAT TTA AGC AGT GTG ATT CCC AAC GCT CAA GGG CTA      920
Asn Ser Ser Thr Asp Leu Ser Ser Val Ile Pro Asn Ala Gln Gly Leu
275                 280                 285                 290

AAC AGC GCG TTT AGC ACA TTA GAA AGC GCT CAA AAC ACT CTA AAA GGC      968
Asn Ser Ala Phe Ser Thr Leu Glu Ser Ala Gln Asn Thr Leu Lys Gly
                295                 300                 305

TAT TTA AAT TCT TCT AGC GCG ACG ATT GGG CAA TTG ACA AAC GGA TCT     1016
Tyr Leu Asn Ser Ser Ser Ala Thr Ile Gly Gln Leu Thr Asn Gly Ser
            310                 315                 320

AAT GCG GTT GTG GGC GCG TTA GAT AAA GCT ATC AAT CAA GTG GAT ATG     1064
Asn Ala Val Val Gly Ala Leu Asp Lys Ala Ile Asn Gln Val Asp Met
        325                 330                 335

GCT TTG GCC GAT CTT AGT GCA GCT GAT ACG CAA AAA ACG CAA GCC GTT     1112
Ala Leu Ala Asp Leu Ser Ala Ala Asp Thr Gln Lys Thr Gln Ala Val
    340                 345                 350

ACG CTT GCA ACT GCT AGT GAT AGT CCA ACG ACA ACG ACA GAT GCC ATC     1160
Thr Leu Ala Thr Ala Ser Asp Ser Pro Thr Thr Thr Thr Asp Ala Ile
355                 360                 365                 370

AAT TTC TTA AAC GCG CTA AAA AGC AAT CTA ATG GCT CAA AAA GAC GCT     1208
Asn Phe Leu Asn Ala Leu Lys Ser Asn Leu Met Ala Gln Lys Asp Ala
                375                 380                 385

TTT TTG AAT GTG CAT AAA AAC ATT CAA ACC GCT GTC GCT CAA GCC CAG     1256
Phe Leu Asn Val His Lys Asn Ile Gln Thr Ala Val Ala Gln Ala Gln
            390                 395                 400

GAA ACC TAC ACG CCA AGC GTG ATC AAC ACC AAT AAT TAC GGG CAA ATG     1304
Glu Thr Tyr Thr Pro Ser Val Ile Asn Thr Asn Asn Tyr Gly Gln Met
        405                 410                 415

TAT GGG GTA GAT GCG ATG GCA GGG TAT AAG TGG TTC TTT GGC AAA ACC     1352
Tyr Gly Val Asp Ala Met Ala Gly Tyr Lys Trp Phe Phe Gly Lys Thr
    420                 425                 430

AAA CGC TTT GGC TTT AGG TCT TAT GGA TAC TAC AGC TAT AAC CAT GCG     1400
Lys Arg Phe Gly Phe Arg Ser Tyr Gly Tyr Tyr Ser Tyr Asn His Ala
435                 440                 445                 450

AAT TTA AGC TTT GTG GGG AGC CAG CTT GGA ATC ATG GAG GGC GCG TCT     1448
Asn Leu Ser Phe Val Gly Ser Gln Leu Gly Ile Met Glu Gly Ala Ser
```

```
                455                 460                 465

CAA GTG AAT AAC TTC ACT TAT GGC GTG GGC TTT GAT GTG CTC TAT AAC    1496
Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu Tyr Asn
            470                 475                 480

TTC TAT GAA AGC AAA GAG GGC TAT AAC ACA GCA GGG TTG TTC TTA GGC    1544
Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe Leu Gly
        485                 490                 495

TTT GGG TTA GGA GGG GAT TCG TTT ATC GTT CAA GGA GAG AGC TAC TTG    1592
Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser Tyr Leu
    500                 505                 510

AAA TCT CAA ATG CAC ATT TGC AAC AAC ACC GCC GGC TGT TCA GCG AGC    1640
Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser Ala Ser
515                 520                 525                 530

ATG AAC ACA AGC TAC TTC CAA ATG CCT GTT GAA TTT GGT TTT AGG AGC    1688
Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe Arg Ser
                535                 540                 545

AAT TTC TCT AAA CAC AGC GGG ATT GAA GTG GGC TTT AAA TTG CCT TTA    1736
Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu Pro Leu
            550                 555                 560

TTC ACC AAC CAA TTC TAT AAA GAA AGG GGC GTA GAT GGA TCG GTA GAT    1784
Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser Val Asp
        565                 570                 575

GTG TTC TAT AAA AGG AAT TTC TCT ATT TAT TTT AAC TAC ATG ATC AAC    1832
Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met Ile Asn
    580                 585                 590

TTC TAAGCCTTTC TATTCTTTCC AATAGAGGGT TTTCTCTCTG TTGGTTTCTT TTT      1888
Phe
595
```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
Met Lys Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser
 1               5                  10                  15
Gly Val Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala
            20                  25                  30
Ala Leu Gln Lys Ser Ser His Val Phe Gly Asn Tyr Ala Glu Lys Asp
        35                  40                  45
Lys Asp Ser Lys Leu Thr Ser Asp Ser Pro Thr Gln Gln Gln Asp Gln
```

```
    50                  55                  60
Lys Val Ala Gln Asn Thr Ala Ser Asn Asp Ser Gln Glu Ala Thr Thr
65                  70                  75                  80
Leu Glu Asn Thr Ala Ser Thr Asp Asn Thr Thr Ala Thr Thr Asp Glu
                85                  90                  95
Thr Tyr Thr Lys Ser Thr Asp Thr Thr Val Ala Gly Ala Ala Gln Lys
            100                 105                 110
Val Glu Thr Asp Asn Thr Ala Val Gln Ser Ala Glu Gln Thr Leu Lys
        115                 120                 125
Thr Asp Val Ala Lys Val Gln Ala Asp Ala Ser Ala Lys Asp Phe Asp
    130                 135                 140
Glu Thr Thr Phe Gln Ala Asp Gln Ala Ala Glu Gln Thr Ala Glu Lys
145                 150                 155                 160
Ala Leu Gln Gln Ala Glu Ser Lys Leu Asn Thr Asp Gln Gln Thr Leu
                165                 170                 175
Asn Thr Ala Leu Gln Asp Gln Thr Lys Thr Pro Thr Pro Ser Thr Pro
            180                 185                 190
Pro Thr Lys Glu Glu Pro Lys His Thr Ala Ser Ser Gly Thr Pro Pro
        195                 200                 205
Ala Pro Glu Ser Pro Pro Ala Lys Lys Asp Glu Thr Ser Gly Thr Pro
    210                 215                 220
Ser Ala Ser Gly Ser Ser Val Ala Ser Gln Leu Thr Lys Asp Thr Thr
225                 230                 235                 240
Met Val Asn Asn Leu Lys Ser Val Ser Val Ser Ala Met Asn Thr Thr
                245                 250                 255
Leu Ser Gly Val Glu Thr Met Ser Gln Gln Thr Ala Thr Ile Gly Asn
            260                 265                 270
Leu Leu Asn Ser Ser Thr Asp Leu Ser Ser Val Ile Pro Asn Ala Gln
        275                 280                 285
Gly Leu Asn Ser Ala Phe Ser Thr Leu Glu Ser Ala Gln Asn Thr Leu
    290                 295                 300
Lys Gly Tyr Leu Asn Ser Ser Ser Ala Thr Ile Gly Gln Leu Thr Asn
305                 310                 315                 320
Gly Ser Asn Ala Val Val Gly Ala Leu Asp Lys Ala Ile Asn Gln Val
                325                 330                 335
Asp Met Ala Leu Ala Asp Leu Ser Ala Ala Asp Thr Gln Lys Thr Gln
            340                 345                 350
Ala Val Thr Leu Ala Thr Ala Ser Asp Ser Pro Thr Thr Thr Thr Asp
        355                 360                 365
Ala Ile Asn Phe Leu Asn Ala Leu Lys Ser Asn Leu Met Ala Gln Lys
    370                 375                 380
Asp Ala Phe Leu Asn Val His Lys Asn Ile Gln Thr Ala Val Ala Gln
385                 390                 395                 400
Ala Gln Glu Thr Tyr Thr Pro Ser Val Ile Asn Thr Asn Asn Tyr Gly
                405                 410                 415
Gln Met Tyr Gly Val Asp Ala Met Ala Gly Tyr Lys Trp Phe Phe Gly
            420                 425                 430
Lys Thr Lys Arg Phe Gly Phe Arg Ser Tyr Gly Tyr Tyr Ser Tyr Asn
        435                 440                 445
His Ala Asn Leu Ser Phe Val Gly Ser Gln Leu Gly Ile Met Glu Gly
    450                 455                 460
Ala Ser Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu
465                 470                 475                 480
Tyr Asn Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe
                485                 490                 495
Leu Gly Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser
            500                 505                 510
Tyr Leu Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser
```

```
        515                 520                 525
Ala Ser Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe
    530                 535                 540
Arg Ser Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu
545                 550                 555                 560
Pro Leu Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser
                565                 570                 575
Val Asp Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met
            580                 585                 590
Ile Asn Phe
        595
```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...1416
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```
TTTAAGAAAC TATTTGCGCA TTTGATGTTA AGGTTTCTCT AAAGC ATG CGT TAT TTT    57
                                                      Met Arg Tyr Phe
                                                       1

CTT GTA GTT TTC TTG TTT TTG TTT GTG GGT TGC ACA AAA AAG GAT TTC     105
Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr Lys Lys Asp Phe
 5                  10                  15                  20

ACG CTC AAA GAT TTA TCC TTG CCC CAA GAG GCT TCA AGC TAT CTT GCA     153
Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser Ser Tyr Leu Ala
                25                  30                  35

AGC TCT CAA AAT GGC AGT AAC AAC AAC CAA AGC ATT GAC CCC CAA GCG     201
Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile Asp Pro Gln Ala
            40                  45                  50

TTA AGA GAA AAT CTG AAA GAG AGC TAT CTC AAA GCG TGG TAT TCC CCA     249
Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala Trp Tyr Ser Pro
        55                  60                  65

TGG CTA GAT ATG AAA GTC AAA AGC AAT AAA AAA GAA GTG TTT TGG ATC     297
Trp Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu Val Phe Trp Ile
    70                  75                  80

CTT AAG GAG ATG AAT AAA TCC ACC GGT TAT GGC GAA GAT CTA AAA CCC     345
Leu Lys Glu Met Asn Lys Ser Thr Gly Tyr Gly Glu Asp Leu Lys Pro
85                  90                  95                  100
```

```
AAC GCA AAA GCT TTC AAT GAC GCA CTC ATT AAG AGC ATG GAT ATT GAG      393
Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser Met Asp Ile Glu
                105                 110                 115

CAT TAC CCT AGC GTT AAG ATT AGG GCT GTT GTA GCG CGA GAT AGC GAT      441
His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala Arg Asp Ser Asp
            120                 125                 130

GTG AGG GCT GTG CCT ACT AAC AAA CCT TAT TAT CTT TCT CAA AAA GGC      489
Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu Ser Gln Lys Gly
        135                 140                 145

TAT CCT TTT GAT AGG TAT CAA AAT TCG CTG ATT TTT CAA GGC ACG CCG      537
Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe Gln Gly Thr Pro
    150                 155                 160

GTT TTA ATC ACG CAT TTT AAT CTA GAT AAA ACT TAT GCC CAC ATT CAA      585
Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr Ala His Ile Gln
165                 170                 175                 180

AGC AGT TTT GTT TAT GGC TGG ATC AAA GTT AGC GAT TTA GTC TAC ATG      633
Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp Leu Val Tyr Met
                185                 190                 195

CAC GAT AAA GAC ATA GAG CTT TTA ACC CAT CTT AAA GAT TAT GTC ATG      681
His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys Asp Tyr Val Met
            200                 205                 210

CCT ATA AAA GAT AAA ATC CCC CTT TAT ACA GAC TAT GGG GAT TTT TAC      729
Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr Gly Asp Phe Tyr
        215                 220                 225

ACC AAC GCC AGA GTG GGC GAA TTG TTC GCT CTC ATC CCC CAA AGT CAA      777
Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile Pro Gln Ser Gln
    230                 235                 240

AAA ACA CCT CAA AAA CCC CAA AAA AAG GAA TTG AAA GCC TAT GGT TTT      825
Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys Ala Tyr Gly Phe
245                 250                 255                 260

TTG AGA GAC GCT AAG GGT TAT GCA GCT TTA CAA AGC GTG ATC TTA GAA      873
Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser Val Ile Leu Glu
                265                 270                 275

GAA AAG GAT TTT TTT GTT TTC CCT AAG GCT TTT AAC AGC GAG AAC ATG      921
Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn Ser Glu Asn Met
            280                 285                 290

GCG TAT TTT ATA GAC ACC ATG TTA GGG CAA AAA TAC GGC TGG GGC GGG      969
Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr Gly Trp Gly Gly
        295                 300                 305

CTA TTG GGT AAT AGG GAT TGC TCG GCT TTC ACC AGA GAT AGT TTT GCT     1017
Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg Asp Ser Phe Ala
    310                 315                 320

AAT TTT GGT ATT TTG CTC CCC AGA AAT TCC TAT GCG CAA AGC CGT TAT     1065
Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala Gln Ser Arg Tyr
```

```
325                 330                 335                 340

GCG AAC AAT TAT GTG GAT TTA AGC TCT ATG AAA GCC AAA GAA AAA GAA    1113
Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala Lys Glu Lys Glu
                345                 350                 355

GAC TAC ATC CTT AAA AAC GCC ACG CCT TTT GGA ACG CTC ATC TAT TTA    1161
Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr Leu Ile Tyr Leu
            360                 365                 370

AAA GGG CAT ATC ATG CTT TAT TTA GGC GCA CAC AAC CAT CAA GCG ATA    1209
Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn His Gln Ala Ile
        375                 380                 385

GTC GCT CAC AGC ATT TGG TCG GTG CAA ACC CAA AAG CAT TTT AAA ACC    1257
Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys His Phe Lys Thr
    390                 395                 400

TTG AGC CAT AAA ATA GGA GGC GTG GTG ATC ACT TCG TTA TGG TTA GCT    1305
Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser Leu Trp Leu Ala
405                 410                 415                 420

GAA GAG CAT AAT GGG GCG TTT TCT AAA AAG AAA TTA TTG ATT GAT AGG    1353
Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu Leu Ile Asp Arg
                425                 430                 435

GTG CTT GGA ATG AGC GAT TTG AAA GAT TTT GTC AAT AAA ACT TCA AGC    1401
Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn Lys Thr Ser Ser
            440                 445                 450

CCT TTA AAT GCG AAT TGATTTTCTT ATATTATGAT TACGATTTAT CAATTTAAAA C  1457
Pro Leu Asn Ala Asn
        455

ATTTGGAGAA AGA                                                     1470
```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 457 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```
Met Arg Tyr Phe Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr
 1               5                  10                  15
Lys Lys Asp Phe Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser
            20                  25                  30
Ser Tyr Leu Ala Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile
        35                  40                  45
Asp Pro Gln Ala Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala
    50                  55                  60
Trp Tyr Ser Pro Trp Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu
```

```
65                  70                  75                  80
Val Phe Trp Ile Leu Lys Glu Met Asn Lys Ser Thr Gly Tyr Gly Glu
                85                  90                  95
Asp Leu Lys Pro Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser
            100                 105                 110
Met Asp Ile Glu His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala
        115                 120                 125
Arg Asp Ser Asp Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu
    130                 135                 140
Ser Gln Lys Gly Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe
145                 150                 155                 160
Gln Gly Thr Pro Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr
                165                 170                 175
Ala His Ile Gln Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp
            180                 185                 190
Leu Val Tyr Met His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys
        195                 200                 205
Asp Tyr Val Met Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr
    210                 215                 220
Gly Asp Phe Tyr Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile
225                 230                 235                 240
Pro Gln Ser Gln Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys
                245                 250                 255
Ala Tyr Gly Phe Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser
            260                 265                 270
Val Ile Leu Glu Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn
        275                 280                 285
Ser Glu Asn Met Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr
    290                 295                 300
Gly Trp Gly Gly Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg
305                 310                 315                 320
Asp Ser Phe Ala Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala
                325                 330                 335
Gln Ser Arg Tyr Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala
            340                 345                 350
Lys Glu Lys Glu Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr
        355                 360                 365
Leu Ile Tyr Leu Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn
    370                 375                 380
His Gln Ala Ile Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys
385                 390                 395                 400
His Phe Lys Thr Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser
                405                 410                 415
Leu Trp Leu Ala Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu
            420                 425                 430
Leu Ile Asp Arg Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn
        435                 440                 445
Lys Thr Ser Ser Pro Leu Asn Ala Asn
    450                 455
```

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...182
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```
CTTTTACTTT ATAATTATCG TTGGCATTTT AATATTCAAA GGAGCTTGAA ATG AGA      56
                                                          Met Arg
                                                            1

ATT TCT CTT TTA GCT GTA ATT TTA GCG TTA TTG TTT GTG GCT TGC CAC     104
Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala Cys His
          5                  10                  15

GAA ACT AAA AAA CAA ATC TTA CAA AAC GAA GCC GAT AGC ACC CCT TCA     152
Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr Pro Ser
     20                  25                  30

GAA AAA ACC ATT TGG CAA CCT GAA CAA AAA TAAAAATTGT AAAAATACTC AAA   205
Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
35                  40

GGCATTTTTT AAAATAAACG CAATAAAAAA                                    235
```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```
Met Arg Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala
 1               5                  10                  15
Cys His Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr
            20                  25                  30
Pro Ser Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1298
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```
CCAGCGATGC GTCCTGTTAA AAACGATTTT AATGTGGAGA GTGAAGAATA  ATG GCG      56
                                                        Met Ala
                                                         1

TAT TTT TTA GAA CAA ACG GAT AGT GAA ATT TTT GAG CTT ATC TTT GAA      104
Tyr Phe Leu Glu Gln Thr Asp Ser Glu Ile Phe Glu Leu Ile Phe Glu
          5                  10                  15

GAA TAC AAG CGG CAA AAT GAG CAT TTA GAA ATG ATA GCG AGC GAG AAT      152
Glu Tyr Lys Arg Gln Asn Glu His Leu Glu Met Ile Ala Ser Glu Asn
     20                  25                  30

TAC ACT TTT GCA AGC GTT ATG GAG GCT ATG GGG AGT GTT TTA ACG AAT      200
Tyr Thr Phe Ala Ser Val Met Glu Ala Met Gly Ser Val Leu Thr Asn
35                   40                  45                  50

AAA TAC GCT GAA GGC TAC CCT AAC AAG CGC TAT TAT GGA GGC TGT GAA      248
Lys Tyr Ala Glu Gly Tyr Pro Asn Lys Arg Tyr Tyr Gly Gly Cys Glu
                55                  60                  65

GTG GTG GAT AAA ATA GAA AGC CTA GCC ATA GAA AGG GCT AAA AAG CTT      296
Val Val Asp Lys Ile Glu Ser Leu Ala Ile Glu Arg Ala Lys Lys Leu
           70                  75                  80

TTT AAT TGC CAG TTC GCT AAC GTG CAA GCG CAT TCA GGC TCA CAA GCC      344
Phe Asn Cys Gln Phe Ala Asn Val Gln Ala His Ser Gly Ser Gln Ala
      85                  90                  95

AAT AAC GCT GTC TAT CAC GCT CTT TTA AAG CCT TAT GAC AAG ATT TTA      392
Asn Asn Ala Val Tyr His Ala Leu Leu Lys Pro Tyr Asp Lys Ile Leu
 100                 105                 110

GGC ATG GAT TTA AGC TGT GGA GGG CAT TTA ACG CAT GGC GCT AAA GTG      440
Gly Met Asp Leu Ser Cys Gly Gly His Leu Thr His Gly Ala Lys Val
115                 120                 125                 130

AGT TTA ACC GGC AAG CAT TAT CAG AGC TTT TCT TAT GGC GTG AAT TTG      488
Ser Leu Thr Gly Lys His Tyr Gln Ser Phe Ser Tyr Gly Val Asn Leu
                135                 140                 145

GAT GGC TAT ATT GAT TAT GAA GAG GCG CTA AAA ATC GCT CAA AGC GTT      536
Asp Gly Tyr Ile Asp Tyr Glu Glu Ala Leu Lys Ile Ala Gln Ser Val
           150                 155                 160

AAG CCA GAA ATC ATC GTG TGC GGG TTT TCA GCC TAT CCA AGG GAG ATT      584
Lys Pro Glu Ile Ile Val Cys Gly Phe Ser Ala Tyr Pro Arg Glu Ile
      165                 170                 175

GAT TTT AAG AAA TTT AGA GAA ATC GCT GAT GAA GTG GGG GCG TTA CTA      632
```

```
Asp Phe Lys Lys Phe Arg Glu Ile Ala Asp Glu Val Gly Ala Leu Leu
    180                 185                 190

TTA GGC GAT ATA GCC CAT GTG GCA GGG CTT GTG GTA ACC GGT GAG CAT      680
Leu Gly Asp Ile Ala His Val Ala Gly Leu Val Val Thr Gly Glu His
195                 200                 205                 210

GCC CAT CCT TTC CCG CAT TGC CAT GTG GTT TCA AGC ACC ACT CAT AAG      728
Ala His Pro Phe Pro His Cys His Val Val Ser Ser Thr Thr His Lys
                215                 220                 225

ACC TTA AGA GGG CCT AGA GGG GGG ATT ATT TTA ACT AAT GAT GAA GAG      776
Thr Leu Arg Gly Pro Arg Gly Gly Ile Ile Leu Thr Asn Asp Glu Glu
            230                 235                 240

ATA GCG GCT AAG ATT GAC AAA GCG ATT TTT CCA GGA ACT CAA GGC GGG      824
Ile Ala Ala Lys Ile Asp Lys Ala Ile Phe Pro Gly Thr Gln Gly Gly
        245                 250                 255

CCT TTG ATG CAT GTG ATT GCT GCT AAA GCG GTG GGT TTT AAA GAG AAT      872
Pro Leu Met His Val Ile Ala Ala Lys Ala Val Gly Phe Lys Glu Asn
    260                 265                 270

CTA AAA CCA GAA TTT AAA GCT TAT GCA CAA TTA GTG AAA TCT AAC ATG      920
Leu Lys Pro Glu Phe Lys Ala Tyr Ala Gln Leu Val Lys Ser Asn Met
275                 280                 285                 290

CAA GTT TTG GCT AAA GCG TTA AAA GAA AAA AAC CAT AAG TTA GTG AGT      968
Gln Val Leu Ala Lys Ala Leu Lys Glu Lys Asn His Lys Leu Val Ser
                295                 300                 305

GGT GGC ACT TCT AAC CAT TTG CTT TTA ATG GAT TTT TTA GAT AAG CCT     1016
Gly Gly Thr Ser Asn His Leu Leu Leu Met Asp Phe Leu Asp Lys Pro
            310                 315                 320

TAT AGC GGG AAA GAC GCT GAT ATT GCA TTA GGG AAT GCC GGA ATC ACC     1064
Tyr Ser Gly Lys Asp Ala Asp Ile Ala Leu Gly Asn Ala Gly Ile Thr
        325                 330                 335

GTG AAT AAA AAC ACC ATT CCT GGT GAA ACG CGC AGC CCT TTT GTA ACG     1112
Val Asn Lys Asn Thr Ile Pro Gly Glu Thr Arg Ser Pro Phe Val Thr
    340                 345                 350

AGC GGG ATA AGG ATT GGC TCA GCG GCA TTG AGC GCA AGG GGC ATG GGA     1160
Ser Gly Ile Arg Ile Gly Ser Ala Ala Leu Ser Ala Arg Gly Met Gly
355                 360                 365                 370

GCT AAG GAA TTT GAA ATC ATA GGG AAT AAA ATA TCA GAT ATT TTG AAT     1208
Ala Lys Glu Phe Glu Ile Ile Gly Asn Lys Ile Ser Asp Ile Leu Asn
                375                 380                 385

GAT ATT AAT AAT GTT AGT TTG CAA TTG CAT GTG AAA GAA GAA TTG AAA     1256
Asp Ile Asn Asn Val Ser Leu Gln Leu His Val Lys Glu Glu Leu Lys
            390                 395                 400

GCC ATG GTC AAT CAA TTC CCT GTG TAC CAC CAA CCT ATT TTT TAAGGGAGT  1307
Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe
        405                 410                 415
```

CAAGATGACA GAAATGGAAT TAAAGCTCAT TAAGATAGAC ACAA 1351

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```
Met Ala Tyr Phe Leu Glu Gln Thr Asp Ser Glu Ile Phe Glu Leu Ile
 1               5                  10                  15
Phe Glu Glu Tyr Lys Arg Gln Asn Glu His Leu Glu Met Ile Ala Ser
            20                  25                  30
Glu Asn Tyr Thr Phe Ala Ser Val Met Glu Ala Met Gly Ser Val Leu
        35                  40                  45
Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Asn Lys Arg Tyr Tyr Gly Gly
    50                  55                  60
Cys Glu Val Val Asp Lys Ile Glu Ser Leu Ala Ile Glu Arg Ala Lys
65                  70                  75                  80
Lys Leu Phe Asn Cys Gln Phe Ala Asn Val Gln Ala His Ser Gly Ser
                85                  90                  95
Gln Ala Asn Asn Ala Val Tyr His Ala Leu Leu Lys Pro Tyr Asp Lys
            100                 105                 110
Ile Leu Gly Met Asp Leu Ser Cys Gly Gly His Leu Thr His Gly Ala
        115                 120                 125
Lys Val Ser Leu Thr Gly Lys His Tyr Gln Ser Phe Ser Tyr Gly Val
    130                 135                 140
Asn Leu Asp Gly Tyr Ile Asp Tyr Glu Glu Ala Leu Lys Ile Ala Gln
145                 150                 155                 160
Ser Val Lys Pro Glu Ile Ile Val Cys Gly Phe Ser Ala Tyr Pro Arg
                165                 170                 175
Glu Ile Asp Phe Lys Lys Phe Arg Glu Ile Ala Asp Glu Val Gly Ala
            180                 185                 190
Leu Leu Leu Gly Asp Ile Ala His Val Ala Gly Leu Val Val Thr Gly
        195                 200                 205
Glu His Ala His Pro Phe Pro His Cys His Val Val Ser Ser Thr Thr
    210                 215                 220
His Lys Thr Leu Arg Gly Pro Arg Gly Gly Ile Ile Leu Thr Asn Asp
225                 230                 235                 240
Glu Glu Ile Ala Ala Lys Ile Asp Lys Ala Ile Phe Pro Gly Thr Gln
                245                 250                 255
Gly Gly Pro Leu Met His Val Ile Ala Ala Lys Ala Val Gly Phe Lys
            260                 265                 270
Glu Asn Leu Lys Pro Glu Phe Lys Ala Tyr Ala Gln Leu Val Lys Ser
        275                 280                 285
Asn Met Gln Val Leu Ala Lys Ala Leu Lys Glu Lys Asn His Lys Leu
    290                 295                 300
Val Ser Gly Gly Thr Ser Asn His Leu Leu Leu Met Asp Phe Leu Asp
305                 310                 315                 320
Lys Pro Tyr Ser Gly Lys Asp Ala Asp Ile Ala Leu Gly Asn Ala Gly
                325                 330                 335
Ile Thr Val Asn Lys Asn Thr Ile Pro Gly Glu Thr Arg Ser Pro Phe
```

```
            340                 345                 350
Val Thr Ser Gly Ile Arg Ile Gly Ser Ala Ala Leu Ser Ala Arg Gly
        355                 360                 365
Met Gly Ala Lys Glu Phe Glu Ile Ile Gly Asn Lys Ile Ser Asp Ile
    370                 375                 380
Leu Asn Asp Ile Asn Asn Val Ser Leu Gln Leu His Val Lys Glu Glu
385                 390                 395                 400
Leu Lys Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe
                405                 410                 415
```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1460
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```
TGAAAAACCA CTCCTTTAAA AAAACGATCG CTCTTTCCTT ACTAGCGAGC ATG TCT      56
                                                          Met Ser
                                                            1

TTG TGC AGG GCT GAA GAA GAT GGG GCG TTT TTT GTC ATA GAT TAC CAG     104
Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp Tyr Gln
          5                  10                  15

ACG AGT TTG GCC AGA CAG GAA TTG AAA AAT CCA GGC TTC ACC CAA GCG     152
Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe Thr Gln Ala
     20                  25                  30

CAA GAA TTA AGG CAG TTG ATC AGA GAT GGG GCT GTG AGG TTG CAA ACT     200
Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu Gln Thr
35                  40                  45                  50

TCT GCC ATT CCC TTA TCC TAC TAC TTG GAT ATT TTA GGG AAT AAA ACA     248
Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn Lys Thr
                55                  60                  65

GCA ACT CTT TTG CGT GAA AGC CTG AAA AAC AAT GCA CAA CCA TCA CAA     296
Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro Ser Gln
          70                  75                  80

CCA AAC GCG CAA CCA CCG CAA CAA AAC GGA CCA TCA AAC CAA GCC TTA     344
Pro Asn Ala Gln Pro Pro Gln Gln Asn Gly Pro Ser Asn Gln Ala Leu
          85                  90                  95

GCC AAT TTA GAG CAA TCT CTA GGG ATT TTA GGA AAA CTA TTG GAT CTA     392
```

```
Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu Asp Leu
    100                 105                 110

TCC CAA CAA TAC GCT AGT CAG GGT GTC ATT AAG CCT TTG GTG GTG GAT      440
Ser Gln Gln Tyr Ala Ser Gln Gly Val Ile Lys Pro Leu Val Val Asp
115                 120                 125                 130

GTG GGG AAA GAA CAA ATC GGT ATC ACG GAT AGC ATG CTC TTG GTG GCT      488
Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu Val Ala
                135                 140                 145

CAA AAC ATC GTT TTA GCT TTA GGG CAA GTG GAT TTG AGC AAA ATC CAA      536
Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys Ile Gln
            150                 155                 160

CAA AAC AAT AAC GAA CAG CTA TAC GAA AAT ATT ATG AAA GTC ATG CTT      584
Gln Asn Asn Asn Glu Gln Leu Tyr Glu Asn Ile Met Lys Val Met Leu
        165                 170                 175

TTA GGC GCG GGC GGG ACT AAT GGG GCG TAT AAT GGC GTG AGT GTG GGC      632
Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn Gly Val Ser Val Gly
    180                 185                 190

GAC ATT GCC ACG GGC ATG CAA AAT TTT TCT TCG CAA ACG GGC TTG ATA      680
Asp Ile Ala Thr Gly Met Gln Asn Phe Ser Ser Gln Thr Gly Leu Ile
195                 200                 205                 210

GGG GCT AAT TCT ACG GTT AGC GAG CTG AAT GCT TTG ATT AAG AGC GGG      728
Gly Ala Asn Ser Thr Val Ser Glu Leu Asn Ala Leu Ile Lys Ser Gly
                215                 220                 225

ATT TCT TTG GAT CGT GAG ACT TTG GGG TTA GGG AGT TTT ATT GAA AAA      776
Ile Ser Leu Asp Arg Glu Thr Leu Gly Leu Gly Ser Phe Ile Glu Lys
            230                 235                 240

AAT ATC TGT AGC GGT GCA TCG TCT TGT TTT AGT GGG AAT CAG CTT ATC      824
Asn Ile Cys Ser Gly Ala Ser Ser Cys Phe Ser Gly Asn Gln Leu Ile
        245                 250                 255

TAT AAG AAA GGG CTA GAC AGA ACC ATA AAC ATC ATT AAT ACG GTA TTA      872
Tyr Lys Lys Gly Leu Asp Arg Thr Ile Asn Ile Ile Asn Thr Val Leu
    260                 265                 270

GGT CAG TTT GAA TCT TCG GCT AGT TCT CTT TAT AAG ATT TCT TAT ATC      920
Gly Gln Phe Glu Ser Ser Ala Ser Ser Leu Tyr Lys Ile Ser Tyr Ile
275                 280                 285                 290

CCT AAC CTC TTT TCG CTC AAG GAT TAC CAG TCA GCG AGC ATG AAC GGC      968
Pro Asn Leu Phe Ser Leu Lys Asp Tyr Gln Ser Ala Ser Met Asn Gly
                295                 300                 305

TTT GGG GCT AAG ATG GGC TAT AAA CAA TTT TTC ACC CAT AAG AAA AAT     1016
Phe Gly Ala Lys Met Gly Tyr Lys Gln Phe Phe Thr His Lys Lys Asn
            310                 315                 320

GTT GGC TTA AGG TAT TAC GGG TTT TTG GAT TAT GGC TAT GCG AAC TTT     1064
Val Gly Leu Arg Tyr Tyr Gly Phe Leu Asp Tyr Gly Tyr Ala Asn Phe
        325                 330                 335
```

```
GGC GAT ACG AAT TTA AAA GTG GGG GCG AAT CTT GTT ACT TAT GGG GTA    1112
Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu Val Thr Tyr Gly Val
    340                 345                 350

GGA ACG GAT TTT TTA TAC AAT GTG TAT GAA CGC TCT AGA AGG AGG GAA    1160
Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg Ser Arg Arg Arg Glu
355                 360                 365                 370

AGG ACT ACG ATC GGT CTT TTC TTT GGC GCT CAA ATT GCA GGG CAA ACT    1208
Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln Ile Ala Gly Gln Thr
                375                 380                 385

TGG AGC ACT AAT GTA ACG AAC TTA TTG AGC GGG CAA AGG CCT GAT GTC    1256
Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro Asp Val
            390                 395                 400

AAG TCC AGT TCG TTC CAA TTC TTG TTT GAT TTG GGC GTG CGC ACC AAC    1304
Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg Thr Asn
        405                 410                 415

TTT GCA AAA ACC AAT TTC AAT AAG CAC AGG CTA GAC CAA GGG ATA GAA    1352
Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly Ile Glu
    420                 425                 430

TTT GGG GTG AAA ATC CCT GTT ATC GCT CAT AAA TAT TTT GCA ACC CAA    1400
Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala Thr Gln
435                 440                 445                 450

GGC TCA AGC GCG AGC TAT ATG AGG AAT TTT AGC TTC TAT GTG GGC TAT    1448
Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val Gly Tyr
                455                 460                 465

TCA GTC GGT TTT TAAGGAAGGC TCTTGATGAA AAATACCAAT ACAAAAGAGA TAAAG  1505
Ser Val Gly Phe
            470

AATACAAG                                                          1513
```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```
Met Ser Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp
 1               5                  10                  15
Tyr Gln Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe Thr
            20                  25                  30
Gln Ala Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu
        35                  40                  45
Gln Thr Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn
```

```
    50                  55                  60
Lys Thr Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro
65                  70                  75                  80
Ser Gln Pro Asn Ala Gln Pro Pro Gln Gln Asn Gly Pro Ser Asn Gln
                85                  90                  95
Ala Leu Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu
            100                 105                 110
Asp Leu Ser Gln Gln Tyr Ala Ser Gln Gly Val Ile Lys Pro Leu Val
        115                 120                 125
Val Asp Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu
    130                 135                 140
Val Ala Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys
145                 150                 155                 160
Ile Gln Gln Asn Asn Asn Glu Gln Leu Tyr Glu Asn Ile Met Lys Val
                165                 170                 175
Met Leu Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn Gly Val Ser
            180                 185                 190
Val Gly Asp Ile Ala Thr Gly Met Gln Asn Phe Ser Ser Gln Thr Gly
        195                 200                 205
Leu Ile Gly Ala Asn Ser Thr Val Ser Glu Leu Asn Ala Leu Ile Lys
    210                 215                 220
Ser Gly Ile Ser Leu Asp Arg Glu Thr Leu Gly Leu Gly Ser Phe Ile
225                 230                 235                 240
Glu Lys Asn Ile Cys Ser Gly Ala Ser Ser Cys Phe Ser Gly Asn Gln
                245                 250                 255
Leu Ile Tyr Lys Lys Gly Leu Asp Arg Thr Ile Asn Ile Ile Asn Thr
            260                 265                 270
Val Leu Gly Gln Phe Glu Ser Ser Ala Ser Ser Leu Tyr Lys Ile Ser
        275                 280                 285
Tyr Ile Pro Asn Leu Phe Ser Leu Lys Asp Tyr Gln Ser Ala Ser Met
    290                 295                 300
Asn Gly Phe Gly Ala Lys Met Gly Tyr Lys Gln Phe Phe Thr His Lys
305                 310                 315                 320
Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Leu Asp Tyr Gly Tyr Ala
                325                 330                 335
Asn Phe Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu Val Thr Tyr
            340                 345                 350
Gly Val Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg Ser Arg Arg
        355                 360                 365
Arg Glu Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln Ile Ala Gly
    370                 375                 380
Gln Thr Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro
385                 390                 395                 400
Asp Val Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg
                405                 410                 415
Thr Asn Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly
            420                 425                 430
Ile Glu Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala
        435                 440                 445
Thr Gln Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val
    450                 455                 460
Gly Tyr Ser Val Gly Phe
465                 470
```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...452
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```
AAGACCCTAA ATACACACAA AATAAAACAA AATAAATCCA ATCAAATCCC ATG TGC      56
                                                        Met Cys
                                                          1

CAA ATC CAA TGC TTG CTT ATT TTA CTT TCT ATC AAT ATA GTT AGC GCG     104
Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val Ser Ala
          5                  10                  15

ATC ATC GTT TAT TTT TTC CAA GCA TTT CAA GGG GTT TTG AAT TTT GAA     152
Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn Phe Glu
     20                  25                  30

GGG GGT TTT TTA GGG TTT TTT ATC GTG GCG TTG TCT TCG TAT TAC GGC     200
Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr Tyr Gly
35                   40                  45                  50

GTT AAA AAG CGT TTG GAT TTA AGG AAA CAA AAT TCA ATA GAA AAA GAA     248
Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu Lys Glu
                55                  60                  65

GAA AAG CAA AAA TTC CAA AAA TTC GCC CTG GGC TTG GAA ATG TCT TTC     296
Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met Ser Phe
           70                  75                  80

AAT GTG TGG CGT TTA GGA GGG TAT GGG GTT TTA CTA GGC ATT TTA GGA     344
Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile Leu Gly
      85                  90                  95

ACG CTT TTA TTC TTG CAT CTT TTT AAC GGG TTA ATC TTT CTT ATT GGC     392
Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu Ile Gly
100                 105                 110

GTG TTT GTG AGC TCG CTC TCT AGC GCG TTA TTA CGA TTT TTG AAT AAT     440
Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu Asn Asn
115                 120                 125                 130

AAT GGT AAG TTT TGACACAAAC TCACATGGAT TTTAACCCCT TTAATCCTCT TTTAA   497
Asn Gly Lys Phe

TTTTTAAT                                                            505
```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```
Met Cys Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val
 1               5                  10                  15
Ser Ala Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn
            20                  25                  30
Phe Glu Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr
        35                  40                  45
Tyr Gly Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu
    50                  55                  60
Lys Glu Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met
65                  70                  75                  80
Ser Phe Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile
                85                  90                  95
Leu Gly Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu
            100                 105                 110
Ile Gly Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu
        115                 120                 125
Asn Asn Asn Gly Lys Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...458
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```
TTTTTGCACT ATCGTTGTTT GCGCTGTGGT GTTTGGCACG CTTGAAAAAA ATG CTC      56
                                                          Met Leu
                                                            1

AAG AGT ACC ATC AAA GAA GAT TAT TTG ATG CTG ATG TCT AGA GAA GTG     104
Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg Glu Val
  5                  10                  15
```

```
AGT GCT TTT GTG GGG ACT CTT TTC TTC ATT GGC TTG AGT TGC TAT GCG      152
Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys Tyr Ala
    20                  25                  30

ATC TAT CAT GGC AAC ATG CCC GAT TAT TTG AGA CCG GCT TTG ATA GAC      200
Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu Ile Asp
35                  40                  45                  50

ACT ATT AAG GCA GCG AGT GAT TCC ATC TAT TCC AGC TGC GAC TAC ATG      248
Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp Tyr Met
                55                  60                  65

GAT TAT TTT TTG AAG GCT AGA AAG ATG TTA GAG GGG TTT GCT TGG TGG      296
Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala Trp Trp
            70                  75                  80

AGC ATG TTC AAA GCG GAG AGC ATG GGC TTA AAT AAG GGG TTT ATG GTT      344
Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe Met Val
        85                  90                  95

GCG GGC TGG GTA GCG TTT ATC ATC TAT AAC GCT CTT AGC GGG ATA GCC      392
Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly Ile Ala
    100                 105                 110

ATC AGC AGG CTG AGC GCT CAA ATC ATT TAT TGG TTA TCA AAA TAT TTT      440
Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys Tyr Phe
115                 120                 125                 130

AGG AGT GAG TAT GGA AAA TGATGTTAAA GAAGATCTAG AGCAAGCAAG ACCAAAGT   496
Arg Ser Glu Tyr Gly Lys
                135

TAGAGCCAGA AAAGC                                                    511
```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
Met Leu Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg
 1               5                  10                  15
Glu Val Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys
            20                  25                  30
Tyr Ala Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu
        35                  40                  45
Ile Asp Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp
    50                  55                  60
Tyr Met Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala
65                  70                  75                  80
Trp Trp Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe
```

```
                85                  90                  95
Met Val Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly
            100                 105                 110
Ile Ala Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys
        115                 120                 125
Tyr Phe Arg Ser Glu Tyr Gly Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...2150
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
GAGTTACACA CTCTTTGAGA ACAAAACGCC AAACCATTTA GGAAATTACC ATG CTA      56
                                                        Met Leu
                                                          1

AGA TTC GTT AGT AAA ACG ATT TGC TTG TCT TTA ATC GGC TTG TTC AAC     104
Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu Phe Asn
        5                  10                  15

CCT TTA GAA GCC TTT CAA AAA CAC CAA AAA GAC GGC TTT TTT ATA GAA     152
Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe Ile Glu
    20                  25                  30

GCT GGG TTT GAA ACT GGG TTA TTA GAA GGA ACG CAA ACT AAA GAA GAA     200
Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys Glu Glu
35                  40                  45                  50

GTC ATA ACC ACC CAA AAA ATC TAT GAA AAC CCC CTA ACC CAC CCA CAA     248
Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His Pro Gln
                55                  60                  65

ACT AAA GAA CAG CCT AAA GAA CAA AAT AAA AGC GAT ACG GCC ACC CCA     296
Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala Thr Pro
            70                  75                  80

CAA AGC GCT TAC GGA AAA TAC TAC ATA CCC CAA AGC ACC ATT TTA AAA     344
Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile Leu Lys
        85                  90                  95

AAT GCA ACG GCT TTA TTC ACC ACG GAC AAG ATA GAA AAT GGC TTA ACT     392
Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly Leu Thr
    100                 105                 110
```

```
TTT TAT TCT CAA AAC CCT GTG TAT GCG AAT ATG GTT AAT GGG AGC GTA      440
Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly Ser Val
115                 120                 125                 130

ACC ATA CAA AAC TTT CTG CCT TAT AAT TTA AAC AAT GTT GAA CTG AGT      488
Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu Leu Ser
                135                 140                 145

TTT AAA GAC GCT CAA GGC AAG GTG GTC AAT TTA GGC GTG ATA GAG ACC      536
Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile Glu Thr
            150                 155                 160

ATC CCT AAA CAA TCT CAA ATT ACC TTG CCT GCA AGC TTG TTT AAT GAT      584
Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe Asn Asp
        165                 170                 175

TCA GAA TTT GAA CAA GCT GAT AGC TTT AAT TAC CAA CAA CTT CAA GCC      632
Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu Gln Ala
    180                 185                 190

ACT GCC ACA CAA TTT TCT GAC GCT AAC ACG CAA AGT TTG TTT CAA AAG      680
Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe Gln Lys
195                 200                 205                 210

CTC AGC AAG ATC ACA ACC AAT GTA ACA ATG AGT TAT GAA AAC GCC GAT      728
Leu Ser Lys Ile Thr Thr Asn Val Thr Met Ser Tyr Glu Asn Ala Asp
                215                 220                 225

ACC AAC AAT TTT AAA GGT AAT TGC CAT GAT TGT GTG TCA GAT TTC ACC      776
Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp Phe Thr
            230                 235                 240

CCA CAA ACC GCA GAA GAA TTG ACC AAT TTA ATG CTA GAT ATG ATT GCG      824
Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met Ile Ala
        245                 250                 255

GTG TTT GAC TCT AAA TCG TGG GAA GAA GCC GTT TTA AAC GCT CCT TTC      872
Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala Pro Phe
    260                 265                 270

CAA TTT TCT AAC AGC TCA TCA GAG TGC GGC TCT GAC TTT CCT AAG TGC      920
Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro Lys Cys
275                 280                 285                 290

GTG AAT CCT TTC AAT AAC GGG CGT GTC GCT CCC ATC TAT GAA AAA TAC      968
Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu Lys Tyr
                295                 300                 305

GTG CTA ACC CCA CAA TCC GTT ATA GAT GCG TTT AGA AGA ACG ATC AAT     1016
Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr Ile Asn
            310                 315                 320

CTT GAA GTG AAT ATC CTA AAA TCA GGG TTT GTA GGG CTA GGG TAT GAA     1064
Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly Tyr Glu
        325                 330                 335

CTT GAT GAT AAT GAT GGT AAT CTG GGG ATA GAA GCT TCT GCC TTA AAT     1112
Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala Leu Asn
```

0098175A2 .I>

340 345 350

CCT GAA AAA TTG TTT GGT AAA ACT TTG AAC AAA GTT GAT ATT GTG GAA 1160
Pro Glu Lys Leu Phe Gly Lys Thr Leu Asn Lys Val Asp Ile Val Glu
355 360 365 370

TTA AGA GAC ATT ATC CAT GAA TTT AGC CAC ACT AAA GGC TAT ACG CAT 1208
Leu Arg Asp Ile Ile His Glu Phe Ser His Thr Lys Gly Tyr Thr His
375 380 385

AAT GGG AAC ATG ACT TAT CAA AGA GTG CGC TTG TGT CAA GAA AAC GGC 1256
Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu Asn Gly
390 395 400

GGA GCC ATA CAA GAA TGT GAG GGT GGG AAA GAA GAG TTA GTC AAT GGA 1304
Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val Asn Gly
405 410 415

AAA GAA GAA CTA AAA TTT ACA AAT GGG AAA GAA GTG AAA GAT CAG GAT 1352
Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp Gln Asp
420 425 430

GGT TAC ACC TAT GAT GTA TGT TCT TTT TAT AAG GAC AAC CAC CAA GTC 1400
Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His Gln Val
435 440 445 450

TAT ACA GCG AGC AAT TAC CCC AAT TCC ATT TAT ACG AAT TGC GCT CAA 1448
Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys Ala Gln
455 460 465

GTC CCT GCT GGG CTT ATA GGG GTT ACC ACC GCT GTC TGG CAA CAG CTC 1496
Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln Gln Leu
470 475 480

ATC AAT CAA AAC GCT CTG CCC ATT AAT TTC GCT AAT CTA AAT AGC CCA 1544
Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn Ser Pro
485 490 495

ACC AAC CAC TTA AAC GCC GGG TTG AAC GCA CAA AAT TTT GCA ACC TCT 1592
Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala Thr Ser
500 505 510

ATA GTC AGC GCG ATC GCG CAA AAT TTT TCC ACC ACT TCC ACC ACC ACT 1640
Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr Thr Thr
515 520 525 530

TAC CGC TCT TCA AGT AAG AAT TTT AGA AGC CCT ATT TTA GGG GTT AAT 1688
Tyr Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly Val Asn
535 540 545

GTT AAA ATA GGC TAC CAA CAT TAT TTC AAT GAC TAC ATA GGG TTA GCC 1736
Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly Leu Ala
550 555 560

TAT TAC GGC ATT ATC AAA TAC AAT TAC GCC AAA ACT AAC GAT GAA AAA 1784
Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp Glu Lys
565 570 575

```
ATC CAG CAA TTA AGC TAT GGT GGG GGA ATG GAT GTG TTG TTT GAT TTC    1832
Ile Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe Asp Phe
    580                 585                 590

ATC ACC ACT TAC GCT AAC AAA AAG CAA GAC AAC CCA ACT AAA AAA GTT    1880
Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys Lys Val
595                 600                 605                 610

TTT GCT TCC TCT TTT GGG GTG TTT GGG GGG TTA AGG GGC TTA TAC AAT    1928
Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu Tyr Asn
                615                 620                 625

AGC TAT TAT GTC TTC AAC CAA GTC AAA GGA AGC GGT AAT TTA GAT ATA    1976
Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu Asp Ile
            630                 635                 640

GTT ACT GGG TTT AAT TAC CGC TAC AAG CAT TCT AAA TAT TCT GTA GGC    2024
Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser Val Gly
        645                 650                 655

ATT AGC GTT CCT TTA ATC CAA AGC GGT ATT AAA ATC GCT TCT AAT AAT    2072
Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser Asn Asn
    660                 665                 670

GGC ATC TAT GCG AAC TCC GTT GTT TTG AAT GAA GGG GGC AGT CAT TTT    2120
Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser His Phe
675                 680                 685                 690

AAA GTG TTT TTT AAT TAC GGG TGG ATT TTT TAGGATTTAA AATCCCCAAT AAC  2173
Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe
                695                 700

CCCCTAAACT TGTGCGATAC TCGCTACAAA                                   2203
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 700 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
Met Leu Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu
 1               5                  10                  15
Phe Asn Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe
            20                  25                  30
Ile Glu Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys
        35                  40                  45
Glu Glu Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His
    50                  55                  60
Pro Gln Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala
65                  70                  75                  80
Thr Pro Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile
```

```
                85                  90                  95
Leu Lys Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly
            100                 105                 110
Leu Thr Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly
        115                 120                 125
Ser Val Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu
    130                 135                 140
Leu Ser Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile
145                 150                 155                 160
Glu Thr Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe
                165                 170                 175
Asn Asp Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu
            180                 185                 190
Gln Ala Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe
        195                 200                 205
Gln Lys Leu Ser Lys Ile Thr Thr Asn Val Thr Met Ser Tyr Glu Asn
    210                 215                 220
Ala Asp Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp
225                 230                 235                 240
Phe Thr Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met
                245                 250                 255
Ile Ala Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala
            260                 265                 270
Pro Phe Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro
        275                 280                 285
Lys Cys Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu
    290                 295                 300
Lys Tyr Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr
305                 310                 315                 320
Ile Asn Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly
                325                 330                 335
Tyr Glu Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala
            340                 345                 350
Leu Asn Pro Glu Lys Leu Phe Gly Lys Thr Leu Asn Lys Val Asp Ile
        355                 360                 365
Val Glu Leu Arg Asp Ile Ile His Glu Phe Ser His Thr Lys Gly Tyr
    370                 375                 380
Thr His Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu
385                 390                 395                 400
Asn Gly Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val
                405                 410                 415
Asn Gly Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp
            420                 425                 430
Gln Asp Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His
        435                 440                 445
Gln Val Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys
    450                 455                 460
Ala Gln Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln
465                 470                 475                 480
Gln Leu Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn
                485                 490                 495
Ser Pro Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala
            500                 505                 510
Thr Ser Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr
        515                 520                 525
Thr Thr Tyr Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly
    530                 535                 540
Val Asn Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly
```

```
545                 550                 555                 560
Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp
                565                 570                 575
Glu Lys Ile Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe
            580                 585                 590
Asp Phe Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys
        595                 600                 605
Lys Val Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu
    610                 615                 620
Tyr Asn Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu
625                 630                 635                 640
Asp Ile Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser
                645                 650                 655
Val Gly Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser
            660                 665                 670
Asn Asn Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser
        675                 680                 685
His Phe Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe
    690                 695                 700
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...344
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
TCGTTTTGGA AAAAGATATA GCCCATGCGC GTTTCAAGGG TAATGAAAGC ATG GTG      56
                                                        Met Val
                                                          1

TAT GAA GAA AAT TTT GTG CAT GCC GGG TTT GTG CTT ATT GCG TGC AAT     104
Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala Cys Asn
          5                  10                  15

TAT GCG GCC TTG TGC GCG TTG AAT AAA AGA CAC AGC GTG GTG GTT TCT     152
Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val Val Ser
     20                  25                  30

AAT AAC ATC AAT TTT TAT GCC CCC CTA GAA TTG AAT CAA GAA GCA CTC     200
Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu Ala Leu
35                  40                  45                  50

ATT AAA GCG CAA GTG ATT CAA GAT GGC GTG AAA AAA GCT GAA ATA AAA     248
Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu Ile Lys
                55                  60                  65
```

```
ATA GAG GCG TTT GTG TTA GAC ATT CAG GTT TTA GAG GGA ATG ATA GAA     296
Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met Ile Glu
            70                  75                  80

ATT GTG GTG TTT GAT AAA AAG CCT TTT AAA TTC AAT TTT AAA GAA GAG T   345
Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys Glu Glu
        85                  90                  95

AGTTAAATGG TTATTGTTTT AGTCGTGGAT AGTTTTAAAG ACACCAGTAA TG           397
```

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```
Met Val Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala
 1               5                  10                  15
Cys Asn Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val
            20                  25                  30
Val Ser Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu
        35                  40                  45
Ala Leu Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu
    50                  55                  60
Ile Lys Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met
65                  70                  75                  80
Ile Glu Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys
                85                  90                  95
Glu Glu
```

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1208
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```
ATGATAGTAA GGAAATAAGA GTGGAATGCA AGAATCACCC TATTGAAAAG ATG GCA      56
```

```
                                                                  Met Ala
                                                                   1

GAA AAA TTA GAG GAA ACT AAT CCT GAA TGG TTT GAA AAA TGG AGG GAA      104
Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp Arg Glu
          5                  10                  15

AAA CAA TAC ACC CAA ACT GGC GAA TCT AAG CCA TCA AAA CGA ATC AAA      152
Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg Ile Lys
     20                  25                  30

GTT TTT AAA AAC TTT ACG GCA TTT GAT GAC AGA TTG TAT ACA ATT GAA      200
Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr Ile Glu
35                   40                  45                  50

TGT AAT TTA AAA AAT CTG GAT ACC CAT CAA AAA AAG TTT GAA ATT TGT      248
Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu Ile Cys
                55                  60                  65

GGG GCT CTG TAT GAC ATT TAT GAA CAA ATT TTT GAT GAA ACA CCA AGC      296
Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr Pro Ser
           70                  75                  80

TTG AAA GGG CGC GAT TTA GAA ACA TAC AAA GCA CAA GAT TTG TCA AAG      344
Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu Ser Lys
      85                  90                  95

AAA TTC ATG CAT TTA GGT TTT GAA CAG ATC TCA AAA GAT TTA AAC GAC      392
Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu Asn Asp
 100                 105                 110

TCT AGA TTG AAC GCT TTA TTG TGC TAT GAG GAA AAA GTC ATG CAA GCT      440
Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met Gln Ala
115                 120                 125                 130

TTG GCT AAA AAA TAC CCT AGT TTT TTA CAA GAT TTG CAT GAT ATA AAA      488
Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp Ile Lys
                135                 140                 145

AAA TAC AGG AAT AAA GAT AAA CAC GGC GAG AAA CCA CAA GAT GGG TCT      536
Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp Gly Ser
           150                 155                 160

TCT TTA ACG AGA GTG GAA TTA GAA AGA TAC AGA GAT GGA ATT TAT TTT      584
Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile Tyr Phe
      165                 170                 175

CTA GTA GAA AAT CTT TTA AAA AAC CCC TTG ATT AAA GAG AGA GAA AAT      632
Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg Glu Asn
 180                 185                 190

GCT CAA GAA GAA AAA CAT TAT AAG AAA AAT GCA GAG ATT GAC GAC CGA      680
Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp Asp Arg
195                 200                 205                 210

TCC CAG CTA TCA AAC TTA AAC GCA CCC AAA CCC TTA TTT GAA TGT TTT      728
Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu Cys Phe
                215                 220                 225
```

```
GTA GGA GTT AAT CTG GCC AAA GCC AAA TAT TAT TCT AAA AAA GAA GAA      776
Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys Glu Glu
            230                 235                 240

AGA GAA AAA GAA AAG ATG ATC TTG AAT TTT TGT AAG ATA TTT GAA ATT      824
Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe Glu Ile
        245                 250                 255

ATT CTT TTT GAA GCT ATC CAA AAA CAA CCA AAG CCT GAT TTT AAA AAT      872
Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe Lys Asn
    260                 265                 270

AAA GAC GAG CTT TTA GGG GAT TAT CCT AAT CTT AAA AAT TTA GAT TCT      920
Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu Asp Ser
275                 280                 285                 290

TTA AGA GAA GTG AGG GAA GAC TTT TTG AAA AGA GCG TTT AAG AAT GAT      968
Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys Asn Asp
                295                 300                 305

GAA GCG AGT TTG GGA GCG TAT GTG TTA GTG TTG CTT AGC TGT AAG TAT     1016
Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys Lys Tyr
            310                 315                 320

TTT GAG AGC GTG TTT GAA AAA GTT CAA GAA TGG CTA GAT TTT ATC GCT     1064
Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe Ile Ala
        325                 330                 335

AGG CTT ATT GCT TTG AGA GGC CAT GTG CAC AAG ATA ACT AAA GAA CTT     1112
Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys Glu Leu
    340                 345                 350

GAA AGA TTA GAA GAA GAG GAT TTA GAA AAA TTG GAA AAA CAA GCA CTA     1160
Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln Ala Leu
355                 360                 365                 370

GAA TAT TTT AAT AAA ATA GCA AAT AAA ATA TAT CTA AAG GAG AAA CGA T   1209
Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu Lys Arg
                375                 380                 385

GAGCGGGAAT GAAGAATTGG AGCTAAGAGC CAGAGAAACT GAGTTGGATA AA           1261
```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```
Met Ala Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp
 1               5                  10                  15
Arg Glu Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg
```

```
            20                  25                  30
Ile Lys Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr
        35                  40                  45
Ile Glu Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu
    50                  55                  60
Ile Cys Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr
65                  70                  75                  80
Pro Ser Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu
                85                  90                  95
Ser Lys Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu
            100                 105                 110
Asn Asp Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met
        115                 120                 125
Gln Ala Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp
    130                 135                 140
Ile Lys Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp
145                 150                 155                 160
Gly Ser Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile
                165                 170                 175
Tyr Phe Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg
            180                 185                 190
Glu Asn Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp
        195                 200                 205
Asp Arg Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu
    210                 215                 220
Cys Phe Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys
225                 230                 235                 240
Glu Glu Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe
                245                 250                 255
Glu Ile Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe
            260                 265                 270
Lys Asn Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu
        275                 280                 285
Asp Ser Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys
    290                 295                 300
Asn Asp Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys
305                 310                 315                 320
Lys Tyr Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe
                325                 330                 335
Ile Ala Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys
            340                 345                 350
Glu Leu Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln
        355                 360                 365
Ala Leu Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu
    370                 375                 380
Lys Arg
385
```

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 412 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...359
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```
CATTTAATGC TAAGTCTAAT AAGATTGCCC TAGATAGACA TTACGCCAAA ATG TTT      56
                                                        Met Phe
                                                          1

TTG CAA GTT GTA GCA AGA ACT CTA AGA AAG AAT GTC AAT ATA TTA GAA     104
Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile Leu Glu
          5                  10                  15

GAG CAA GGT TTT ATT GAA GTC ATT AAA GGA AAA CAA AGA TAC TTG TAT     152
Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr
     20                  25                  30

GTG TAT CTT AAA GAT TAC AGA GAA TTA GAG GGC TAT AAC TCC GTA GGA     200
Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser Val Gly
35                  40                  45                  50

GCT AAT CAA AAG AAC AAT ATC CCA TCG CCT TTT TTC TTA CAG ATT ATG     248
Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln Ile Met
                55                  60                  65

CGT TTC TTA GAA AAG TTT GCC AAA GAA ATT GAG AGA GTA AAA ATA ACA     296
Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys Ile Thr
            70                  75                  80

ACA AAG AAT GTG TTA TGC ATA TTC CTA GCC AAG AGC TTA TGC AAA GAG     344
Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys Lys Glu
        85                  90                  95

TTA ATA ATG TTG TTT TAAAATTCAC GCCTATTTCT AATCCTAATA CCACTTACAC T   400
Leu Ile Met Leu Phe
    100

TTATCCTACA AG                                                       412
```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
Met Phe Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile
 1               5                  10                  15
Leu Glu Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr
```

```
            20                  25                  30
Leu Tyr Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser
        35                  40                  45
Val Gly Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln
    50                  55                  60
Ile Met Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys
65                  70                  75                  80
Ile Thr Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys
                85                  90                  95
Lys Glu Leu Ile Met Leu Phe
            100
```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1151
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```
TTCTATTAAA ATTAGTGTAT GATTGAGATT ATTTTTGATT AGGATCAACC ATG CAA      56
                                                        Met Gln
                                                          1

AAA GCC TTA TTA CAT TCA TCA TTC TTT TTA CCT TTA TTT TTA TCT TTT     104
Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu Phe Leu Ser Phe
          5                  10                  15

TGT ATC GCT GAA GAA AAT GGG GCG TAT GCG AGC GTG GGT TTT GAA TAT     152
Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe Glu Tyr
    20                  25                  30

TCC ATT AGT CAT GCC GTT GAA CAC AAT AAC CCC TTT TTA AAT CAA GAA     200
Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn Gln Glu
35                  40                  45                  50

CGC ATC CAA ATC ATT TCT AAC GCT CAA AAT AAA ATC TAT AAA CTC CAT     248
Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys Leu His
                55                  60                  65

CAA GTT AAA AAT GAA ATC ACA AGC ATG CCT AAA ACC TTT GCA TAT ATC     296
Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr Phe Ala Tyr Ile
            70                  75                  80

AAC AAC GCT TTA AAA AAC AAC TCC AAA TTA ACC CCC ACT GAA ATG CAA     344
Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro Thr Glu Met Gln
        85                  90                  95
```

```
GCC GAA CAA TAC TAC CTC CAA TCC ACC TTT CAA AAC ATT GAA AAA ATA      392
Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn Ile Glu Lys Ile
    100                 105                 110

GTA ATG CTT AGC GGT GGC GTT TCA TCT AAC CCA CAA TTA GTC CAA GCG      440
Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln Leu Val Gln Ala
115                 120                 125                 130

TTG GAA AAA ATG CAA GAA CCC ATT ACT AAC CCT TTA GAA TTT GAA GAA      488
Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe Glu Glu
                135                 140                 145

AAC TTA AGA AAT TTA GAA GTG CAA TTT GCT CAA TCT CAA AAC CGC ATG      536
Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn Arg Met
            150                 155                 160

CTT TCT TCT TTA TCT TCT CAA ATC GCT GCC ATT TCA AAT TCC TTA AAC      584
Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser Leu Asn
        165                 170                 175

GCG CTT GAT CCT AAC TCT TAT TCT AAA AAC ATT TCA AGC ATG TAT GGG      632
Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met Tyr Gly
    180                 185                 190

GTG AGT TTG AGC GTA GGT TAT AAG CAT TTC TTT ACC AAG AAA AAA AAT      680
Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys Lys Asn
195                 200                 205                 210

CAA GGG TTG CGC TAT TAC TTG TTT TAT GAC TAT GGT TAC ACT AAT TTT      728
Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe
                215                 220                 225

GGT TTT GTG GGC AAT GGC TTT GAT GGT TTA GGC AAA ATG AAT AAC CAT      776
Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn His
            230                 235                 240

CTC TAT GGG CTT GGG ATA GAC TAT CTT TAT AAT TTC ATT GAT AAT GCA      824
Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp Asn Ala
        245                 250                 255

AAA AAA CAC TCT AGC GTA GGT TTT TAT CTG GGT TTT GCT TTA GCG GGG      872
Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu Ala Gly
    260                 265                 270

AGT TCG TGG GTA GGG AGT GGT TTG AGC ATG TGG GTG AGC CAA ACG GAT      920
Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln Thr Asp
275                 280                 285                 290

TTT ATC AAC AAT TAC TTG ACG GGC TAT CAA GCT AAA ATG CAC ACG AGT      968
Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His Thr Ser
                295                 300                 305

TTT TTC CAG ATC CCT TTG AAT TTT GGG GTT CGT GTG AAT GTC AAT AGG     1016
Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asn Arg
            310                 315                 320

CAT AAT GGC TTT GAA ATG GGC TTG AAA ATC CCT TTA GCG ATG AAT TCC     1064
His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met Asn Ser
```

```
        325                 330                 335

TTT TAT GAA ACG CAT GGC AAA GGG CTA AAC ACT TCC CTC TTT TTC AAA    1112
Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser Leu Phe Phe Lys
    340                 345                 350

CGC CTT GTC ATG TTT AAC GTG AGT TAC GTT TAT AGT TTT TAGGGGGGTA AA  1163
Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe
355                 360                 365

TGCCTTCAAA CGCTCTTTTG ATTGAAGAAA TCACTCATTT A                      1204
```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```
Met Gln Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu Phe Leu
 1               5                  10                  15
Ser Phe Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe
            20                  25                  30
Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn
        35                  40                  45
Gln Glu Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys
    50                  55                  60
Leu His Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr Phe Ala
65                  70                  75                  80
Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro Thr Glu
                85                  90                  95
Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn Ile Glu
            100                 105                 110
Lys Ile Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln Leu Val
        115                 120                 125
Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe
    130                 135                 140
Glu Glu Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn
145                 150                 155                 160
Arg Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser
                165                 170                 175
Leu Asn Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met
            180                 185                 190
Tyr Gly Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys
        195                 200                 205
Lys Asn Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr
    210                 215                 220
Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn
225                 230                 235                 240
Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp
                245                 250                 255
Asn Ala Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu
```

```
            260                 265                 270
Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln
        275                 280                 285
Thr Asp Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His
    290                 295                 300
Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val
305                 310                 315                 320
Asn Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met
                325                 330                 335
Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser Leu Phe
            340                 345                 350
Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe
        355                 360                 365
```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1634
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```
TTATTTTTAC AGAGTAATTT ATCTATTCTC AGGTAAAGTA AGGAAGAGGA ATG AAA      56
                                                          Met Lys
                                                            1

TTA AAG AAA CGA AAA GTT GCG GCT GCA TTG CTA AAG CGT TTT ACC TTG      104
Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe Thr Leu
          5                  10                  15

CCA CTA TTG TTC ACT ACG GGT TCA TTA GGG GCG GTT ACT TAT GAA GTG      152
Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr Glu Val
     20                  25                  30

CAT GGA GAT TTT ATC AAT TTT GCT AAA GTG GGT TTT AAC CAT TCG CCC      200
His Gly Asp Phe Ile Asn Phe Ala Lys Val Gly Phe Asn His Ser Pro
35                  40                  45                  50

ATT AAT CCT GTT AAA GGT ATC TAT CCC ACA GAA ACT TTT GTT AAC CTT      248
Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val Asn Leu
                55                  60                  65

ACG GGT AAG CTA GAG GGG TCT GTG CAT TTA GGT AGG GGA TGG ACC GTG      296
Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp Thr Val
          70                  75                  80

AAT TTA GGC GGT GTT TTG GGC GGA CAG GCT TAT GAT GGC ACT AAG TAT      344
```

```
Asn Leu Gly Gly Val Leu Gly Gly Gln Ala Tyr Asp Gly Thr Lys Tyr
        85                  90                  95

GAT AGG TGG GCG AAG GAT TTT ACC CCC CCA AGC TAT TGG GAT AAA ACT     392
Asp Arg Trp Ala Lys Asp Phe Thr Pro Pro Ser Tyr Trp Asp Lys Thr
    100                 105                 110

TCT TGC GGT ACT GAT TCT ATG AGT CTT TGT ATG AAT GCC ACT AAA ATG     440
Ser Cys Gly Thr Asp Ser Met Ser Leu Cys Met Asn Ala Thr Lys Met
115                 120                 125                 130

TGG CAG CAA TCA GGG CCA GGT GGC GTC ATT AAC CCT AGA GGT ATT GGT     488
Trp Gln Gln Ser Gly Pro Gly Gly Val Ile Asn Pro Arg Gly Ile Gly
                135                 140                 145

TGG GAA TAC ATG GGT GAG TGG AAC GGC TTG TTC CCT AAC TAC TAT CCG     536
Trp Glu Tyr Met Gly Glu Trp Asn Gly Leu Phe Pro Asn Tyr Tyr Pro
            150                 155                 160

GCT AAC GCC TAC TTG CCT GGT GGC TCA AGG CGC TAT CAA GTC TAT AAA     584
Ala Asn Ala Tyr Leu Pro Gly Gly Ser Arg Arg Tyr Gln Val Tyr Lys
        165                 170                 175

GCA AAT TTG ACC TAT GAT AGC GAC AGG GTC CAT ATG GTA ATG GGG CGT     632
Ala Asn Leu Thr Tyr Asp Ser Asp Arg Val His Met Val Met Gly Arg
    180                 185                 190

TTT GAC ATT ACC GAG CAG GAG CAA ATG GAT TGG ATT TAC CAA TTG TTC     680
Phe Asp Ile Thr Glu Gln Glu Gln Met Asp Trp Ile Tyr Gln Leu Phe
195                 200                 205                 210

CAA GGG TTT TAT GGG ACT TTC AAG CTC ACT AAG AAT ATG AAA TTC TTG     728
Gln Gly Phe Tyr Gly Thr Phe Lys Leu Thr Lys Asn Met Lys Phe Leu
                215                 220                 225

CTC TTT AGT GGT TGG GGT CGT GGT ATC GCT GAT GGT CAG TGG TTG TTC     776
Leu Phe Ser Gly Trp Gly Arg Gly Ile Ala Asp Gly Gln Trp Leu Phe
            230                 235                 240

CCT ATC TAT CGT GAA AAG CCT TGG GGG GTT CAT AAA GCG GGT ATT ATT     824
Pro Ile Tyr Arg Glu Lys Pro Trp Gly Val His Lys Ala Gly Ile Ile
        245                 250                 255

TAT CGC CCT ACA AAG AAT TTG ATG ATC CAC CCT TAT GTG TAT CTT ATC     872
Tyr Arg Pro Thr Lys Asn Leu Met Ile His Pro Tyr Val Tyr Leu Ile
    260                 265                 270

CCA ATG GTA GGC ACA TTG CCT GGT GCT AAA ATA GAA TAC GAT ACC AAT     920
Pro Met Val Gly Thr Leu Pro Gly Ala Lys Ile Glu Tyr Asp Thr Asn
275                 280                 285                 290

CCT GAA TTT AGC GGT AGG GGC ATT AGG AAC AGA ACG ACT TTC TAT GCG     968
Pro Glu Phe Ser Gly Arg Gly Ile Arg Asn Arg Thr Thr Phe Tyr Ala
                295                 300                 305

TTG TAT GAC TAT CGT TGG AAT AAC GCT GAA TAC GGT CGT TAC GCG CCC    1016
Leu Tyr Asp Tyr Arg Trp Asn Asn Ala Glu Tyr Gly Arg Tyr Ala Pro
            310                 315                 320
```

```
GCT CGT TAT AAC ACT TGG GAT CCG TTC TTG GAT AAT GGT AAG TGG CGT    1064
Ala Arg Tyr Asn Thr Trp Asp Pro Phe Leu Asp Asn Gly Lys Trp Arg
        325                 330                 335

GGC TTG CAA GGT CCT GGT GGT GCG ACG CTC CTT TTA CGC CAC CAT ATA    1112
Gly Leu Gln Gly Pro Gly Gly Ala Thr Leu Leu Leu Arg His His Ile
    340                 345                 350

GAT ATT AAC AAC TAC TTT GTG GTT GGT GGT GCT TAT CTC AAC ATT GGT    1160
Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn Ile Gly
355                 360                 365                 370

AAC CCT AAC ATG AAC TTA GGT ACT TGG GGT AAC CCT GTG GCT GTT GAT    1208
Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala Val Asp
                375                 380                 385

GGT ATC GAA CAA TGG GTC GGT AGT ATC TAT AGC TTA GGG TTT GCG GGG    1256
Gly Ile Glu Gln Trp Val Gly Ser Ile Tyr Ser Leu Gly Phe Ala Gly
            390                 395                 400

ATT GAC AAC ATT ACC GAT GCT GAC GCG TTC ACC GAG TAT GTT AAA GGT    1304
Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val Lys Gly
        405                 410                 415

GGA GGC AAG CAT GGT AAG TTT AGT TGG AGC GTT TAT CAG CGC TTC ACT    1352
Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg Phe Thr
    420                 425                 430

ACC GCT CCA AGG GCT TTG GAA TAT GGT ATC GGT ATG TAT CTA GAC TAT    1400
Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu Asp Tyr
435                 440                 445                 450

CAG TTC AGC AAG CAT GTT AAA GCG GGT CTC AAA CTC GTA TGG TTA GAG    1448
Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp Leu Glu
                455                 460                 465

TTC CAA ATT CGT GCG GGT TAC AAC CCT GGA ACC GGT TTC CTT GGG CCA    1496
Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu Gly Pro
            470                 475                 480

AAC GGT CAG CCG CTT AAC TTG AAT ACT GGT TTG TTT GAG TCT TCA GCG    1544
Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser Ser Ala
        485                 490                 495

TTC GCT CAA GGC CCT CAA AAC ATG GGC GGT ATC GCA AAA AGC ATC ACT    1592
Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser Ile Thr
    500                 505                 510

CAA GAC AGA AGC CAT TTG ATG ACA CAC ATT AGT TAT AGT TTC TAAGAGAGT  1643
Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe
515                 520                 525

TCTCCCCCTA TCTCTTAGAT ATGCCTTTTT GTATTTTTAT TTTA                   1687
```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```
Met Lys Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe
 1               5                  10                  15
Thr Leu Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr
            20                  25                  30
Glu Val His Gly Asp Phe Ile Asn Phe Ala Lys Val Gly Phe Asn His
        35                  40                  45
Ser Pro Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val
    50                  55                  60
Asn Leu Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp
65                  70                  75                  80
Thr Val Asn Leu Gly Gly Val Leu Gly Gly Gln Ala Tyr Asp Gly Thr
                85                  90                  95
Lys Tyr Asp Arg Trp Ala Lys Asp Phe Thr Pro Pro Ser Tyr Trp Asp
            100                 105                 110
Lys Thr Ser Cys Gly Thr Asp Ser Met Ser Leu Cys Met Asn Ala Thr
        115                 120                 125
Lys Met Trp Gln Gln Ser Gly Pro Gly Gly Val Ile Asn Pro Arg Gly
    130                 135                 140
Ile Gly Trp Glu Tyr Met Gly Glu Trp Asn Gly Leu Phe Pro Asn Tyr
145                 150                 155                 160
Tyr Pro Ala Asn Ala Tyr Leu Pro Gly Gly Ser Arg Arg Tyr Gln Val
                165                 170                 175
Tyr Lys Ala Asn Leu Thr Tyr Asp Ser Asp Arg Val His Met Val Met
            180                 185                 190
Gly Arg Phe Asp Ile Thr Glu Gln Glu Gln Met Asp Trp Ile Tyr Gln
        195                 200                 205
Leu Phe Gln Gly Phe Tyr Gly Thr Phe Lys Leu Thr Lys Asn Met Lys
    210                 215                 220
Phe Leu Leu Phe Ser Gly Trp Gly Arg Gly Ile Ala Asp Gly Gln Trp
225                 230                 235                 240
Leu Phe Pro Ile Tyr Arg Glu Lys Pro Trp Gly Val His Lys Ala Gly
                245                 250                 255
Ile Ile Tyr Arg Pro Thr Lys Asn Leu Met Ile His Pro Tyr Val Tyr
            260                 265                 270
Leu Ile Pro Met Val Gly Thr Leu Pro Gly Ala Lys Ile Glu Tyr Asp
        275                 280                 285
Thr Asn Pro Glu Phe Ser Gly Arg Gly Ile Arg Asn Arg Thr Thr Phe
    290                 295                 300
Tyr Ala Leu Tyr Asp Tyr Arg Trp Asn Asn Ala Glu Tyr Gly Arg Tyr
305                 310                 315                 320
Ala Pro Ala Arg Tyr Asn Thr Trp Asp Pro Phe Leu Asp Asn Gly Lys
                325                 330                 335
Trp Arg Gly Leu Gln Gly Pro Gly Gly Ala Thr Leu Leu Leu Arg His
            340                 345                 350
His Ile Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn
        355                 360                 365
Ile Gly Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala
    370                 375                 380
Val Asp Gly Ile Glu Gln Trp Val Gly Ser Ile Tyr Ser Leu Gly Phe
```

```
385                 390                 395                 400
Ala Gly Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val
                405                 410                 415
Lys Gly Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg
            420                 425                 430
Phe Thr Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu
        435                 440                 445
Asp Tyr Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp
    450                 455                 460
Leu Glu Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu
465                 470                 475                 480
Gly Pro Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser
                485                 490                 495
Ser Ala Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser
            500                 505                 510
Ile Thr Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe
        515                 520                 525
```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...359
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```
TTTTGTCTGA TTTGTTGCTA CCAAAACCAT TACCAACCAA AGCAGATCCC  ATG TTT      56
                                                        Met Phe
                                                         1

TTG ATA CTA TCG AAT CCA TTC TTC AAC ACT TCT GCC ATA AAA TTC TTG      104
Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys Phe Leu
          5                  10                  15

ATA TTG TCC ATA GGC AAG TTG AAT TTT TTC CCT AAT ATT TCA TTA AGT      152
Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser Leu Ser
    20                  25                  30

CCC ATC ATT AAC ATC AGG AAG AAC AAA AAA TTT AAT ATC ATA GAA AAC      200
Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile Glu Asn
35                  40                  45                  50

AAA TCA CTG GAT AAA CCT GTA AAA AGA TTT GTT CCG CCA CCC AAC AAA      248
Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro Asn Lys
                55                  60                  65

GAA GCT AAA ATT TTT CCC ATG ATC AGT CCT TTT ATT TTT GGT TGT GTA      296
Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly Cys Val
            70                  75                  80
```

```
AGT TCT TGC TTG TTC GGA TCT CTA ATG CGT GTT TTA GTA GGA AGC ATT     344
Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly Ser Ile
        85                  90                  95

TCA CAA TGG CAT ACC TAAAGCTACT AAGAAAATTC TTGAATCTAT TGGTAAGATT A   400
Ser Gln Trp His Thr
    100

CTCATGAAAT CA                                                       412
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```
Met Phe Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys
 1               5                  10                  15
Phe Leu Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser
            20                  25                  30
Leu Ser Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile
        35                  40                  45
Glu Asn Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro
    50                  55                  60
Asn Lys Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly
65                  70                  75                  80
Cys Val Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly
                85                  90                  95
Ser Ile Ser Gln Trp His Thr
            100
```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 67...405
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```
TCCAATCCGT CTAATATCTC TTTATTTTCG CTCAATTCTT TAACCATAAC GGGTTTTTTA    60
GCGCTT GTG GGG GTT ACT GGG CTA AAG TTT GGA GCG TTT TGC ACT TCT      108
```

```
        Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser
         1               5                  10

TTT TCT TCT TTT TTT AGA TTT TCC TTT ATC ATT TCT TCT ATC CTT CCT     156
Phe Ser Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro
15                  20                  25                  30

TCT ATC ATT TCT TCT TGC GTG TTT TCT TGT GGG TTT TCT TCT TTT TTA     204
Ser Ile Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu
                35                  40                  45

GGG TGG TTG GGG GTT TTT TGG TTT TCT GTT TTG TTG TCA TTT TCT ATT     252
Gly Trp Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile
            50                  55                  60

ATG GGT GCA AGT GTG GGC ATG ATA GGT TTG GGC GTG GTG GGC GTA AGA     300
Met Gly Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg
        65                  70                  75

GTT TCT TTT GTA GGC GTG GGT TCT CTT TCT TTA GTT TCT TGT TTA ATT     348
Val Ser Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile
    80                  85                  90

TCT TTT AAA GGG GGG TTA GTG GGG TTA GTC AAA TCA TCA AAT CGG TTT     396
Ser Phe Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe
95                  100                 105                 110

CTT TTA GGG TAAAT GGTGTAATGG GTAGGGGGGT GGGAGGAAAT TTGGACT          447
Leu Leu Gly
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser Phe Ser
 1               5                  10                  15
Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro Ser Ile
            20                  25                  30
Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu Gly Trp
        35                  40                  45
Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile Met Gly
    50                  55                  60
Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg Val Ser
65                  70                  75                  80
Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile Ser Phe
                85                  90                  95
Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe Leu Leu
            100                 105                 110
```

Gly

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1127
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
CCAAGAAAGA GTATAATAGC GCATAAGAAT TTAACTGATG AAGAGGTTTA  ATG CTA      56
                                                        Met Leu
                                                         1

GAA AAT AGA GTT AAG ACC AAG CAA ATT TTT ATC GGT GGC GTG GCC ATA      104
Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val Ala Ile
          5                  10                  15

GGG GGT GAT GCT CCC ATA AGC ACG CAA AGC ATG ACC TTT AGC AAA ACC      152
Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser Lys Thr
     20                  25                  30

GCT GAT ATT GAA AGC ACT AAA AAT CAA ATT GAC AGA CTC AAA CTC GCC      200
Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys Leu Ala
35                   40                  45                  50

GGG GCC GAT TTA GTG AGG GTG GCG GTG AGT AAT GAA AAG GAC GCT CTA      248
Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp Ala Leu
                55                  60                  65

GCC TTA AAA GAA TTG AAA AAA GTG TCC CCT TTG CCT TTA ATC GCT GAT      296
Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile Ala Asp
            70                  75                  80

ATT CAT TTC CAT TAT AAA TTC GCT CTC ATT GCC GCT CAA AGC GTG GAT      344
Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser Val Asp
        85                  90                  95

GCG ATC AGG ATT AAC CCC GGA AAC ATC GGC TCT AAA GAG AAG ATC AAA      392
Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys Ile Lys
    100                 105                 110

GCG GTG GTT GAT GCT TGT AAA GAA AAA AAC ATT CCT ATA AGA ATT GGC      440
Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg Ile Gly
115                 120                 125                 130

GTG AAT GCT GGG AGT TTA GAA AAG CAG TTT GAT CAA AAA TAC GGA CCC      488
Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr Gly Pro
```

```
                135                 140                 145

ACC CCA AAA GGC ATG GTA GAA AGC GCT TTG TAT AAC GCC AAA CTT TTA      536
Thr Pro Lys Gly Met Val Glu Ser Ala Leu Tyr Asn Ala Lys Leu Leu
            150                 155                 160

GAA GAT TTG GAT TTT ACC AAT TTT AAG ATT TCT TTA AAA GCG AGC GAT      584
Glu Asp Leu Asp Phe Thr Asn Phe Lys Ile Ser Leu Lys Ala Ser Asp
        165                 170                 175

GTG ATT CGC ACC ATA GAA GCT TAC AGG ATG CTT CGC CCT CTT GTG ATC      632
Val Ile Arg Thr Ile Glu Ala Tyr Arg Met Leu Arg Pro Leu Val Ile
    180                 185                 190

TAT CCT TTC CAT TTG GGG GTT ACG GAG GCG GGG AAT CTT TTT AGC TCC      680
Tyr Pro Phe His Leu Gly Val Thr Glu Ala Gly Asn Leu Phe Ser Ser
195                 200                 205                 210

AGT ATC AAA TCC GCT ATG GCT TTA GGG GGG CTT TTA ATG GAG GGC ATT      728
Ser Ile Lys Ser Ala Met Ala Leu Gly Gly Leu Leu Met Glu Gly Ile
                215                 220                 225

GGG GAT ACG ATG CGC GTA TCC ATC ACA GGG GAA TTA GAA AAT GAA ATC      776
Gly Asp Thr Met Arg Val Ser Ile Thr Gly Glu Leu Glu Asn Glu Ile
            230                 235                 240

AAA GTG GCC AGA GCA ATT TTA CGC CAT AGC GGG CGG TTG AAA GAA GGG      824
Lys Val Ala Arg Ala Ile Leu Arg His Ser Gly Arg Leu Lys Glu Gly
        245                 250                 255

ATT AAT TGG ATT TCT TGC CCC ACT TGC GGG CGC ATT GAA GCC AAT TTA      872
Ile Asn Trp Ile Ser Cys Pro Thr Cys Gly Arg Ile Glu Ala Asn Leu
    260                 265                 270

GTG GAT ATG GCG ATC AAG GTA GAA AAA CGC TTA AGC CAC ATC AAA ACC      920
Val Asp Met Ala Ile Lys Val Glu Lys Arg Leu Ser His Ile Lys Thr
275                 280                 285                 290

CCT TTA GAC ATT AGC GTG ATG GGT TGC GTG GTG AAT GCT TTG GGT GAA      968
Pro Leu Asp Ile Ser Val Met Gly Cys Val Val Asn Ala Leu Gly Glu
                295                 300                 305

GCC AAG CAT GCA GAC ATG GCG ATC GCT TTT GGG AAT CGC AGC GGT TTG     1016
Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser Gly Leu
            310                 315                 320

ATC ATT AAA GAG GGT AAA GTC ATT CAC AAA CTG GCT GAA AAG GAT TTA     1064
Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys Asp Leu
        325                 330                 335

TTT GAA ACT TTT GTG ATA GAA GTG GAA AAT TTA GCT AAA GAA AGA GAA     1112
Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu Arg Glu
    340                 345                 350

AAA AGT TTA AAG GAT TAGGCATGAT CAATAAGTTT AAAAATTTTG TGAGCAACTA C   1168
Lys Ser Leu Lys Asp
355
```

CAGCAATCTA AC 1180

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```
Met Leu Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val
 1               5                  10                  15
Ala Ile Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser
            20                  25                  30
Lys Thr Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys
        35                  40                  45
Leu Ala Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp
    50                  55                  60
Ala Leu Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile
65                  70                  75                  80
Ala Asp Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser
                85                  90                  95
Val Asp Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys
            100                 105                 110
Ile Lys Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg
        115                 120                 125
Ile Gly Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr
    130                 135                 140
Gly Pro Thr Pro Lys Gly Met Val Glu Ser Ala Leu Tyr Asn Ala Lys
145                 150                 155                 160
Leu Leu Glu Asp Leu Asp Phe Thr Asn Phe Lys Ile Ser Leu Lys Ala
                165                 170                 175
Ser Asp Val Ile Arg Thr Ile Glu Ala Tyr Arg Met Leu Arg Pro Leu
            180                 185                 190
Val Ile Tyr Pro Phe His Leu Gly Val Thr Glu Ala Gly Asn Leu Phe
        195                 200                 205
Ser Ser Ser Ile Lys Ser Ala Met Ala Leu Gly Gly Leu Leu Met Glu
    210                 215                 220
Gly Ile Gly Asp Thr Met Arg Val Ser Ile Thr Gly Glu Leu Glu Asn
225                 230                 235                 240
Glu Ile Lys Val Ala Arg Ala Ile Leu Arg His Ser Gly Arg Leu Lys
                245                 250                 255
Glu Gly Ile Asn Trp Ile Ser Cys Pro Thr Cys Gly Arg Ile Glu Ala
            260                 265                 270
Asn Leu Val Asp Met Ala Ile Lys Val Glu Lys Arg Leu Ser His Ile
        275                 280                 285
Lys Thr Pro Leu Asp Ile Ser Val Met Gly Cys Val Val Asn Ala Leu
    290                 295                 300
Gly Glu Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser
305                 310                 315                 320
Gly Leu Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys
                325                 330                 335
Asp Leu Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu
```

```
            340                 345                 350
Arg Glu Lys Ser Leu Lys Asp
        355
```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1346
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```
GCCTATGAAA TCTTAAAGCG TTATCCGGCT AAAGCAAAGG TATAAATAAC ATG AAA      56
                                                          Met Lys
                                                            1

AAA TTT TTA ATC ACT TTA TTA TTA GGA GTT TTT ATG GGG TTA CAA GCG      104
Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu Gln Ala
          5                  10                  15

AGC GCT TTG ACA CAC CAA GAA ATC AAT CAA GCT AAA GTC CCT GTG ATT      152
Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro Val Ile
     20                  25                  30

TAT GAA GAA AAC CAT TTG TTG CCT ATG GGG TTT ATC CAT TTA GCC TTT      200
Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu Ala Phe
35                   40                  45                  50

AGG GGG GGT GGG AGC TTA AGC GAT AAA AAC CAG TTG GGT TTG GCG AAA      248
Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu Ala Lys
                55                  60                  65

TTA TTC GCG CAA GTT TTA AAC GAA GGC ACT AAA GAG CTT GGT GCG GTG      296
Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly Ala Val
            70                  75                  80

GGG TTT GCG CAA CTT TTA GAG CAA AAA GCG ATC AGT TTG AAT GTG GAT      344
Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn Val Asp
        85                  90                  95

ACC AGC ACA GAA GAT TTG CAA ATC ACT TTA GAA TTT TTA AAA GAA TAC      392
Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys Glu Tyr
    100                 105                 110

GAA GAT GAA GCC ATT ACG CGC TTA AAA GAG CTT TTA AAA TCC CCT AAT      440
Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Leu Lys Ser Pro Asn
```

```
115                 120                 125                 130

TTC ACG CAA AAC GCT TTA GAA AAA GTC AAA ACC CAA ATG TTA GCC GCA      488
Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr Gln Met Leu Ala Ala
                135                 140                 145

CTT TTA CAA AAA GAA AGC GAT TTT GAC TAT TTG GCT AAA TTG ACT TTA      536
Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu Ala Lys Leu Thr Leu
            150                 155                 160

AAG CAA GAG CTT TTT GCT AAC ACC CCT TTA GCT AAC GCA GCC TTA GGC      584
Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala Asn Ala Ala Leu Gly
        165                 170                 175

ACT AAA GAG AGC ATT CAA AAA ATC AAG CTA GAC GAT TTG AAA CAG CAA      632
Thr Lys Glu Ser Ile Gln Lys Ile Lys Leu Asp Asp Leu Lys Gln Gln
    180                 185                 190

TTT GCT AAG GTC TTT GAA CTC AAT AAG CTC GTG GTG GTG CTT GGG GGC      680
Phe Ala Lys Val Phe Glu Leu Asn Lys Leu Val Val Val Leu Gly Gly
195                 200                 205                 210

GAT TTG AAA ATC GAT CAA ACC CTT AAG CGT TTG AAT AAC GCC CTT AAT      728
Asp Leu Lys Ile Asp Gln Thr Leu Lys Arg Leu Asn Asn Ala Leu Asn
                215                 220                 225

TTC TTG CCA CAA GGT AAA GCG TAT GAA GAG CCT TAT TTT GAA ACG AGC      776
Phe Leu Pro Gln Gly Lys Ala Tyr Glu Glu Pro Tyr Phe Glu Thr Ser
            230                 235                 240

GAT AAA AAA AGC GAA AAA GTC CTC TAT AAA GAC ACT GAG CAG GCT TTC      824
Asp Lys Lys Ser Glu Lys Val Leu Tyr Lys Asp Thr Glu Gln Ala Phe
        245                 250                 255

GTG TAT TTT GGT GCG CCC TTT AAA ATC AAG GAT TTA AAA CAG GAT TTA      872
Val Tyr Phe Gly Ala Pro Phe Lys Ile Lys Asp Leu Lys Gln Asp Leu
    260                 265                 270

GCG AAA TCT AAA GTC ATG ATG TTT GTG CTT GGT GGG GGG TTT GGC TCT      920
Ala Lys Ser Lys Val Met Met Phe Val Leu Gly Gly Gly Phe Gly Ser
275                 280                 285                 290

CGT TTA ATG GAA AAA ATC AGG GTT CAA GAG GGA TTA GCT TAT AGC GTG      968
Arg Leu Met Glu Lys Ile Arg Val Gln Glu Gly Leu Ala Tyr Ser Val
                295                 300                 305

TAT ATC CGC TCC AAT TTT TCT AAA GTG GCG CAT TTT GCG AGC GGG TAT     1016
Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His Phe Ala Ser Gly Tyr
            310                 315                 320

TTG CAA ACC AAG CTC AGC ACT CAA ACT AAA AGC GTT GCC TTA GTT AAA     1064
Leu Gln Thr Lys Leu Ser Thr Gln Thr Lys Ser Val Ala Leu Val Lys
        325                 330                 335

AAA ATC GTT AAG GAA TTT ATA GAA AAA GGC ATG ACG CAA CAA GAA TTA     1112
Lys Ile Val Lys Glu Phe Ile Glu Lys Gly Met Thr Gln Gln Glu Leu
    340                 345                 350
```

```
GAC GAC GCT AAA AAG TTT TTA CTA GGC TCT GAG CCT TTA AGG AAT GAA    1160
Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu Arg Asn Glu
355                 360                 365                 370

ACG ATC TCT AGC CGC TTG AAC ACC ACT TAC AAT TAT TTT TAT TTA GGT    1208
Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly
                375                 380                 385

TTG CCT TTA AAT TTT AAC CAA ACG CTG CTC AAT CAA ATC CAA AAA ATG    1256
Leu Pro Leu Asn Phe Asn Gln Thr Leu Leu Asn Gln Ile Gln Lys Met
            390                 395                 400

AGT TTG AAA GAA ATC AAT GAT TTC ATT AAA GCC CAC ACC GAA ATC AAC    1304
Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Ala His Thr Glu Ile Asn
        405                 410                 415

GAC TTG ACT TTT GCT ATT GTG AGC AAT AAA AAG AAG GAC AAA TGATGCCAT  1355
Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys Lys Asp Lys
    420                 425                 430

TTGAAGCTGT AATCGGGCTA GAAGTCCATG TCCAACTCAA CACC                   1399
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```
Met Lys Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu
 1               5                  10                  15
Gln Ala Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro
            20                  25                  30
Val Ile Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu
        35                  40                  45
Ala Phe Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu
    50                  55                  60
Ala Lys Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly
65                  70                  75                  80
Ala Val Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn
                85                  90                  95
Val Asp Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys
            100                 105                 110
Glu Tyr Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Leu Lys Ser
        115                 120                 125
Pro Asn Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr Gln Met Leu
    130                 135                 140
Ala Ala Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu Ala Lys Leu
145                 150                 155                 160
Thr Leu Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala Asn Ala Ala
                165                 170                 175
Leu Gly Thr Lys Glu Ser Ile Gln Lys Ile Lys Leu Asp Asp Leu Lys
```

```
            180                 185                 190
Gln Gln Phe Ala Lys Val Phe Glu Leu Asn Lys Leu Val Val Val Leu
        195                 200                 205
Gly Gly Asp Leu Lys Ile Asp Gln Thr Leu Lys Arg Leu Asn Asn Ala
    210                 215                 220
Leu Asn Phe Leu Pro Gln Gly Lys Ala Tyr Glu Glu Pro Tyr Phe Glu
225                 230                 235                 240
Thr Ser Asp Lys Lys Ser Glu Lys Val Leu Tyr Lys Asp Thr Glu Gln
                245                 250                 255
Ala Phe Val Tyr Phe Gly Ala Pro Phe Lys Ile Lys Asp Leu Lys Gln
            260                 265                 270
Asp Leu Ala Lys Ser Lys Val Met Met Phe Val Leu Gly Gly Gly Phe
        275                 280                 285
Gly Ser Arg Leu Met Glu Lys Ile Arg Val Gln Glu Gly Leu Ala Tyr
    290                 295                 300
Ser Val Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His Phe Ala Ser
305                 310                 315                 320
Gly Tyr Leu Gln Thr Lys Leu Ser Thr Gln Thr Lys Ser Val Ala Leu
                325                 330                 335
Val Lys Lys Ile Val Lys Glu Phe Ile Glu Lys Gly Met Thr Gln Gln
            340                 345                 350
Glu Leu Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu Arg
        355                 360                 365
Asn Glu Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe Tyr
    370                 375                 380
Leu Gly Leu Pro Leu Asn Phe Asn Gln Thr Leu Leu Asn Gln Ile Gln
385                 390                 395                 400
Lys Met Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Ala His Thr Glu
                405                 410                 415
Ile Asn Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys Lys Asp Lys
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...521
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```
GAAGAGCCAG AAAATTTAGA AACCTCTTCG GCACAAAATT TGTTTGAGTG ATG CGT      56
                                                          Met Arg
                                                            1

TTC TTT TCA TTC TTT TAT TTT TTA TTT TAT TTT TTA GGG GTT TCT TTG     104
Phe Phe Ser Phe Phe Tyr Phe Leu Phe Tyr Phe Leu Gly Val Ser Leu
  5                   10                  15
```

```
CAA GCT CTC AGC CCC CTA GAA GAT CAA GAA TTT TTA ATT TCG TAC CGC      152
Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser Tyr Arg
    20                  25                  30

TTG AAA ATC GTT GAT TCT AGA GTG ATG GGC GAA GAG TAT TCT GTC TCT      200
Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser Val Ser
35                  40                  45                  50

AAA CCT ATC GTT AGC CGC ATT AAA ACA GCC CCC TAT GTT TTA GAC TAT      248
Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu Asp Tyr
                55                  60                  65

CAT TGC TCC ATC ATC ACT CGT AAC TTA CCC AAT TTG AAA AAC CCC TTG      296
His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn Pro Leu
            70                  75                  80

CTC CCA ATA AAG TTA GAA CGC TTC CTT TTA GAA ATC GCG TTA AAA AAA      344
Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu Lys Lys
        85                  90                  95

GAA AAA GAG CGG GTC ATA GAC TGC ATT TTA AAA AGC CAG GTC GCT ATC      392
Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val Ala Ile
    100                 105                 110

ACG CAT TAT GAT CAT AGC TAT AAA AAC GGC ACC ACT ACC ACA AGC ATT      440
Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr Ser Ile
115                 120                 125                 130

CTT GCC CTC AAA GCC TTA AGC GTT AGA GCG AGT TTA GTG GGA GAT GCG      488
Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly Asp Ala
                135                 140                 145

CTG TTT TTA GAT ATT TTT AGA AAG GAA GAA GAA TGAAAATCGC CATTGTAGAA     541
Leu Phe Leu Asp Ile Phe Arg Lys Glu Glu Glu
            150                 155

GATGATATTA ACATGCGTAA AAGCCTGGAG CTT                                 574
```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
Met Arg Phe Phe Ser Phe Phe Tyr Phe Leu Phe Tyr Phe Leu Gly Val
 1               5                  10                  15
Ser Leu Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser
            20                  25                  30
Tyr Arg Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser
        35                  40                  45
Val Ser Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu
```

```
    50                  55                  60
Asp Tyr His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn
65                  70                  75                  80
Pro Leu Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu
                85                  90                  95
Lys Lys Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val
            100                 105                 110
Ala Ile Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr
        115                 120                 125
Ser Ile Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly
    130                 135                 140
Asp Ala Leu Phe Leu Asp Ile Phe Arg Lys Glu Glu Glu
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...950
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
ATCATGAGAA AACGCTTCAC TCCACTTTTG TTATTCAGGA AATAATACAG ATG AGA      56
                                                          Met Arg
                                                            1

AAA ACG ATT TCA GCG TTG TTT TTA TCA GCG TGC ATA GGG TTA TCG TCT     104
Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu Ser Ser
          5                  10                  15

GTT TAT GCA GAT AAC GCT TTG ATT TTG CAA ACC GAT TTT AGT CTA AAA     152
Val Tyr Ala Asp Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser Leu Lys
    20                  25                  30

GAT GGG GCC GTC TCG GCG ATG AAA GGC GTC GCT TTC AGC GTT GAT TCC     200
Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val Asp Ser
35                  40                  45                  50

CAT CTT AAA ATC TTT GAT TTA ACG CAC GAA ATC CCC CCG TAT AAC ATC     248
His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr Asn Ile
                55                  60                  65

TGG GAA GGC GCT TAC CGC TTG TAT CAG ACC GCC AGT TAT TGG CCA AAA     296
Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp Pro Lys
            70                  75                  80

GGT TCG GTA TTT GTG AGC GTA GTT GAT CCG GGC GTA GGC ACT AAG CGT     344
```

```
Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr Lys Arg
        85                  90                  95

AAA TCG GTG GTA CTA AAA ACT AAA AAC GGC CAG TAT TTC GTC TCG CCG      392
Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val Ser Pro
    100                 105                 110

GAT AAC GGC ACG CTG ACT TTG GTG GCA CAA ACT TTG GGG ATT GAT AGC      440
Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile Asp Ser
115                 120                 125                 130

GTG CGT GAA ATT GAT GAA AAA GCT AAC CGC TTG AAA GGT TCT GAA AAA      488
Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser Glu Lys
                135                 140                 145

TCC TAT ACT TTC CAT GGT CGT GAT GTG TAT GCT TAC ACC GGT GCA CGC      536
Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly Ala Arg
            150                 155                 160

TTG GCT TCT GGG GCG ATC ACA TTC GAG CAG GTC GGG CCA GAG CTT CCC      584
Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu Leu Pro
        165                 170                 175

CCA AAA GTC GTT GAA ATT CCT TAC CAA AAA GCG AAA GCC ACA AAA GGG      632
Pro Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr Lys Gly
    180                 185                 190

GAA GTG AAA GGT AAT ATC CCG ATT TTG GAT ATT CAA TAT GGC AAT GTT      680
Glu Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly Asn Val
195                 200                 205                 210

TGG AGC AAC ATC AGC GAT AAA TTA CTC AAT CAA GCA AAA ATC AAA CTC      728
Trp Ser Asn Ile Ser Asp Lys Leu Leu Asn Gln Ala Lys Ile Lys Leu
                215                 220                 225

AAT GAC ACG CTG TGT GTA ACG ATT TTT AAA GGT TCT AAG AAA CAA TAC      776
Asn Asp Thr Leu Cys Val Thr Ile Phe Lys Gly Ser Lys Lys Gln Tyr
            230                 235                 240

GAA GGG AAA ATG CCG TAT GTC GCA AGC TTT GGC GAT GTG CCA GAA GGC      824
Glu Gly Lys Met Pro Tyr Val Ala Ser Phe Gly Asp Val Pro Glu Gly
        245                 250                 255

CAG CCG TTA GTT TAT TTA AAC AGC TTG TTA AAT GTT TCC GTG GCG CTG      872
Gln Pro Leu Val Tyr Leu Asn Ser Leu Leu Asn Val Ser Val Ala Leu
    260                 265                 270

AAT AGG GAT AAT TTC GCG CAA AAA TAT CAA ATC AAA TCC GGT GCT GAC      920
Asn Arg Asp Asn Phe Ala Gln Lys Tyr Gln Ile Lys Ser Gly Ala Asp
275                 280                 285                 290

TGG AAT ATT GAT ATA AAG AAG TGC GCT AAG TAAAGCGCTG TTTAGAAAAT TAA    973
Trp Asn Ile Asp Ile Lys Lys Cys Ala Lys
                295                 300

GGGGCGTGAA ACGCCCTAAC CGCTAAAGAT                                    1003
```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
Met Arg Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu
 1               5                  10                  15
Ser Ser Val Tyr Ala Asp Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser
            20                  25                  30
Leu Lys Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val
        35                  40                  45
Asp Ser His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr
    50                  55                  60
Asn Ile Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp
65                  70                  75                  80
Pro Lys Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr
                85                  90                  95
Lys Arg Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val
            100                 105                 110
Ser Pro Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile
        115                 120                 125
Asp Ser Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser
    130                 135                 140
Glu Lys Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly
145                 150                 155                 160
Ala Arg Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu
                165                 170                 175
Leu Pro Pro Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr
            180                 185                 190
Lys Gly Glu Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly
        195                 200                 205
Asn Val Trp Ser Asn Ile Ser Asp Lys Leu Leu Asn Gln Ala Lys Ile
    210                 215                 220
Lys Leu Asn Asp Thr Leu Cys Val Thr Ile Phe Lys Gly Ser Lys Lys
225                 230                 235                 240
Gln Tyr Glu Gly Lys Met Pro Tyr Val Ala Ser Phe Gly Asp Val Pro
                245                 250                 255
Glu Gly Gln Pro Leu Val Tyr Leu Asn Ser Leu Leu Asn Val Ser Val
            260                 265                 270
Ala Leu Asn Arg Asp Asn Phe Ala Gln Lys Tyr Gln Ile Lys Ser Gly
        275                 280                 285
Ala Asp Trp Asn Ile Asp Ile Lys Lys Cys Ala Lys
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1160
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```
ATTATTTTTA ATCTTGCATG AAATCTTAAA TATAGAATTA GTCCCTTTGG ATG GGA      56
                                                          Met Gly
                                                            1

TTT TCN CTC GCG CTA GGC TAT TTG TGT TTG TTT ATA TTC GTT TTA AGC      104
Phe Xaa Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val Leu Ser
          5                  10                  15

GCT TCT TTA ATC TCT GAA AAA GCC TTA TCC AAG CAG TAT TTG CAA ACC      152
Ala Ser Leu Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu Gln Thr
     20                  25                  30

GCT AAA GAT AAA ATC ACC TCT TTA AAG AAT TTA AAA GTC ATC GCC ATT      200
Ala Lys Asp Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile Ala Ile
35                  40                  45                  50

ACC GGA AGC TTT GGG AAA ACC AGC ACC AAA AAT TTC TTG CTT CAA ATC      248
Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu Gln Ile
                55                  60                  65

TTA CAA ACC ACA TTC AAC GCG CAT GCA AGC CCC AAA AGC GTC AAT ACC      296
Leu Gln Thr Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr
            70                  75                  80

CTT TTA GGG CTT GCG AAT GAT ATT AAT CAG AAT TTA GAC GAT AGG AGT      344
Leu Leu Gly Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser
        85                  90                  95

GAA ATC TAT ATC GCT GAA GCC GGG GCA AGG AAT AAG GGC GAT ATT AAA      392
Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys
    100                 105                 110

GAA ATC ACC TGT CTC ATT GAA CCG CAC CTT GTT GTG GTT GCA GAA GTG      440
Glu Ile Thr Cys Leu Ile Glu Pro His Leu Val Val Val Ala Glu Val
115                 120                 125                 130

GGC GAA CAG CAT TTA GAA TAC TTT AAA ACT TTA GAA AAT ATT TGC GAG      488
Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu
                135                 140                 145

ACT AAA GCG GAA TTA TTG GAT TCC AAA CGC TTA GAA AAA GCC TTT TGT      536
Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys
            150                 155                 160

TAC TCG GTG GAA AAG ATC AAG CCC TAT GCC CCT AAA GAT AGC CCT TTA      584
Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu
        165                 170                 175
```

```
ATA GAC TAT TCT AGC CTG GTT AAA AAC ATC CAA TCC ACT TTA AAA GGC      632
Ile Asp Tyr Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly
    180                 185                 190

ACT TCT TTT GAA ATG CTT ATA GGT AGC GTT TGG GAA AGA TTT GAA ACA      680
Thr Ser Phe Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr
195                 200                 205                 210

AAG GTT CTA GGG GAG TTT AGC GCT TAT AAT ATC GCT TCA GCC ATT TTA      728
Lys Val Leu Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu
                215                 220                 225

ATC GCT AAG CAT TTA GGC TTA GAG ACC GAA AGG ATC AAA CGG CTT GTT      776
Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val
            230                 235                 240

TTA GAA CTC AAC CCT ATT GCT CAT CGT TTG CAA CTT TTG GAA GTG AAT      824
Leu Glu Leu Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn
        245                 250                 255

CAA AAA ATC ATC ATA GAC GAT AGC TTT AAT GGG AAT TTA AAG GGC ATG      872
Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met
    260                 265                 270

TTA GAG GGC ATT CGT TTA GCG AGT TTG CAC AAA GGG CGT AAA GTC ATT      920
Leu Glu Gly Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile
275                 280                 285                 290

GTA ACA CCG GGC TTA GTG GAA AGC AAT ACA GAA AGT AAT GAG GCT TTA      968
Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu
                295                 300                 305

GCG CAA AAA ATA GAC GGG GTT TTT GAT GTC GCT ATC ATC ACA GGG GAG     1016
Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu
            310                 315                 320

TTG AAT TCC AAA ACG ATT GCT TCA CAA TTG AAA ACC CCC CAA AAA ATC     1064
Leu Asn Ser Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile
        325                 330                 335

TTA CTC AAG GAT AAG GCG CAA TTG GAA AAT ATC TTA CAA GCC ACC ACG     1112
Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr
    340                 345                 350

ATT CAA GGC GAT TTG ATT TTA TTC GCT AAT GAC GCC CCT AAT TAC ATT T   1161
Ile Gln Gly Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile
355                 360                 365                 370

AGGAAATGAA CATGCAACAT TTATACGCTC CTTGGCGCGA AAGTTATTTG AA          1213
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
Met Gly Phe Xaa Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val
 1               5                  10                  15
Leu Ser Ala Ser Leu Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu
            20                  25                  30
Gln Thr Ala Lys Asp Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile
        35                  40                  45
Ala Ile Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu
    50                  55                  60
Gln Ile Leu Gln Thr Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val
65                  70                  75                  80
Asn Thr Leu Leu Gly Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp
                85                  90                  95
Arg Ser Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp
            100                 105                 110
Ile Lys Glu Ile Thr Cys Leu Ile Glu Pro His Leu Val Val Val Ala
        115                 120                 125
Glu Val Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile
    130                 135                 140
Cys Glu Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala
145                 150                 155                 160
Phe Cys Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser
                165                 170                 175
Pro Leu Ile Asp Tyr Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu
            180                 185                 190
Lys Gly Thr Ser Phe Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe
        195                 200                 205
Glu Thr Lys Val Leu Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala
    210                 215                 220
Ile Leu Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg
225                 230                 235                 240
Leu Val Leu Glu Leu Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu
                245                 250                 255
Val Asn Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys
            260                 265                 270
Gly Met Leu Glu Gly Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys
        275                 280                 285
Val Ile Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu
    290                 295                 300
Ala Leu Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr
305                 310                 315                 320
Gly Glu Leu Asn Ser Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln
                325                 330                 335
Lys Ile Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala
            340                 345                 350
Thr Thr Ile Gln Gly Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn
        355                 360                 365
Tyr Ile
    370
```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1303 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1250
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```
CCTTGTGGTC TCATTTGTTT CTGTTTTACT TGTAGCTTGG AGGACTAGGC ATG TAT      56
                                                          Met Tyr
                                                            1

AAA TTA GGG GTG TTT TTG TTA GCC ACC TTA CTA TCA GCT AAC ACG CAA     104
Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn Thr Gln
          5                  10                  15

AAA GTG AGC GAT ATT GCT AAA GAT ATC CAA CAT AAA GAA ACC CTT TTG     152
Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr Leu Leu
     20                  25                  30

AAA AAA ACC CAT GAA GAA AAA AAC CAA CTA AAC AGC CGT TTG AGT TCT     200
Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu Ser Ser
35                   40                  45                  50

TTA GGC GAA GCG ATC CGC TCT AAA GAG CTT CAA AAG GCT GAG ATG GAG     248
Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu Met Glu
                55                  60                  65

CGC CAA ATG ATC GCT TTA AAA AAG AGT CTT GAA AAA AAT CGT AAC GAA     296
Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg Asn Glu
          70                  75                  80

AGT TTG GCG CAA GAA AAA GTC CTA ACC AAC TAC CGC AAG TCT TTA GAT     344
Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser Leu Asp
     85                  90                  95

CAT TTG CAA AAA AAG CGA TCA TTT TTA CAA AAG AGG GTG TTT GAT ACG     392
His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe Asp Thr
100                 105                 110

CTT TTA CAG GAT TTC CTT TTT TCA CAA GCC CTA AAG GGG CAG AAT TTA     440
Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln Asn Leu
115                 120                 125                 130

GCC TCT TCT AAT GAT GTT GTT TTG CAA GTG GCG TTT GAA AAC TTG CAC     488
Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn Leu His
                135                 140                 145

CAA AGC ACT CTG TCT AAA ATG TCG CAA CTG AGC CAA GAA GAA AAG GAA     536
Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu Lys Glu
          150                 155                 160
```

```
CTC AAT ACG CAA GCT TTA AAA GTC AAA AAC AGC ATT CAA AAA ATC TCA      584
Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys Ile Ser
        165                 170                 175

TCC ATC ATA GAT GAG CAA AAA ACT CGT GAA GTA ACC TTA AAA TCC TTG      632
Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys Ser Leu
    180                 185                 190

AAA ACC GAA CAA GAT AAG CTC ATT TTG AGC ATG CAA AAA GAT TAT GCG      680
Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp Tyr Ala
195                 200                 205                 210

ATC TAC AAC CAA CGC CTA ACC CTT TTA GAA AAA GAG CGC CAG AAT TTA      728
Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln Asn Leu
                215                 220                 225

AAC GCT CTT TTA AAA CGC TTG AAT ATC ATC AAA CAA AAC AGA GAA AAT      776
Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg Glu Asn
            230                 235                 240

GAA GAA AAA GTC AGT TTG AAA AAA TCT TCT CAA GCC TTA GAA GTC AAA      824
Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu Val Lys
        245                 250                 255

CAA GTG GCT AGC TCT TAT CAA AAT ATC AAC ACC ACG AGC TAT AAC GGA      872
Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr Asn Gly
    260                 265                 270

CCA AAA ACG ATC GCT CCC TTG AAC GAT TAT GAA GTG GTG CAA AAA TTT      920
Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln Lys Phe
275                 280                 285                 290

GGC CCC TAT ATT GAC CCG GTT TAT AAT TTA AAA ATT TTT AGC GAG TCT      968
Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser Glu Ser
                295                 300                 305

ATT ACG CTC GTG TCA AAA ACC CCA AAC GCT TTG GTG CGT AAT GTT TTA     1016
Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn Val Leu
            310                 315                 320

GAC GGG AAA ATC GTG TTC GCT AAA GAA ATC AAC ATG CTT AAA AAA GTC     1064
Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys Lys Val
        325                 330                 335

GTT ATC ATT GAG CAT AAA AAT GGG ATC CGC ACG ATT TAT TCT CAA TTG     1112
Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser Gln Leu
    340                 345                 350

GAT AAA ATC GCT CCC ACC ATT AAA AGC GGC ATG CGG ATC CAA AAA GGC     1160
Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln Lys Gly
355                 360                 365                 370

TAT GTT TTA GGG CGC ATT GAT CAA CGC TTG GGC TTT GAA GTT ACC ATG     1208
Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val Thr Met
                375                 380                 385

AGA GAA AAA CAC ATC AAC CCC TTA GAA CTC ATC GCA CGC AAT TAAACAAAT   1259
Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn
```

390 395 400

CGTTTTTATT GCCGATATTG GCTAAAGAAT TTATGCAAAC AAAT 1303

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met Tyr Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn
1 5 10 15
Thr Gln Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr
20 25 30
Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu
35 40 45
Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu
50 55 60
Met Glu Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg
65 70 75 80
Asn Glu Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser
85 90 95
Leu Asp His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe
100 105 110
Asp Thr Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln
115 120 125
Asn Leu Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn
130 135 140
Leu His Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu
145 150 155 160
Lys Glu Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys
165 170 175
Ile Ser Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys
180 185 190
Ser Leu Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp
195 200 205
Tyr Ala Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln
210 215 220
Asn Leu Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg
225 230 235 240
Glu Asn Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu
245 250 255
Val Lys Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr
260 265 270
Asn Gly Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln
275 280 285
Lys Phe Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser
290 295 300
Glu Ser Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn
305 310 315 320
Val Leu Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys

```
                325                 330                 335
Lys Val Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser
            340                 345                 350
Gln Leu Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln
        355                 360                 365
Lys Gly Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val
    370                 375                 380
Thr Met Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn
385                 390                 395                 400
```

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...308
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```
AGGATTTAAG ATTGCGTTTG AAGTTAGCTA GCGTATGCTT GGGCGTTTTG ATG AGT      56
                                                          Met Ser
                                                            1

GGT TGT GCG TCT TCT TCG CCA ACT GGC ACT CTT ATC ACT ATG GTA ACG     104
Gly Cys Ala Ser Ser Ser Pro Thr Gly Thr Leu Ile Thr Met Val Thr
          5                  10                  15

ATG CCA GTT TCT GGG AAT GAT GCA CAA TAC TCC AAA GAA GGG CGT GCG     152
Met Pro Val Ser Gly Asn Asp Ala Gln Tyr Ser Lys Glu Gly Arg Ala
    20                  25                  30

AGT TGT TGG AGT GTT TTT AGT CTT GTG GCT GCC GGT AAT TGT TCG GTA     200
Ser Cys Trp Ser Val Phe Ser Leu Val Ala Ala Gly Asn Cys Ser Val
35                  40                  45                  50

GAA AAA GCG GCT AAA AGT GGC GGT GTT ACC AAG ATT AAA ATG GTG AGC     248
Glu Lys Ala Ala Lys Ser Gly Gly Val Thr Lys Ile Lys Met Val Ser
                55                  60                  65

CGT GAG ACA AAC AAC TTT TTA GGT ATT GTT GGC AAA TAC ACC ACG ATC     296
Arg Glu Thr Asn Asn Phe Leu Gly Ile Val Gly Lys Tyr Thr Thr Ile
            70                  75                  80

GTT CAA GGC GAC TAGTTTTAAT ATTTAGAGAG CGTAGTTGAA TCGTCTTTCG TTCCA   353
Val Gln Gly Asp
        85

CTCTAGGC                                                            361
```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
Met Ser Gly Cys Ala Ser Ser Ser Pro Thr Gly Thr Leu Ile Thr Met
 1               5                  10                  15
Val Thr Met Pro Val Ser Gly Asn Asp Ala Gln Tyr Ser Lys Glu Gly
            20                  25                  30
Arg Ala Ser Cys Trp Ser Val Phe Ser Leu Val Ala Ala Gly Asn Cys
        35                  40                  45
Ser Val Glu Lys Ala Ala Lys Ser Gly Gly Val Thr Lys Ile Lys Met
    50                  55                  60
Val Ser Arg Glu Thr Asn Asn Phe Leu Gly Ile Val Gly Lys Tyr Thr
65                  70                  75                  80
Thr Ile Val Gln Gly Asp
                85
```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1511
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
TTTAAACCTG AATTTCATAT TTTTGATTTT TTAAAGGGAT TAGAGTTCTT  ATG ATT      56
                                                        Met Ile
                                                         1

GAA TGG ATG CAA AAT CAT AGA AAA TAT TTA GTG GTT ACA ATA TGG ATA     104
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
        5                  10                  15

AGC ACG ATC GCT TTT ATT GCC GCT GGG ATG ATA GGC TGG GGG CAA TAC     152
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
    20                  25                  30

AGC TTT TCT TTA GAT AGC GAT AGC GCT GCC AAA GTG GGA CAG ATT AAG     200
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
```

```
35                  40                  45                  50

ATT TCT CAA GAA GAA TTA GCC CAA GAA TAC CGC CGC CTT AAA GAC GCA      248
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
                55                  60                  65

TAT GCT GAG TCT ATC CCT GAT TTT AAA GAA CTC ACC AAA GAT CAA ATC      296
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Lys Asp Gln Ile
            70                  75                  80

AAA GCC ATG CAT TTA GAA AAA AGC GCT TTA GAT TCG CTC ATC AAT CAA      344
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
        85                  90                  95

GCC TTA TTG AGA AAT CTC GCT TTA GAT TTA GGG CTT GGC GCT ACA AAG      392
Ala Leu Leu Arg Asn Leu Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
    100                 105                 110

CAA GAA GTG GCG AAA GAG ATC AGA AAA ACG AGC GTT TTC CAA AAA GAT      440
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Ser Val Phe Gln Lys Asp
115                 120                 125                 130

GGC GTT TTT GAT GAA GAA TTG TAT AAA AAT ATC TTA AAG CAA AGC CAT      488
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
                135                 140                 145

TAC CGC CCC AAA CAT TTT GAA GAA AGC GTT GAA AGG CTT TTA ATC CTT      536
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
            150                 155                 160

CAA AAA ATC AGC ACT CTA TTC CCC AAA ACC ACT ACC CCT TTG GAG CAA      584
Gln Lys Ile Ser Thr Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
        165                 170                 175

TCC AGC CTA TCG CTT TGG GCA AAA TTG CAA GAC AAA TTA GAC ATT CTT      632
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
    180                 185                 190

ATC CTA AAC CCT AGT GAT GTT AAA ATC TCT CTT AAT GAA GAA GAG ATG      680
Ile Leu Asn Pro Ser Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
195                 200                 205                 210

AAA AAA TAT TAC GAG TCC CAT AAA AAG GAT TTT AAA AAG CCC ACG AGC      728
Lys Lys Tyr Tyr Glu Ser His Lys Lys Asp Phe Lys Lys Pro Thr Ser
                215                 220                 225

TTT AAA ACA CGC TCT TTA TAT TTT GAC GCT AGT TTG GAA AAA CCT GAT      776
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Pro Asp
            230                 235                 240

TTG AAG GAG TTG GAG GAA TAC TAC CAT AAA AAC AAG GTG TCT TAT TTG      824
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
        245                 250                 255

GAC AAA GAG GGG AAA TTG CAG GAT TTT AAA AGC GTT CAA GAG CAA GTC      872
Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln Val
    260                 265                 270
```

```
AAG CAT GAT TTA AGC ATG CAA AAA GCG AAT GAA AAA GCC TTA AGG AGC      920
Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu Arg Ser
275                 280                 285                 290

TAT ATC GCT CTA AAA AAA GCG AAC GCG CAA AAC TAC ACC ACA CAA GAT      968
Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr Gln Asp
                295                 300                 305

TTT GAA GAG AAC AAC TCC CCC TAT ACT GCT GAA ATC ACG CAA AAA CTC     1016
Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys Leu
            310                 315                 320

ACC GCT CTC AAA CCC CTT GAA ATC CTA AAG CCA GAG CCT TTT AAA GAT     1064
Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe Lys Asp
        325                 330                 335

GGT TTT ATT GTG GTG CAA CTC ATC TCT CAA ATT AAA GAC GAA TTG CAA     1112
Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu Leu Gln
    340                 345                 350

AAT TTT AAT GAA GCT AAA AGC GCT CTT AAA ACC CGC CTA ACT CAA GAA     1160
Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln Glu
355                 360                 365                 370

AAA ACC CTT ATG GCG TTG CAA ACT TTA GCC AAA GAA AAG CTT AAG GAT     1208
Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys Asp
                375                 380                 385

TTT AAG GGC AAA AGC GTG GGC TAT GTA AGC CCT AAT TTT GGA GGC ACT     1256
Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly Thr
            390                 395                 400

ATT AGT GAG CTT AAC CAA GAA GAA AGT GCT AAG TTT ATC AAC GCT CTT     1304
Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Ala Leu
        405                 410                 415

TTT AAC CGC CAG GAA AAA AAG GGG TTT ATC GCT ATT AAT AAT AAA GTG     1352
Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn Lys Val
    420                 425                 430

GTG CTC TAT CAA ATC ACA GAA CAA AAT TTC AAC CAC TCA TTT AGT GCA     1400
Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe Ser Ala
435                 440                 445                 450

GAA GAA AGC CAG TAT ATG CAG CGT TTA GTC AAT AAC ACT AAA ACG GAT     1448
Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr Asp
                455                 460                 465

TTT TTT GAT AAA GCG TTG ATA GAA GAA TTG AAA AAA CGC TAT AAG ATA     1496
Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys Ile
            470                 475                 480

GTC AAA TAC ATT CAA TAAATGCAAG GGGAAATCAT GGAACATAAA GAAATCGTTA T  1552
Val Lys Tyr Ile Gln
        485

AGGGGTTGAT CT                                                      1564
```

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```
Met Ile Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile
 1               5                  10                  15
Trp Ile Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly
            20                  25                  30
Gln Tyr Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln
        35                  40                  45
Ile Lys Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys
    50                  55                  60
Asp Ala Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Lys Asp
65                  70                  75                  80
Gln Ile Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile
                85                  90                  95
Asn Gln Ala Leu Leu Arg Asn Leu Ala Leu Asp Leu Gly Leu Gly Ala
            100                 105                 110
Thr Lys Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Ser Val Phe Gln
        115                 120                 125
Lys Asp Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln
    130                 135                 140
Ser His Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu
145                 150                 155                 160
Ile Leu Gln Lys Ile Ser Thr Leu Phe Pro Lys Thr Thr Thr Pro Leu
                165                 170                 175
Glu Gln Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp
            180                 185                 190
Ile Leu Ile Leu Asn Pro Ser Asp Val Lys Ile Ser Leu Asn Glu Glu
        195                 200                 205
Glu Met Lys Lys Tyr Tyr Glu Ser His Lys Lys Asp Phe Lys Lys Pro
    210                 215                 220
Thr Ser Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys
225                 230                 235                 240
Pro Asp Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser
                245                 250                 255
Tyr Leu Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu
            260                 265                 270
Gln Val Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu
        275                 280                 285
Arg Ser Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr
    290                 295                 300
Gln Asp Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln
305                 310                 315                 320
Lys Leu Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe
                325                 330                 335
Lys Asp Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu
            340                 345                 350
Leu Gln Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr
```

```
        355                 360                 365
Gln Glu Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu
    370                 375                 380
Lys Asp Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly
385                 390                 395                 400
Gly Thr Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn
                405                 410                 415
Ala Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn
            420                 425                 430
Lys Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe
        435                 440                 445
Ser Ala Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys
    450                 455                 460
Thr Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr
465                 470                 475                 480
Lys Ile Val Lys Tyr Ile Gln
                485
```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1382
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```
CAAAAAGATG GATTTTTGAG CGTCAAAGAG GCTATAGGAG CGGATTTAAG ATG AAA      56
                                                          Met Lys
                                                            1

CAT TTT TCT GTT AAA AGA CTT TTA GGG CTT AGT TCT GTC TTG TTA GTC      104
His Phe Ser Val Lys Arg Leu Leu Gly Leu Ser Ser Val Leu Leu Val
  5                 10                  15

ACT TTA GGA GCG AGC ATG CAC GCA CAA TCT TAC TTA CCC AAA CAT GAG      152
Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys His Glu
    20                  25                  30

AGC GTT ACC TTA AAA AAC GGG TTG CAA GTC GTG AGC GTC CCC CTA GAA      200
Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro Leu Glu
35                  40                  45                  50

AAT AAA ACC GGG GTT ATA GAA GTG GAT GTG CTT TAT AAA GTC GGC TCT      248
Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val Gly Ser
                55                  60                  65

AGA AAC GAA ACC ATG GGA AAG AGC GGG ATC GCT CAC ATG TTA GAG CAT      296
```

```
Arg Asn Glu Thr Met Gly Lys Ser Gly Ile Ala His Met Leu Glu His
            70                  75                  80

TTG AAT TTT AAA AGC ACC AAA AAC CTT AAA GCC GGC GAA TTT GAT AAA      344
Leu Asn Phe Lys Ser Thr Lys Asn Leu Lys Ala Gly Glu Phe Asp Lys
        85                  90                  95

ATC GTT AAG CGT TTT GGG GGC GTG AGT AAC GCT TCT ACG AGT TTT GAT      392
Ile Val Lys Arg Phe Gly Gly Val Ser Asn Ala Ser Thr Ser Phe Asp
    100                 105                 110

ATT ACG CGC TAC TTC ATT AAA ACC AGT CAG GCT AAC TTG GAT AAG TCT      440
Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp Lys Ser
115                 120                 125                 130

TTA GAA TTG TTC GCT GAA ACC ATG GGT TCA TTG AAT TTA AAA GAA GAT      488
Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys Glu Asp
                135                 140                 145

GAG TTT TTG CCT GAG CGT CAA GTG GTC GCT GAA GAA AGG CGA TGG CGC      536
Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg Trp Arg
            150                 155                 160

ACT GAT AAT TCC CCT ATC GGC ATG CTT TAT TTC CGC TTT TTT AAC ACC      584
Thr Asp Asn Ser Pro Ile Gly Met Leu Tyr Phe Arg Phe Phe Asn Thr
        165                 170                 175

GCT TAT GTC TAT CAC CCC TAC CAT TGG ACG CCC ATT GGT TTT ATG GAT      632
Ala Tyr Val Tyr His Pro Tyr His Trp Thr Pro Ile Gly Phe Met Asp
    180                 185                 190

GAT ATT CAA AAT TGG ACT TTA AAA GAC ATT AAA AAA TTC CAT TCG CTC      680
Asp Ile Gln Asn Trp Thr Leu Lys Asp Ile Lys Lys Phe His Ser Leu
195                 200                 205                 210

TAT TAT CAG CCT AAA AAC GCT ATC GTT TTG GTG GTA GGC GAT GTC AAT      728
Tyr Tyr Gln Pro Lys Asn Ala Ile Val Leu Val Val Gly Asp Val Asn
                215                 220                 225

TCC CAA AAG GTT TTT GAA TTG AGT AAA AAG CAT TTT GAA TCC TTA AAA      776
Ser Gln Lys Val Phe Glu Leu Ser Lys Lys His Phe Glu Ser Leu Lys
            230                 235                 240

AAC CTT GAT GAA AAA GCT ATC CCC ACC CCT TAC ATG AAA GAG CCT AAG      824
Asn Leu Asp Glu Lys Ala Ile Pro Thr Pro Tyr Met Lys Glu Pro Lys
        245                 250                 255

CAA GAT GGA GCC AGA ACG GCA GTC GTG CAT AAA GAT GGG GTC CAT TTA      872
Gln Asp Gly Ala Arg Thr Ala Val Val His Lys Asp Gly Val His Leu
    260                 265                 270

GAA TGG GTG GCC CTT GGG TAT AAA GTG CCT GCT TTC AAG CAT AAA GAT      920
Glu Trp Val Ala Leu Gly Tyr Lys Val Pro Ala Phe Lys His Lys Asp
275                 280                 285                 290

CAA GTC GCC TTA GAC GCA CTA AGT AGG CTT TTA GGC GAA GGC AAA AGC      968
Gln Val Ala Leu Asp Ala Leu Ser Arg Leu Leu Gly Glu Gly Lys Ser
                295                 300                 305
```

```
TCG TGG TTG CAA AGC GAA TTA GTG GAT AAA AAA CGC TTG GCT TCT CAA    1016
Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala Ser Gln
            310                 315                 320

GCT TTC TCG CAC AAC ATG CAA TTA CAA GAT GAA AGC GTG TTT TTA TTC    1064
Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe Leu Phe
        325                 330                 335

ATT GCG GGG GGT AAT CCT AAT GTC AAA GCC GAA GCC TTA CAA AAA GAA    1112
Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln Lys Glu
    340                 345                 350

ATC GTA GCG CTT TTA GAA AAG CTG AAA AAA GGC GAA ATC ACT CAA GCG    1160
Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr Gln Ala
355                 360                 365                 370

GAA TTA GAC AAG CTC AAA ATC AAT CAA AAA GCT GAC TTT ATT TCT AAT    1208
Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile Ser Asn
                375                 380                 385

TTA GAA AGT TCT AGC GAT GTT GCG GGG CTT TTT GCG GAC TAT TTA GTG    1256
Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr Leu Val
            390                 395                 400

CAA AAC GAT ATT CAA GGC TTG ACG GAT TAC CAG CGA CAA TTT TTG GAT    1304
Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe Leu Asp
        405                 410                 415

TTA AAA GTG AGC GAT TTG GTG CGT GTG GCC AAT GAA TAT TTT AAA GAC    1352
Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe Lys Asp
    420                 425                 430

ACC CAA TCA ACC ACC GTG TTT TTG AAA CCT TAAAAGAGCC TTATAACATG CAA  1405
Thr Gln Ser Thr Thr Val Phe Leu Lys Pro
435                 440

TTTCATTCAT CTAGCGCGTT GATTACGCCT                                   1435
```

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```
Met Lys His Phe Ser Val Lys Arg Leu Leu Gly Leu Ser Ser Val Leu
 1               5                  10                  15
Leu Val Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys
            20                  25                  30
His Glu Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro
        35                  40                  45
Leu Glu Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val
```

```
    50                  55                  60
Gly Ser Arg Asn Glu Thr Met Gly Lys Ser Gly Ile Ala His Met Leu
65                  70                  75                  80
Glu His Leu Asn Phe Lys Ser Thr Lys Asn Leu Lys Ala Gly Glu Phe
                85                  90                  95
Asp Lys Ile Val Lys Arg Phe Gly Gly Val Ser Asn Ala Ser Thr Ser
            100                 105                 110
Phe Asp Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp
        115                 120                 125
Lys Ser Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys
    130                 135                 140
Glu Asp Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg
145                 150                 155                 160
Trp Arg Thr Asp Asn Ser Pro Ile Gly Met Leu Tyr Phe Arg Phe Phe
                165                 170                 175
Asn Thr Ala Tyr Val Tyr His Pro Tyr His Trp Thr Pro Ile Gly Phe
            180                 185                 190
Met Asp Asp Ile Gln Asn Trp Thr Leu Lys Asp Ile Lys Lys Phe His
        195                 200                 205
Ser Leu Tyr Tyr Gln Pro Lys Asn Ala Ile Val Leu Val Val Gly Asp
    210                 215                 220
Val Asn Ser Gln Lys Val Phe Glu Leu Ser Lys Lys His Phe Glu Ser
225                 230                 235                 240
Leu Lys Asn Leu Asp Glu Lys Ala Ile Pro Thr Pro Tyr Met Lys Glu
                245                 250                 255
Pro Lys Gln Asp Gly Ala Arg Thr Ala Val Val His Lys Asp Gly Val
            260                 265                 270
His Leu Glu Trp Val Ala Leu Gly Tyr Lys Val Pro Ala Phe Lys His
        275                 280                 285
Lys Asp Gln Val Ala Leu Asp Ala Leu Ser Arg Leu Leu Gly Glu Gly
    290                 295                 300
Lys Ser Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala
305                 310                 315                 320
Ser Gln Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe
                325                 330                 335
Leu Phe Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln
            340                 345                 350
Lys Glu Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr
        355                 360                 365
Gln Ala Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile
    370                 375                 380
Ser Asn Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr
385                 390                 395                 400
Leu Val Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe
                405                 410                 415
Leu Asp Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe
            420                 425                 430
Lys Asp Thr Gln Ser Thr Thr Val Phe Leu Lys Pro
        435                 440
```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...197
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
ATATAATCTT TTCTTAATTT TGAAGTTTAG CAAATTTTAA GGAAGTAACC ATG ATG      56
                                                        Met Met
                                                         1

AAA AAA ACC CTT TTT ATC TCT TTG GCT TTA GCG TTA AGC TTG AAT GCG     104
Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu Asn Ala
         5                  10                  15

GGC AAT ATC CAA ATC CAG AGC ATG CCC AAA GTT AAA GAG CGA GTG AGT     152
Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg Val Ser
    20                  25                  30

GTC CCC TCT AAA GAC GAT ACG GAT CTA TTC TTA CCA CGA TTC TAT TAAGG   202
Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe Tyr
35                  40                  45

ACTCTATTAA GGCGGTGGTG AATATCTCCA CTGAAAAGAA GATTAAAA               250
```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu
 1               5                  10                  15
Asn Ala Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg
            20                  25                  30
Val Ser Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe
        35                  40                  45
Tyr
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...275
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
TTAAGATTGC GGTTATACTG AAAAAAACAA TATGAAATCA AGGAGCTTGT ATG CAA      56
                                                        Met Gln
                                                          1

CAG CGT CAT TTA GGC CCT TTA AAA GTG GGT GCA TTA GCT CTA GGG TGC     104
Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu Gly Cys
        5                  10                  15

ATG GGC ATG ACT TAT GGG TAT GGG GAA GTC CAT GAT AAA AAG CAG ATG     152
Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys Gln Met
    20                  25                  30

GTT AAA CTT ATC CAT AAG GCT TTG GAA TTG GGT ATT AAC TTT TTT GAC     200
Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe Phe Asp
35                  40                  45                  50

ACT GCA GAG GCT TAT GGG GAA GAT AAT GAA AAG CTT TTA GGC GAA CGA     248
Thr Ala Glu Ala Tyr Gly Glu Asp Asn Glu Lys Leu Leu Gly Glu Arg
                55                  60                  65

TCA AGC CTT TTA AAG ACA AGG TTG TGG TAGCGAGCAA GTTTGGGATT TACTACG   302
Ser Ser Leu Leu Lys Thr Arg Leu Trp
            70                  75

CAGATCCTAA TGACAAATAC GCAACC                                       328
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```
Met Gln Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu
 1               5                  10                  15
Gly Cys Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys
            20                  25                  30
Gln Met Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe
        35                  40                  45
Phe Asp Thr Ala Glu Ala Tyr Gly Glu Asp Asn Glu Lys Leu Leu Gly
    50                  55                  60
```

```
Glu Arg Ser Ser Leu Leu Lys Thr Arg Leu Trp
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 649 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...596
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```
CGAATTGCTG TATAGTTAGC GTTTTTAATT CAAAATGAAG TGAGGAAACA ATG AAA      56
                                                          Met Lys
                                                            1

AAA GCG TTA ATA TCC ACC CTT TTT GGT GTT AGT TTG GCG TTT GCA AAA     104
Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe Ala Lys
          5                  10                  15

CCT TAT ACG ATT GAT AAG GCA AAC TCT AGC GTG TGG TTT GAG GTC AAA     152
Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu Val Lys
     20                  25                  30

CAC TTC ACG TTC AAT GAA ACA AGA GGC GCG TTT GAT AAT TTT GAT GGC     200
His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe Asp Gly
35                  40                  45                  50

AAA ATT GAT CTA GAG CCC AAC ACT AAA ATG CTC AGC GTT TTT GAA GGC     248
Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe Glu Gly
                55                  60                  65

AAT ATT GAT GTG AAA AGC GTC AAT ACT AGG GAT AGA AAA AGA GAT AAC     296
Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg Asp Asn
            70                  75                  80

CAC TTG AAA ACA GCG GAC TTT TTT GAT GTG GTA AAA TAC CCC AAA GGG     344
His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro Lys Gly
        85                  90                  95

AGC TTT AAA ATG ACC AAA TAC GAA GAT GGT AAA ATC TAT GGG GAT TTG     392
Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly Asp Leu
    100                 105                 110

ACT CTT CGT GGC GTA ACC AAG CCT GTC GTA TTG GAA GCC AAA ATC CAA     440
Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys Ile Gln
115                 120                 125                 130
```

```
GCC CCC TTA CAA AAC CCC ATG AAT AAA AAA GAA TTC ATG GTG TTA CAA      488
Ala Pro Leu Gln Asn Pro Met Asn Lys Lys Glu Phe Met Val Leu Gln
                135                 140                 145

GCT GAA GGC AAA ATC AAC CGC AAG GAT TTT GGT ATC GGT AAA ACC TTT      536
Ala Glu Gly Lys Ile Asn Arg Lys Asp Phe Gly Ile Gly Lys Thr Phe
            150                 155                 160

AGC GAT GCT GTC GTT GGA GAT GAG GTA AAG ATT GAG CTC AAA CTA GAA      584
Ser Asp Ala Val Val Gly Asp Glu Val Lys Ile Glu Leu Lys Leu Glu
        165                 170                 175

GCT TAC GCC CAA TAATCGTTTT GCAAGAGATA GATATCTTCT TCTCTTGCGT TTTTC    641
Ala Tyr Ala Gln
    180

TAACAGCA                                                            649
```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```
Met Lys Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe
 1               5                  10                  15
Ala Lys Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu
            20                  25                  30
Val Lys His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe
        35                  40                  45
Asp Gly Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe
    50                  55                  60
Glu Gly Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg
65                  70                  75                  80
Asp Asn His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro
                85                  90                  95
Lys Gly Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly
            100                 105                 110
Asp Leu Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys
        115                 120                 125
Ile Gln Ala Pro Leu Gln Asn Pro Met Asn Lys Lys Glu Phe Met Val
    130                 135                 140
Leu Gln Ala Glu Gly Lys Ile Asn Arg Lys Asp Phe Gly Ile Gly Lys
145                 150                 155                 160
Thr Phe Ser Asp Ala Val Val Gly Asp Glu Val Lys Ile Glu Leu Lys
                165                 170                 175
Leu Glu Ala Tyr Ala Gln
            180
```

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...425
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```
TCCGTTCGCA ACAAGAATTT TCTTGTTATC TTAATGTAAA GGTCAAAACG ATG AAA      56
                                                        Met Lys
                                                          1

AAG TTA GCC GCT TTA TTT TTA GTA AGC GTG TTG GGG GTT ATG GGT TTA     104
Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly Leu
        5                  10                  15

AAC GCA TGG GAG CAA ACC CTA AAA GCT AAT GAC TTG GAA GTG AAA ATC     152
Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys Ile
    20                  25                  30

AAA TCC GTG GGT AAC CCC ATT AAA GGC GAT AAC ACT TTC ATT CTC AGC     200
Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu Ser
35                  40                  45                  50

CCC ACT TTA AAA GGT AAG GCT TTA GAA AAA GCT ATC GTT AGG GTG CAG     248
Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val Gln
                55                  60                  65

TTT ATG ATG CCT GAA ATG CCC GGC ATG CCA GCG ATG AAA GAA ATG GCG     296
Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met Ala
            70                  75                  80

CAA GTG AGT GAA AAA AAC GGC CTT TAT GAA GCT AAA ACC AAT CTT TCT     344
Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu Ser
        85                  90                  95

ATG AAC GGG ACA TGG CAG GTT AGG GTG GAT ATT AAA TCT AAA GAG GGT     392
Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu Gly
    100                 105                 110

CAG GTT TAT CGC GCT AAA ACA AGC CTG GAT TTA TAAGAGCATG CTATCTTTTA    445
Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
115                 120                 125

TAAGCGCGTT TGATAAAAGG GGCGTTTCAA TAC                               478
```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```
Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met
 1               5                  10                  15
Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
            20                  25                  30
Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile
        35                  40                  45
Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
    50                  55                  60
Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
65                  70                  75                  80
Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
                85                  90                  95
Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
            100                 105                 110
Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1064
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```
AGCGCTTTAA ATAGCACTTA TTTGTCTTTA CAAAACCTTA AAGGATTAGA ATG AAA      56
                                                          Met Lys
                                                           1

CGG ATT TTA TGG TTA GCC TTG ATT TTA TTT TTT AGC CCC TTA TTC GCT     104
Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu Phe Ala
        5                  10                  15

AAC GCT CAA AAA ACT CAA GAA ATT AAA AAA ACT AAA GAA GCT AAA AGC     152
Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala Lys Ser
    20                  25                  30
```

```
CAA ACC CGT TTT AAT ATT TCC ACC ACT AAG GTC ATA GAA AAA GAA TTT      200
Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys Glu Phe
35                  40                  45                  50

TCT CAA AGC CGG CGC TAT TAC GCG CTT TTA GAG CCC AAT GAA GCG CTG      248
Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu Ala Leu
                55                  60                  65

ATT TTT TCT CAA ACC CTG CGT TTT GAT GGC TAT GTG GAA AAG CTT TAT      296
Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys Leu Tyr
            70                  75                  80

GCG AAT AAA ACC TAT ACC CCC ATT AAA AAG GGC GAC AGG TTA TTG AGC      344
Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu Leu Ser
        85                  90                  95

GTG TAT TCC CCT GAA TTA GTG AGC GCT CAA AGC GAA TTG CTA TCA TCA      392
Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu Ser Ser
    100                 105                 110

TTG AAA TTC AAC CAA CAA GTG GGA GCG ATT AAA GAA AAA TTA AAA CTA      440
Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu Lys Leu
115                 120                 125                 130

TTA GGG TTA GAA AAC TCT AGC ATT GAA AAA ATC ATT AGC AGC CAT AAA      488
Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser His Lys
                135                 140                 145

GTC CAA AAT GAA ATG ACT ATT TAC TCT CAC TTC AAC GGC ATT ATT TTT      536
Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile Ile Phe
            150                 155                 160

AAA AAA AGC CCG GAT CTC AAT GAG GGG AGC TTC ATT AAA AAA GGG CAA      584
Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys Gly Gln
        165                 170                 175

GAG TTG TTT CAA ATC ATA GAT TTA AGC CAA TTG TGG GCG CTG GTT AAA      632
Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu Val Lys
    180                 185                 190

GTC AAT CAA GAG GAT TTA GAA TTT TTA AAA AAC ACG CAT AAA GCG ATC      680
Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys Ala Ile
195                 200                 205                 210

TTG TTT GTA GAA GGG ATT AAA GGC GAG CAA GAA ATC ACG CTT GAA AAT      728
Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu Glu Asn
                215                 220                 225

ATC AAC CCC ATC ATC AAC AAA GAA GAT AAA ATG CTA GAA GCG CGC TTC      776
Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala Arg Phe
            230                 235                 240

AAT GTG CCT AAT GTT AAA CAG ATT TAT TAC CCT AAC ATG TTC GCT CAA      824
Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe Ala Gln
        245                 250                 255

GTA GAA ATC TTT CAA AAA CCA CAA AAA ATG AAG ATT TTG CCT AAA GAA      872
Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro Lys Glu
```

```
    260                 265                 270

GCG GTT TTG ATT AAA GGG GGG AAA GCT ATC GTG TTT AAA AAA GAC GAT      920
Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys Asp Asp
275                 280                 285                 290

TTT GGC TTA AGC CCG TTA GAA ATT AAA GCC GTC CGC TTG AGC GAT GGG      968
Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser Asp Gly
                295                 300                 305

AGT TAT GAG ATT TTA GAG GGT TTA AAG GCG GGC GAA GAA GTC GCT AAT     1016
Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val Ala Asn
            310                 315                 320

AAC GCT TTA TTC GTG CTA GAC GCT GAC GCT CAA AAC AAT GGG GAT TAT T   1065
Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly Asp Tyr
        325                 330                 335

GAATGATAGA AAAGATCATT GATTTAAGCG TTAAAAACAA ACTCCTTACC AC           1117
```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```
Met Lys Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu
 1               5                  10                  15
Phe Ala Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala
            20                  25                  30
Lys Ser Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys
        35                  40                  45
Glu Phe Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu
    50                  55                  60
Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys
65                  70                  75                  80
Leu Tyr Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu
                85                  90                  95
Leu Ser Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu
            100                 105                 110
Ser Ser Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu
        115                 120                 125
Lys Leu Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser
    130                 135                 140
His Lys Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile
145                 150                 155                 160
Ile Phe Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys
                165                 170                 175
Gly Gln Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu
            180                 185                 190
Val Lys Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys
```

```
        195                 200                 205
Ala Ile Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu
    210                 215                 220
Glu Asn Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala
225                 230                 235                 240
Arg Phe Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe
                245                 250                 255
Ala Gln Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro
            260                 265                 270
Lys Glu Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys
        275                 280                 285
Asp Asp Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser
    290                 295                 300
Asp Gly Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val
305                 310                 315                 320
Ala Asn Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly
                325                 330                 335
Asp Tyr
```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1196
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```
AAAACTTAGA TAAAATAACA CGATAAAACC ATAGTAATAA AGATAACCCC ATG AGA      56
                                                        Met Arg
                                                          1

TTT TTT TGC TTT TTC TTA TTT TTT CTA ACC TTT TCA AAC GCA CAG ATA     104
Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala Gln Ile
          5                  10                  15

ATG ATG ACT TTT GAT TCT CAA ACT AAC GCC AAA CTC TCG CGC TCT AAC     152
Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg Ser Asn
     20                  25                  30

GAA CAG CTT TCA GAC ATG CTC TAT AAA CTC AAT GAA AGT TTA AGA ATC     200
Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu Arg Ile
35                  40                  45                  50

TAT CAA AGC GTG CTT TCC AAT AAC CAA GAT CAA CTC AAA GAA ATC AAA     248
Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu Ile Lys
                55                  60                  65
```

```
AAA GCT AAC AGC ACC CTA AAT AGC CAA AGG CGT TTT TTT AAC GCC AGC      296
Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn Ala Ser
            70                  75                  80

CAG ATC CGC CTT ATG GAC ACT GAT GCA CTA TTG AAA CAA AGC GCT TTG      344
Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser Ala Leu
        85                  90                  95

GAA TTA GAA AAA TTA CAA GCT TTA GAA AAA CAC ATA AAA AAG GGC ATG      392
Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys Gly Met
    100                 105                 110

GAA CAA GAA CGC TTA ATA GAA GAA TCC CAA ACG CTT TTT TTA CAA GAG      440
Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu Gln Glu
115                 120                 125                 130

CAT TGC CCT TAT TTG AGC GGC GTT AAG AAT TTA GAA GAG GCT TCA AAC      488
His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala Ser Asn
                135                 140                 145

GCT TTA GAA GTC CAA GAG CAA AAC AAC GCC CTT TTC TTA CTC AAA GAG      536
Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu Lys Glu
            150                 155                 160

CCT AAA CTC GCC CGT TTG CTC TCA CGA TTG GAT TTG ATG AGC GCT TTA      584
Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser Ala Leu
        165                 170                 175

AAC GCC TTG TGC GAT CAG GTT TTA GAA AAC CAA GCC CAT AAC CAA CAA      632
Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn Gln Gln
    180                 185                 190

TCC CAT AAC AAA ATT TTA GAA TAC AAC GCT CTT AAA AAC CAT GAT TTT      680
Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His Asp Phe
195                 200                 205                 210

CAA GCC TAT AAA GCC ATG CGT TTG AAA AAA TTT AAA AAC AAG CTT CAA      728
Gln Ala Tyr Lys Ala Met Arg Leu Lys Lys Phe Lys Asn Lys Leu Gln
                215                 220                 225

AGT CAA ATC CAA GCC CAA GAA GAC GCT CTA AAA ACC TTT TTA CCC TTA      776
Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu Pro Leu
            230                 235                 240

GAA AAA CGC TTG GAA ACT TTA AAA ACG CAT TTT TTA TGC GAT AAA GAA      824
Glu Lys Arg Leu Glu Thr Leu Lys Thr His Phe Leu Cys Asp Lys Glu
        245                 250                 255

AAC CTA AAA TCA TGC GCT AAA GAA TTG CAC CAA CGC TAC CAA AAC GCC      872
Asn Leu Lys Ser Cys Ala Lys Glu Leu His Gln Arg Tyr Gln Asn Ala
    260                 265                 270

CTT ATA GAG CGA GAT AAA GAA TTA AAA AAC GCT AAA AAT AAT AAA GAA      920
Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu
275                 280                 285                 290

AAG CAT GCT CTA ATC TTA GCC AAT TAC GAG CAT ACT TTA AAA ACC TTG      968
Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys Thr Leu
```

```
                295                 300                 305

AAT ATA GAA TTT TTA AGC GAA TTA AAT AAG CAA ATG GCG TTT TTG AAT    1016
Asn Ile Glu Phe Leu Ser Glu Leu Asn Lys Gln Met Ala Phe Leu Asn
            310                 315                 320

GAA ACC ATG GCG TTA AAC GCC CGA GTT TTA GCC CTT TTA GCC AAA CAG    1064
Glu Thr Met Ala Leu Asn Ala Arg Val Leu Ala Leu Leu Ala Lys Gln
        325                 330                 335

CAT GCC AAA ACG CCA AAG CCT TTC AAT TTG AGC GGT GGT TTA AGC GGT    1112
His Ala Lys Thr Pro Lys Pro Phe Asn Leu Ser Gly Gly Leu Ser Gly
    340                 345                 350

GAT TTG AGC GGT GGG AAA GCT CTT ATT AAA AAT ATC CGC TTA GAT CCG    1160
Asp Leu Ser Gly Gly Lys Ala Leu Ile Lys Asn Ile Arg Leu Asp Pro
355                 360                 365                 370

CAT GGA TTC CCT AGC TTT AAA AAT TTT AAG CAA GAG TAGGACAATA TTTGAC  1212
His Gly Phe Pro Ser Phe Lys Asn Phe Lys Gln Glu
                375                 380

AAGCAAAAAC AATTATAGTA AAATAAGAGC ATAACTT                           1249
```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```
Met Arg Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala
 1               5                  10                  15
Gln Ile Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg
            20                  25                  30
Ser Asn Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu
        35                  40                  45
Arg Ile Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu
    50                  55                  60
Ile Lys Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn
65                  70                  75                  80
Ala Ser Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser
                85                  90                  95
Ala Leu Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys
            100                 105                 110
Gly Met Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu
        115                 120                 125
Gln Glu His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala
    130                 135                 140
Ser Asn Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu
145                 150                 155                 160
Lys Glu Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser
```

```
                 165                 170                 175
Ala Leu Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn
             180                 185                 190
Gln Gln Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His
         195                 200                 205
Asp Phe Gln Ala Tyr Lys Ala Met Arg Leu Lys Lys Phe Lys Asn Lys
     210                 215                 220
Leu Gln Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu
225                 230                 235                 240
Pro Leu Glu Lys Arg Leu Glu Thr Leu Lys Thr His Phe Leu Cys Asp
                 245                 250                 255
Lys Glu Asn Leu Lys Ser Cys Ala Lys Glu Leu His Gln Arg Tyr Gln
             260                 265                 270
Asn Ala Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn
         275                 280                 285
Lys Glu Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys
     290                 295                 300
Thr Leu Asn Ile Glu Phe Leu Ser Glu Leu Asn Lys Gln Met Ala Phe
305                 310                 315                 320
Leu Asn Glu Thr Met Ala Leu Asn Ala Arg Val Leu Ala Leu Leu Ala
                 325                 330                 335
Lys Gln His Ala Lys Thr Pro Lys Pro Phe Asn Leu Ser Gly Gly Leu
             340                 345                 350
Ser Gly Asp Leu Ser Gly Gly Lys Ala Leu Ile Lys Asn Ile Arg Leu
         355                 360                 365
Asp Pro His Gly Phe Pro Ser Phe Lys Asn Phe Lys Gln Glu
     370                 375                 380
```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...437
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```
TTGTTGAGAA AATCCGATGT TTTGAGCGAA AAATTCAGGA TCATGAAAAA ATG AAA      56
                                                          Met Lys
                                                            1

AGC ATC AGA AGA GGC GAT GGG CTG AAT GTT GTC CCT TTC ATT GAT ATT     104
Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile Asp Ile
  5                  10                  15

ATG CTC GTT TTG CTA GCG ATT GTG TTG AGC ATT TCT ACT TTT ATT GCA     152
Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala
     20                  25                  30
```

```
CAA GGT AAG ATT AAG GTC AGT CTC CCT AAC GCT AAA AAT GCG GAA AAA      200
Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys
35                  40                  45                  50

TCC CAG CCA AAC GAT CAA AAA GTG GTG GTC ATC TCT GTA GAT GAG CAT      248
Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His
                55                  60                  65

GAC AAT ATT TTC GTA GAT GAC AAA CCG ATG AAT TTA GAA GCT TTG AGC      296
Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser
            70                  75                  80

GCT GTA GTC AAA CAA ACA GAC CCT AAA ACC CTT ATA GAC TTA AAA AGC      344
Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser
        85                  90                  95

GAC AAA AGC TCT CGT TTT GAA ACT TTT ATC AGC ATT ATG GAT ATT TTA      392
Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu
    100                 105                 110

AAA GAG CAT AAT CAT GAA AAT TTC TCC ATC TCC ACG CAA GCT CAG TAAAG    442
Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
115                 120                 125

TTTCAACGAG TGTTAGCTTT TTAATCTCTT TTGCCCTATA CGCTATAG                490
```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```
Met Lys Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile
 1               5                  10                  15
Asp Ile Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe
            20                  25                  30
Ile Ala Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala
        35                  40                  45
Glu Lys Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp
    50                  55                  60
Glu His Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala
65                  70                  75                  80
Leu Ser Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu
                85                  90                  95
Lys Ser Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp
            100                 105                 110
Ile Leu Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala
        115                 120                 125
Gln
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 958 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...905
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```
TCGTTTTGAA ACTTTTATCA GCATTATGGA TATTTTAAAA GAGCATAATC ATG AAA      56
                                                        Met Lys
                                                          1

ATT TCT CCA TCT CCA CGC AAG CTC AGT AAA GTT TCA ACG AGT GTT AGC     104
Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser Val Ser
          5                  10                  15

TTT TTA ATC TCT TTT GCC CTA TAC GCT ATA GGG TTT GGC TAT TTT TTA     152
Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr Phe Leu
     20                  25                  30

CTG CGC GAA GAC GCC CCA GAG CCT TTA GCG CAA GCC GGG ACC ACT AAG     200
Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr Thr Lys
35                   40                  45                  50

GTT ACC ATG AGT TTA GCC AGC ATC AAC ACT AAT TCC AAT ACA AAG ACT     248
Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr Lys Thr
                55                  60                  65

AAT GCT GAG TCG GCT AAA CCC AAA GAA GAG CCT AAA GAA AAA CCC AAG     296
Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys Pro Lys
            70                  75                  80

AAA GAA GAG CCA AAA AAA GAA GAA CCC AAA AAG GAG GTT ACA AAG CCT     344
Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr Lys Pro
         85                  90                  95

AAA CCT AAG CCT AAA CCC AAG CCA AAG CCA AAA CCA AAA CCT AAG CCT     392
Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro
     100                 105                 110

GAA CCC AAA CCT GAA CCA AAA CCC GAG CCT AAG CCT GAG CCT AAA GTT     440
Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Val
115                  120                 125                 130

GAA GAG GTT AAA AAA GAA GAG CCT AAA GAA GAG CCC AAA AAA GAA GAA     488
Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys Glu Glu
                135                 140                 145
```

```
GCT AAA GAG GAA GCT AAA GAA AAA AGC GCT CCT AAA CAA GTA ACA ACT      536
Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val Thr Thr
            150                 155                 160

AAG GAT ATA GTC AAA GAA AAA GAC AAG CAA GAA GAA TCC AAC AAA ACC      584
Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn Lys Thr
        165                 170                 175

TCT GAG GGG GCC ACT TCT GAA GCT CAA GCT TAT AAC CCA GGG GTG AGC      632
Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly Val Ser
    180                 185                 190

AAC GAA TTT TTA ATG AAG ATC CAA ACC GCT ATT TCT TCT AAA AAC CGC      680
Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys Asn Arg
195                 200                 205                 210

TAC CCT AAA ATG GCG CAG ATT AGG GGT ATT GAG GGC GAA GTG TTG GTG      728
Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val Leu Val
                215                 220                 225

AGC TTT ACG ATC AAT GCT GAT GGG AGC GTT ACG GAC ATT AAA GTG GTC      776
Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys Val Val
            230                 235                 240

AAA AGC AAC ACC ACA GAT ATT TTA AAC CAT GCG GCT TTA GAA GCC ATT      824
Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu Ala Ile
        245                 250                 255

AAA AGC GCG GCA CAT CTA TTC CCT AAA CCA GAA GAA ACC GTG CAT CTA      872
Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val His Leu
    260                 265                 270

AAA ATC CCT ATC GCT TAT AGC TTG AAA GAA GAC TGATTAGTCT TTCTTTTAGG    925
Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp
275                 280                 285

GGCGATTCAA GCCTTAAAAG CCGGGTCAAA ATC                                 958
```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```
Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser
 1               5                  10                  15
Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr
            20                  25                  30
Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr
        35                  40                  45
Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr
```

```
    50                  55                  60
Lys Thr Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys
65                  70                  75                  80
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr
                85                  90                  95
Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro
            100                 105                 110
Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro
        115                 120                 125
Lys Val Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys
    130                 135                 140
Glu Glu Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val
145                 150                 155                 160
Thr Thr Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn
                165                 170                 175
Lys Thr Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly
            180                 185                 190
Val Ser Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys
        195                 200                 205
Asn Arg Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val
    210                 215                 220
Leu Val Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys
225                 230                 235                 240
Val Val Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu
                245                 250                 255
Ala Ile Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val
            260                 265                 270
His Leu Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 757 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...704
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```
TTGATGAAAA AAATAACGCT CCTCTTTTTA AAACTCTTTT AGAGGATGCC ATG AGA      56
                                                          Met Arg
                                                            1

GTG TCT TCT AAA GAG ATT TTA CTC ATT GTG GGG GGG AGC AGT TTT TAC     104
Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser Phe Tyr
  5                  10                  15

CTC AAA TCC ATT TTA GAA GGT TTG AGC CGC ATG CCA AAA CTG AGC GGT     152
```

```
Leu Lys Ser Ile Leu Glu Gly Leu Ser Arg Met Pro Lys Leu Ser Gly
    20                  25                  30

GAG GAG GTT GTA AAA ATA GAG CGA GAA ATT GCC ACT CTT TCT AAC CCT      200
Glu Glu Val Val Lys Ile Glu Arg Glu Ile Ala Thr Leu Ser Asn Pro
35                  40                  45                  50

TAT ATA TTT TTA AAA TCC ATT GAC CCT AAC ATG GCT TTT AAA ATC CAT      248
Tyr Ile Phe Leu Lys Ser Ile Asp Pro Asn Met Ala Phe Lys Ile His
                55                  60                  65

CCA AAC GAC ACT TAC CGC ACC CAT AAG GCT TTA GAA ATC TTT TAT GCC      296
Pro Asn Asp Thr Tyr Arg Thr His Lys Ala Leu Glu Ile Phe Tyr Ala
            70                  75                  80

ACC TGC ACG CCC CCA AGC GAG TAT TTT AAG GCC AAC CCT AAA AAA CCC      344
Thr Cys Thr Pro Pro Ser Glu Tyr Phe Lys Ala Asn Pro Lys Lys Pro
        85                  90                  95

TTT GAG CAT GCT ATC TCC TTA TTC GCT CTG TCT ATT GAA AAA AGC GCG      392
Phe Glu His Ala Ile Ser Leu Phe Ala Leu Ser Ile Glu Lys Ser Ala
    100                 105                 110

CTC CAT AAC AAT ATC AAA CGG CGC ACC AAA AAC ATG CTC CAT TCA GGG      440
Leu His Asn Asn Ile Lys Arg Arg Thr Lys Asn Met Leu His Ser Gly
115                 120                 125                 130

CTT GTT GAA GAA ATC AAA GCC CTC TAT ACT CAA TAC CCT AAA GAT TCG      488
Leu Val Glu Glu Ile Lys Ala Leu Tyr Thr Gln Tyr Pro Lys Asp Ser
                135                 140                 145

CAG CCT TTT AAA GCC ATA GGC GTT AAA GAG AGC GTT CTT TTT TTA GAA      536
Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe Leu Glu
            150                 155                 160

AAA CGA CTC ACT TTA AAG GAG CTA GAA GAA GCG ATT ACC TCT AAC ACC      584
Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser Asn Thr
        165                 170                 175

ATG AAA TTA GCC AAG CGC CAA AAC ACT TTC AAT AAA ACC CAA TTC AAT      632
Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln Phe Asn
    180                 185                 190

AAC CTT TAT GTG GGG AGC GCT GAA GAA GTT AGG CAT GCG ATT TTA AAA      680
Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile Leu Lys
195                 200                 205                 210

CAC TCA AAA AGC GGC ATT AAA GGA TAATCTAATG GATACACAAA ACTTACCCGA     734
His Ser Lys Ser Gly Ile Lys Gly
                215

TCAAATTATC CCTATTTTTA TGA                                           757
```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```
Met Arg Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser
 1               5                  10                  15
Phe Tyr Leu Lys Ser Ile Leu Glu Gly Leu Ser Arg Met Pro Lys Leu
            20                  25                  30
Ser Gly Glu Glu Val Val Lys Ile Glu Arg Glu Ile Ala Thr Leu Ser
        35                  40                  45
Asn Pro Tyr Ile Phe Leu Lys Ser Ile Asp Pro Asn Met Ala Phe Lys
    50                  55                  60
Ile His Pro Asn Asp Thr Tyr Arg Thr His Lys Ala Leu Glu Ile Phe
65                  70                  75                  80
Tyr Ala Thr Cys Thr Pro Pro Ser Glu Tyr Phe Lys Ala Asn Pro Lys
                85                  90                  95
Lys Pro Phe Glu His Ala Ile Ser Leu Phe Ala Leu Ser Ile Glu Lys
            100                 105                 110
Ser Ala Leu His Asn Asn Ile Lys Arg Arg Thr Lys Asn Met Leu His
        115                 120                 125
Ser Gly Leu Val Glu Glu Ile Lys Ala Leu Tyr Thr Gln Tyr Pro Lys
    130                 135                 140
Asp Ser Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe
145                 150                 155                 160
Leu Glu Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser
                165                 170                 175
Asn Thr Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln
            180                 185                 190
Phe Asn Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile
        195                 200                 205
Leu Lys His Ser Lys Ser Gly Ile Lys Gly
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...401
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```
CTATATGAAC AAAGCCTTAA AAGACTTGAA AAAAGGAATA ACTCATACCT ATG CGA      56
                                                          Met Arg
```

1

```
AAC AAT AAA ACG CCT TTT TTG AGC GCG ATT TTT ACG GCA TCA ATT AGG      104
Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser Ile Arg
          5                  10                  15

GGT TAC CAA CGC TTT TTT TCG GCT TTC ACC CCT TCA AGC TGC CGG TTT      152
Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys Arg Phe
     20                  25                  30

TAC CCC ACT TGT TCC AAC TAC GCT CTG TGG TTG CTC TGT TTT GAA AGC      200
Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe Glu Ser
35                   40                  45                  50

CCT TTG AGC GCT ATG GGT AAG ATC GCT ATA AGG ATA CTC TCA TGC AAC      248
Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser Cys Asn
                55                  60                  65

CCT TTT TGC TCT GGG GGC ATT GCT TAC CCT ACT ACT CGC TTG AAA CGC      296
Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu Lys Arg
            70                  75                  80

CCA AGC CTG ATC CAA TCT CAT AAA GAT TCT AAT CGC AAT TTT AAA ACC      344
Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe Lys Thr
         85                  90                  95

ATC ACT TTT TGG CTC GTT CCC ACA AAA AGC CAC GCA ACT TAC TAC ATC      392
Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr Tyr Ile
    100                 105                 110

ATT AAG GTT TAATCACAAT GGATAAAAAC AACAATAATC TCCGCTTGAT TTTAGCGAT    450
Ile Lys Val
115

CGCT                                                                 454
```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```
Met Arg Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser
 1               5                  10                  15
Ile Arg Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys
            20                  25                  30
Arg Phe Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe
        35                  40                  45
Glu Ser Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser
    50                  55                  60
Cys Asn Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu
```

```
65                  70                  75                  80
Lys Arg Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe
                85                  90                  95
Lys Thr Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr
            100                 105                 110
Tyr Ile Ile Lys Val
        115
```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1100
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```
TTATAATAAG AAAGTTTTTA TTATTTTTAA TGCTATTTTA GGAGTTCATC  ATG AAA      56
                                                        Met Lys
                                                         1

AAA TCC ATT TTA TTG GGC GTT TGC TTG GCT TTT TCT TGC GCT CAT GCC      104
Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala His Ala
         5                  10                  15

CTA AAC GAT TTA GAA TTG ATC AAA AAA GCG AGG GAA AGC CAG CTA GAA      152
Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln Leu Glu
    20                  25                  30

CCC ATG CCT ATG GGC AAA GCG CTC AAA GAA TAC CAG ATT AAA AAG ACC      200
Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys Lys Thr
35                  40                  45                  50

AGA GAT GTG GGT ATT GGC ACC AAA AAC AGC GAA ATC ATG ACC TCC GCT      248
Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr Ser Ala
                55                  60                  65

CAA GTG GAA TTA GGC AAA ATG CTC TAT TTT GAC CCT AGG ATT TCC ACT      296
Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile Ser Thr
            70                  75                  80

TCC TAC CTC GTG TCT TGC AAC ACA TGC CAT AAT CTG GGC TTA GGC GGG      344
Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu Gly Gly
        85                  90                  95

GTG GAT TTA GTC CCA AGC GCC ATA GGC TCT CAA TGG AAG AAA AAC CCC      392
Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys Asn Pro
    100                 105                 110
```

```
CAC CTT TTA AGC TCC CCA ACG GTG TAT AAC TCT GTG TTT AAC GAT GTG      440
His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn Asp Val
115                 120                 125                 130

CAG TTT TGG GAT GGC AGG GTT ACG CAT TTA AAC GAA CAG GCG CAA GGG      488
Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala Gln Gly
                135                 140                 145

CCC ATC CAG TCT TCT TTT GAA ATG GGG GCT GAT CCC AAA GTG GTG GTA      536
Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val Val Val
            150                 155                 160

GAA AAA ATC AAT TCC ATG CCA GGC TAT GTC AAG CTC TTT AGA AAA GCC      584
Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg Lys Ala
        165                 170                 175

TAT GGC TCT AAA GTC AAA ATT GAT TTT AAA TTG ATC GCT GAT AGT ATC      632
Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp Ser Ile
    180                 185                 190

GCT ATG TTT GAA GCC ACG CTT ATT ACC CCA AGC CGT TAC GAC GAT TTT      680
Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp Asp Phe
195                 200                 205                 210

TTA AGA GGC AAT CCT AAA GCG CTC AGC AAA GCC GAA AAA GAG GGG CTG      728
Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu Gly Leu
                215                 220                 225

AAT TTA TTC ATT TCT AAA GGC TGT GTG GCT TGC CAT AAC GGC ATT AAT      776
Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly Ile Asn
            230                 235                 240

CTT GGG GGA ACG ATG CAG CCT TTT GGG GTG GTC AAA CCT TAT AAA TTC      824
Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr Lys Phe
        245                 250                 255

GCT AAT GTG GGC GAT TTC AAA GGC GAT AAA AAC GGG CTT GTG AAA GTG      872
Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val Lys Val
    260                 265                 270

CCT ACT TTA AGG AAT ATC ACC GAA ACG ATG CCC TAT TTC CAT AAC GGG      920
Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His Asn Gly
275                 280                 285                 290

CAA TTC TGG GAT GTT AAG GAT GCG ATT AAA GAA ATG GGC TCT ATC CAG      968
Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser Ile Gln
                295                 300                 305

TTA GGC ATT GAA ATC AGC GAT GAA GAA GCG AAA AAA ATT GAA ACT TTC     1016
Leu Gly Ile Glu Ile Ser Asp Glu Glu Ala Lys Lys Ile Glu Thr Phe
            310                 315                 320

TTT GGA GCC TTA AGG GGT AAA AAA CCT AAA ATA ATC TAC CCA GAA CTC     1064
Phe Gly Ala Leu Arg Gly Lys Lys Pro Lys Ile Ile Tyr Pro Glu Leu
        325                 330                 335

CCC ATA ATG ACA GAC AAA ACC CCT AAA CCC TCT TTT TGATTTAAAA AAGTCC   1116
Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe
```

340 345 350

TTTTAGGGGT CTTTGGCGCT AAATCTAAAA AATACTC 1153

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```
Met Lys Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala
 1               5                  10                  15
His Ala Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln
            20                  25                  30
Leu Glu Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys
        35                  40                  45
Lys Thr Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr
    50                  55                  60
Ser Ala Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile
65                  70                  75                  80
Ser Thr Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu
                85                  90                  95
Gly Gly Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys
            100                 105                 110
Asn Pro His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn
        115                 120                 125
Asp Val Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala
    130                 135                 140
Gln Gly Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val
145                 150                 155                 160
Val Val Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg
                165                 170                 175
Lys Ala Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp
            180                 185                 190
Ser Ile Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp
        195                 200                 205
Asp Phe Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu
    210                 215                 220
Gly Leu Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly
225                 230                 235                 240
Ile Asn Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr
                245                 250                 255
Lys Phe Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val
            260                 265                 270
Lys Val Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His
        275                 280                 285
Asn Gly Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser
    290                 295                 300
Ile Gln Leu Gly Ile Glu Ile Ser Asp Glu Glu Ala Lys Lys Ile Glu
305                 310                 315                 320
Thr Phe Phe Gly Ala Leu Arg Gly Lys Lys Pro Lys Ile Ile Tyr Pro
```

```
                325                 330                 335
Glu Leu Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...374
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```
GTTAGAGATT TCTCCCAATT CTCAAGTGGG AGCGAGCGTG AAAATCCGCT ATG AAA      56
                                                          Met Lys
                                                            1

GCA ATC TTT AGC CTC TTT TTC CTT CTT ATT GTT TTA AAA GCA AAC CCC     104
Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala Asn Pro
          5                  10                  15

ATA AAC CCT TTA TTA GAG CCG TTA TAT TTC CCC AGT TAC GCG CAA TTT     152
Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala Gln Phe
     20                  25                  30

TTA AAC TTA GCA CCT CAC TTT GTC ATT AAA AAA AAG CGC GCT TAT AGA     200
Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala Tyr Arg
35                   40                  45                  50

CCC TTT CAA TGG GGG AAT ACC ATT ATC ATC AAA CGC CAT GAT TTA GAA     248
Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp Leu Glu
                55                  60                  65

GAA CGC CAA AGC AAC CAG CCA AGC GAT ATT TTC CGC CAA AAC GCT GAA     296
Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn Ala Glu
            70                  75                  80

ATC AAT GTG TCT TCT CAA ACT TTT TTA AAA GGA ATG AGC AAC GCT TCT     344
Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn Ala Ser
        85                  90                  95

TCA CGA ACA GTG CTT GAT TCA GCC GCT CAG TAAAATGCTA AAACTTTTTT TAA   397
Ser Arg Thr Val Leu Asp Ser Ala Ala Gln
    100                 105

TCACATTTTT CTTGGTATTT TCTTAATCC                                    426
```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```
Met Lys Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala
 1               5                  10                  15
Asn Pro Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala
            20                  25                  30
Gln Phe Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala
        35                  40                  45
Tyr Arg Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp
    50                  55                  60
Leu Glu Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn
65                  70                  75                  80
Ala Glu Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn
                85                  90                  95
Ala Ser Ser Arg Thr Val Leu Asp Ser Ala Ala Gln
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...746
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```
AGCGTGAGCC CAATTACGCC ACGCCTATGT CTAGATAGGG GAGGTTGGAA ATG TTT      56
                                                          Met Phe
                                                            1

AGT TTT TTA GAA AAA AAC CCG TTC TTT TTC ACT CTT GCG TTT ATT TTT     104
Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe Ile Phe
        5                  10                  15

GTG TTT GCG ATC GCG GGC TTG GTG GAG ATT TTG CCC AAC TTC TTC AAA     152
Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe Phe Lys
    20                  25                  30

TCC GCT CGC CCG ATT GAA GGC TTA CGG CCT TAT ACG GTT TTA GAG ACA     200
```

```
Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu Glu Thr
35                  40                  45                  50

GCG GGG AGG CAA ATT TAT ATC CAA GAA GGT TGC TAT CAT TGC CAT TCC      248
Ala Gly Arg Gln Ile Tyr Ile Gln Glu Gly Cys Tyr His Cys His Ser
                55                  60                  65

CAG CTT ATT CGC CCT TTC CAA GCT GAG GTG GAT CGA TAT GGC GCG TAT      296
Gln Leu Ile Arg Pro Phe Gln Ala Glu Val Asp Arg Tyr Gly Ala Tyr
            70                  75                  80

AGT TTG AGT GGG GAA TAC GCG TAT GAC AGG CCA TTT TTG TGG GGT TCT      344
Ser Leu Ser Gly Glu Tyr Ala Tyr Asp Arg Pro Phe Leu Trp Gly Ser
        85                  90                  95

AAA AGG ATT GGC CCT GAT TTG CAC AGG GTA GGG GAT TAT CGC ACA ACC      392
Lys Arg Ile Gly Pro Asp Leu His Arg Val Gly Asp Tyr Arg Thr Thr
    100                 105                 110

GAT TGG CAT GAA AAG CAC ATG TTT GAT CCT AAA AGC GTT GTG CCG CAC      440
Asp Trp His Glu Lys His Met Phe Asp Pro Lys Ser Val Val Pro His
115                 120                 125                 130

AGC ATC ATG CCC GCC TAT AAG CAT TTA TTT ACA AAA AAG AGC GAT TTT      488
Ser Ile Met Pro Ala Tyr Lys His Leu Phe Thr Lys Lys Ser Asp Phe
                135                 140                 145

GAC ACC GCT TAT GCA GAA GCT TTG ACG CAA AAA AAG GTT TTT GGC GTG      536
Asp Thr Ala Tyr Ala Glu Ala Leu Thr Gln Lys Lys Val Phe Gly Val
            150                 155                 160

CCT TAT GAC ACA GAA AAC GGC GTG AAA TTA GGG AGC GTA GAA GAA GCG      584
Pro Tyr Asp Thr Glu Asn Gly Val Lys Leu Gly Ser Val Glu Glu Ala
        165                 170                 175

AAA AAA GCC TAT TTA GAA GAA GCT AAA AAA ATC ACA GCC GAT ATG AAA      632
Lys Lys Ala Tyr Leu Glu Glu Ala Lys Lys Ile Thr Ala Asp Met Lys
    180                 185                 190

GAC AAG AGG GTG CTA GAA GCG ATT GAG AGA GGT GAA GTG TTA GAA ATT      680
Asp Lys Arg Val Leu Glu Ala Ile Glu Arg Gly Glu Val Leu Glu Ile
195                 200                 205                 210

GTG GCT TTG ATC GCT TAT TTG AAT AGC TTG GGT AAT TCC AGG ATC AAC      728
Val Ala Leu Ile Ala Tyr Leu Asn Ser Leu Gly Asn Ser Arg Ile Asn
                215                 220                 225

GCC AAT CAA AAC GCT AAA TAAGGGGTGA ATGATGGATT TAGAAAGTTT GAGAGGTT    784
Ala Asn Gln Asn Ala Lys
            230

TTGCGTATGC GTTTT                                                    799
```

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

```
Met Phe Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe
 1               5                  10                  15
Ile Phe Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe
            20                  25                  30
Phe Lys Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu
        35                  40                  45
Glu Thr Ala Gly Arg Gln Ile Tyr Ile Gln Glu Gly Cys Tyr His Cys
    50                  55                  60
His Ser Gln Leu Ile Arg Pro Phe Gln Ala Glu Val Asp Arg Tyr Gly
65                  70                  75                  80
Ala Tyr Ser Leu Ser Gly Glu Tyr Ala Tyr Asp Arg Pro Phe Leu Trp
                85                  90                  95
Gly Ser Lys Arg Ile Gly Pro Asp Leu His Arg Val Gly Asp Tyr Arg
            100                 105                 110
Thr Thr Asp Trp His Glu Lys His Met Phe Asp Pro Lys Ser Val Val
        115                 120                 125
Pro His Ser Ile Met Pro Ala Tyr Lys His Leu Phe Thr Lys Lys Ser
    130                 135                 140
Asp Phe Asp Thr Ala Tyr Ala Glu Ala Leu Thr Gln Lys Lys Val Phe
145                 150                 155                 160
Gly Val Pro Tyr Asp Thr Glu Asn Gly Val Lys Leu Gly Ser Val Glu
                165                 170                 175
Glu Ala Lys Lys Ala Tyr Leu Glu Glu Ala Lys Lys Ile Thr Ala Asp
            180                 185                 190
Met Lys Asp Lys Arg Val Leu Glu Ala Ile Glu Arg Gly Glu Val Leu
        195                 200                 205
Glu Ile Val Ala Leu Ile Ala Tyr Leu Asn Ser Leu Gly Asn Ser Arg
    210                 215                 220
Ile Asn Ala Asn Gln Asn Ala Lys
225                 230
```

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...269
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```
CTTGGGTAAT TCCAGGATCA ACGCCAATCA AAACGCTAAA TAAGGGGTGA ATG ATG      56
                                                        Met Met
                                                          1

GAT TTA GAA AGT TTG AGA GGT TTT GCG TAT GCG TTT TTT ACC ATT CTT     104
Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr Ile Leu
         5                  10                  15

TTT ACG CTC TTT TTG TAT GCC TAT ATT TTT AGC ATG TAT AGA AAG CAA     152
Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg Lys Gln
    20                  25                  30

AAA AAA GGC ATT ATG GAT TAT GAG CGA TAC GGA TAC TTA GCG TTA AAT     200
Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala Leu Asn
35                  40                  45                  50

GAT GCT TTA GAA GAC GAG TTG ATT GAA CCA CGC CAT AAA AAA GTT CAT     248
Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys Val His
                55                  60                  65

GAT AAT GGC ATA AAG GAA AGT TGAAATGGAT TTTTTAAACG ACCATATAAA TGTT  303
Asp Asn Gly Ile Lys Glu Ser
            70

TTTGGCTTGA TTGCAGCGC                                               322
```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```
Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr
 1               5                  10                  15
Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg
            20                  25                  30
Lys Gln Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala
        35                  40                  45
Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys
    50                  55                  60
Val His Asp Asn Gly Ile Lys Glu Ser
65                  70
```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...968
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```
TTACTGATTT TTCTTTGTGT GAGCTTTGGC TTAGTTTTGT AAGGAATGAG ATG ATA      56
                                                          Met Ile
                                                            1

AAG AGT TGG ACT AAA AAG TGG TTT TTG ATT TTA TTT TTA ATG GCA AGT      104
Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser
        5                  10                  15

TGT TCC AGT TAT TTG GTG GCT ACA ACC GGT GAG AAA TAT TTT AAA ATG      152
Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met
    20                  25                  30

GCT ACT CAA GCC TTT AAG AGA GGG GAC TAC CAT AAA GCG GTG GCT TTT      200
Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe
35                  40                  45                  50

TAT AAG AGG AGC TGT AAT TTA AGG GTG GGG GTT GGT TGC ACG AGT TTA      248
Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu
                55                  60                  65

GGC TCT ATG TAT GAA GAT GGC GAT GGC GTG GAT CAG AAT ATT ACA AAA      296
Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys
            70                  75                  80

GCC GTT TTT TAT TAC AGA AGA GGG TGT AAT TTA AGG AAT CAT CTC GCT      344
Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala
        85                  90                  95

TGC GCG AGT CTA GGC TCT ATG TAT GAA GAT GGC GAT GGT GTG CAA AAA      392
Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys
    100                 105                 110

AAC CTT CCA AAG GCT ATC TAT TAT TAC AGG AGA GGG TGC CAC TTA AAG      440
Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys
115                 120                 125                 130

GGT GGG GTG AGC TGT GGG AGT TTA GGT TTT ATG TAT TTT AAT GGC ACG      488
Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr
                135                 140                 145

GGC GTT AAG CAA AAT TAT GCC AAA GCC CTT TTT CTT TCT AAA TAC GCT      536
Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala
            150                 155                 160

TGC AGT TTG AAT TAC GGC ATT AGT TGT AAC TTT GTA GGG TAT ATG TAT      584
Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr
        165                 170                 175
```

```
AGG AAC GCC AAA GGC GTA CAG AAG GAT TTG AAA AAA GCC CTT GCG AAT      632
Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn
    180                 185                 190

TTT AAA AGA GGG TGC CAT TTG AAA GAC GGA GCG AGT TGT GTG AGC TTG      680
Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu
195                 200                 205                 210

GGA TAC ATG TAT GAA GTC GGT ATG GAT GTC AAA CAA AAT GGA GAG CAA      728
Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln
                215                 220                 225

GCC TTG AAT CTT TAT AAA AAG GGT TGT TAT TTA AAA AGG GGG AGC GGT      776
Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly
            230                 235                 240

TGT CAT AAT GTG GCG GTG ATG TAT TAC ACC GGT AAG GGC GTT CCA AAG      824
Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys
        245                 250                 255

GAT TTA GAT AAA GCC ATT TCG TAT TAT AAG AAA GGT TGC ACT CTA GGC      872
Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly
    260                 265                 270

TTT AGT GGT AGC TGT AAA GTG TTA GAA GAA GTG ATT GGC AAG AAG TCT      920
Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser
275                 280                 285                 290

GAT GAT TTG CAA GAT GAC GCG CAA AAC GAC ACG CAA GAT GAT ATG CAA T    969
Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln
                295                 300                 305

AAGTTAAAGC TTATGGACTA ATGATTAAAA CTCATCTTAT AGAAATCTTT CT          1021
```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```
Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met
 1               5                  10                  15
Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe
            20                  25                  30
Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val
        35                  40                  45
Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr
    50                  55                  60
Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile
65                  70                  75                  80
Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His
```

```
                85                  90                  95
Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val
            100                 105                 110
Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His
        115                 120                 125
Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn
    130                 135                 140
Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys
145                 150                 155                 160
Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr
                165                 170                 175
Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu
            180                 185                 190
Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val
        195                 200                 205
Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly
    210                 215                 220
Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly
225                 230                 235                 240
Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val
                245                 250                 255
Pro Lys Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr
            260                 265                 270
Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys
        275                 280                 285
Lys Ser Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp
    290                 295                 300
Met Gln
305
```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...947
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```
CTATAATGTG AATTTAATGA TGAAAATTAG TTTAGAGTGG AGAACACACA ATG AAA      56
                                                          Met Lys
                                                            1

AAA AAT ATC TTA AAT TTA GCG TTA GTG GGT GCG TTG AGC ACG TCG TTT     104
Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr Ser Phe
  5                  10                  15

TTG ATG GCT AAG CCG GCT CAT AAC GCA AAT AAC GCT ACG CAT AAC ACG     152
```

```
Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His Asn Thr
    20                  25                  30

AAA AAA ACG ACT GAT TCT TCA GCA GGC GTG TTA GCG ACA GTG GAT GGC      200
Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val Asp Gly
35                  40                  45                  50

AGA CCT ATC ACT AAA AGC GAT TTT GAC ATG ATT AAG CAA CGA AAT CCT      248
Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg Asn Pro
                55                  60                  65

AAT TTT GAT TTT GAC AAG CTT AAA GAG AAA GAA AAA GAA GCC TTG ATT      296
Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala Leu Ile
            70                  75                  80

GAT CAA GCT ATT CGC ACC GCC CTT GTA GAA AAT GAA GCT AAA ACC GAG      344
Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys Thr Glu
        85                  90                  95

AAA TTG GAC AGC ACT CCA GAA TTT AAA GCG ATG ATG GAA GCG GTT AAA      392
Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala Val Lys
    100                 105                 110

AAA CAG GCT TTA GTG GAA TTT TGG GCT AAA AAA CAG GCT GAA GAA GTG      440
Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu Glu Val
115                 120                 125                 130

AAA AAA GTC CAA ATC CCA GAA AAA GAA ATG CAA GAT TTT TAC AAC GCT      488
Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr Asn Ala
                135                 140                 145

AAC AAA GAT CAG CTT TTT GTC AAG CAA GAA GCC CAT GCT AGG CAT ATT      536
Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg His Ile
            150                 155                 160

TTA GTG AAA ACC GAA GAT GAG GCT AAA CGG ATT ATT TCT GAG ATT GAC      584
Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu Ile Asp
        165                 170                 175

AAA CAG CCA AAG GCT AAA AAA GAA GCT AAA TTC ATT GAG TTA GCC AAT      632
Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu Ala Asn
    180                 185                 190

CGG GAT ACG ATT GAT CCT AAC AGC AAG AAC GCG CAA AAT GGC GGT GAT      680
Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly Gly Asp
195                 200                 205                 210

TTG GGG AAA TTC CAA AAG AAC CAA ATG GCT CCG GAT TTT TCT AAA GCC      728
Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser Lys Ala
                215                 220                 225

GCT TTC GCT TTA ACT CCT GGG GAT TAC ACT AAA ACC CCT GTT AAA ACA      776
Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val Lys Thr
            230                 235                 240

GAG TTT GGT TAT CAT ATT ATC TAT TTG ATT TCT AAA GAT AGC CCT GTA      824
Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser Pro Val
        245                 250                 255
```

```
ACT TAT ACT TAT GAA CAG GCT AAA CCT ACC ATT AAG GGG ATG TTA CAA      872
Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met Leu Gln
    260                 265                 270

GAA AAG CTT TTC CAA GAA CGC ATG AAT CAA CGC ATT GAG GAA CTA AGA      920
Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu Leu Arg
275                 280                 285                 290

AAG CAC GCT AAA ATT GTT ATC AAC AAG TAATTGATGA GGTGTTATCA TGTTAGT    974
Lys His Ala Lys Ile Val Ile Asn Lys
                295

TAAAGGCAAT GAAATTTTAT TGAAAG                                        1000
```

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```
Met Lys Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr
 1               5                  10                  15
Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His
            20                  25                  30
Asn Thr Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val
        35                  40                  45
Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg
    50                  55                  60
Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala
65                  70                  75                  80
Leu Ile Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys
                85                  90                  95
Thr Glu Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala
            100                 105                 110
Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu
        115                 120                 125
Glu Val Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr
    130                 135                 140
Asn Ala Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg
145                 150                 155                 160
His Ile Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu
                165                 170                 175
Ile Asp Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu
            180                 185                 190
Ala Asn Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly
        195                 200                 205
Gly Asp Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser
    210                 215                 220
Lys Ala Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val
225                 230                 235                 240
Lys Thr Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser
```

```
                245                 250                 255
Pro Val Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met
            260                 265                 270
Leu Gln Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu
        275                 280                 285
Leu Arg Lys His Ala Lys Ile Val Ile Asn Lys
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...323
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```
CAGCGTTGGT GTATTTTGGA GGAAGTTAGG AAAATATTGA AGGAGTATTG ATG AAA      56
                                                        Met Lys
                                                          1

AAG GTT GTT TTT TTA TTG TTA GTT ATA CTA GGG GGT TTA GAA GCG CAA     104
Lys Val Val Phe Leu Leu Leu Val Ile Leu Gly Gly Leu Glu Ala Gln
          5                  10                  15

AGT ACT TAT TGC AGT GAT CAT TGC GAA GGC ACG CCA GAT AGC CGT ATC     152
Ser Thr Tyr Cys Ser Asp His Cys Glu Gly Thr Pro Asp Ser Arg Ile
     20                  25                  30

CCT CCT ATG GGG TTT CAT TTC AGT TTT GTG CAT TCA GTG AAA TAT TAC     200
Pro Pro Met Gly Phe His Phe Ser Phe Val His Ser Val Lys Tyr Tyr
35                  40                  45                  50

TTG CAA GAT CCG CAA GAG CGC GAT CAC AAG CTT GAA AAA TGC CAT CAA     248
Leu Gln Asp Pro Gln Glu Arg Asp His Lys Leu Glu Lys Cys His Gln
                55                  60                  65

GCC TTT GAT TCG ACT CTT AAG GTT AAT TTT ATT ACG AAT CTT TTA AAA     296
Ala Phe Asp Ser Thr Leu Lys Val Asn Phe Ile Thr Asn Leu Leu Lys
            70                  75                  80

AGG ATT GCA AGC ATG CGC AAA TGG CTT TAGAGCAAGC CCAAAAAGGG ACTCCAT   350
Arg Ile Ala Ser Met Arg Lys Trp Leu
        85                  90

AAAAGGGGTT TCTTTAGGGA TTTTAT                                       376
```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```
Met Lys Lys Val Val Phe Leu Leu Leu Val Ile Leu Gly Gly Leu Glu
 1               5                  10                  15
Ala Gln Ser Thr Tyr Cys Ser Asp His Cys Glu Gly Thr Pro Asp Ser
            20                  25                  30
Arg Ile Pro Pro Met Gly Phe His Phe Ser Phe Val His Ser Val Lys
        35                  40                  45
Tyr Tyr Leu Gln Asp Pro Gln Glu Arg Asp His Lys Leu Glu Lys Cys
    50                  55                  60
His Gln Ala Phe Asp Ser Thr Leu Lys Val Asn Phe Ile Thr Asn Leu
65                  70                  75                  80
Leu Lys Arg Ile Ala Ser Met Arg Lys Trp Leu
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1127
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
TTTTTAGTTA TAATGGCGGA CACCATTAAA ATTAAAACAA AGGTTATTCA ATG AAG      56
                                                          Met Lys
                                                            1

GTA TTA TCT TAT TTG AAA AAT TTT TAT CTT TTT TTA GCG ATA GGA GCA     104
Val Leu Ser Tyr Leu Lys Asn Phe Tyr Leu Phe Leu Ala Ile Gly Ala
          5                  10                  15

ATT ATG CAA GCG AGT GAA AAC ATG GGA TCT CAA CAC CAA AAA ACC GAT     152
Ile Met Gln Ala Ser Glu Asn Met Gly Ser Gln His Gln Lys Thr Asp
     20                  25                  30

GAA AGA GTG ATT TAC TTG GCT GGG GGG TGT TTT TGG GGG CTA GAG GCG     200
Glu Arg Val Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Leu Glu Ala
35                  40                  45                  50
```

```
TAT ATG GAG AGG ATT TAT GGC GTC ATA GAC GCA AGC TCT GGT TAC GCT      248
Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly Tyr Ala
                55                  60                  65

AAC GGC AAG ACT TCA AGC ACG AAT TAT GAG AAA TTG CAT GAA AGT GAT      296
Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu Ser Asp
            70                  75                  80

CAT GCT GAA AGC GTG AAA GTC ATT TAT GAT CCT AAA AAA ATC AGT TTG      344
His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile Ser Leu
        85                  90                  95

GAC AAA TTG TTG CGT TAC TAT TTT AAG GTG GTT GAT CCG GTG AGC GTG      392
Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val Ser Val
    100                 105                 110

AAC AAG CAG GGT AAT GAT GTG GGC AGG CAG TAT CGC ACG GGG ATT TAT      440
Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly Ile Tyr
115                 120                 125                 130

TAT GTC AAT AGC GCG GAT AAA GAA GTG ATA GAT CAT GCC TTA AAA GCG      488
Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu Lys Ala
                135                 140                 145

TTA CAG AAA GAA GTG AAA GGT AAA ATC GCT ATT GAA GTA GAG CCT TTA      536
Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu Pro Leu
            150                 155                 160

AAA AAT TAT GTG AGG GCT GAA GAG TAT CAT CAG GAT TAT TTG AAG AAA      584
Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu Lys Lys
        165                 170                 175

CAC CCT AGT GGT TAT TGC CAT ATT GAT TTG AAA AAG GCG GAT GAA GTG      632
His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp Glu Val
    180                 185                 190

ATT GTG GAT GAC GAT AAA TAC ACC AAA CCT AGC GAT GAA GTT TTA AAG      680
Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val Leu Lys
195                 200                 205                 210

AAA AAA CTC ACC AAA CTC CAG TAT GAG GTT ACG CAA AAC AAA CAC ACT      728
Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys His Thr
                215                 220                 225

GAG AAA CCC TTT GAA AAC GAG TAT TAC AAC AAA GAA GAA GAG GGC ATT      776
Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu Gly Ile
            230                 235                 240

TAT GTG GAT ATT ACC ACA GGC GAG CCG TTA TTT TCT TCA GCG GAT AAA      824
Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala Asp Lys
        245                 250                 255

TAC GAC TCC GGT TGC GGG TGG CCA AGC TTT TCT AAG CCT ATC AAT AAA      872
Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile Asn Lys
    260                 265                 270

GAT GTG GTG AAA TAC GAA GAC GAT GAG AGC CTT AAT AGG AAA CGC ATT      920
Asp Val Val Lys Tyr Glu Asp Asp Glu Ser Leu Asn Arg Lys Arg Ile
```

```
275                 280                 285                 290

GAA GTG TTG AGC CGT ATT GGT AAG GCG CAT TTA GGG CAT GTG TTT AAC     968
Glu Val Leu Ser Arg Ile Gly Lys Ala His Leu Gly His Val Phe Asn
                295                 300                 305

GAT GGG CCT AAA GAA TTA GGG GGC TTA AGG TAT TGC ATC AAC AGC GCG    1016
Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn Ser Ala
            310                 315                 320

GCT TTA AGG TTT ATC CCC TTA AAA GAC ATG GAA AAA GAG GGT TAT GGC    1064
Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly Tyr Gly
        325                 330                 335

GAG TTT ATC CCT TAT ATC AAA AAG GGT GAA TTG AAA AAA TAC ATC AAT    1112
Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr Ile Asn
    340                 345                 350

GAT AAA AAG TCG CAT TAAGGGGTAA TGACTAAGCC CCCTAAGGGG GGTTAAAATG A  1168
Asp Lys Lys Ser His
355

GGGGTTTAAG CG                                                      1180
```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```
Met Lys Val Leu Ser Tyr Leu Lys Asn Phe Tyr Leu Phe Leu Ala Ile
 1               5                  10                  15
Gly Ala Ile Met Gln Ala Ser Glu Asn Met Gly Ser Gln His Gln Lys
            20                  25                  30
Thr Asp Glu Arg Val Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Leu
        35                  40                  45
Glu Ala Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly
    50                  55                  60
Tyr Ala Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu
65                  70                  75                  80
Ser Asp His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile
                85                  90                  95
Ser Leu Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val
            100                 105                 110
Ser Val Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly
        115                 120                 125
Ile Tyr Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu
    130                 135                 140
Lys Ala Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu
145                 150                 155                 160
Pro Leu Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu
```

```
                 165                 170                 175
Lys Lys His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp
            180                 185                 190
Glu Val Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val
        195                 200                 205
Leu Lys Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys
    210                 215                 220
His Thr Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu
225                 230                 235                 240
Gly Ile Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala
                245                 250                 255
Asp Lys Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile
            260                 265                 270
Asn Lys Asp Val Val Lys Tyr Glu Asp Asp Glu Ser Leu Asn Arg Lys
        275                 280                 285
Arg Ile Glu Val Leu Ser Arg Ile Gly Lys Ala His Leu Gly His Val
    290                 295                 300
Phe Asn Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn
305                 310                 315                 320
Ser Ala Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly
                325                 330                 335
Tyr Gly Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr
            340                 345                 350
Ile Asn Asp Lys Lys Ser His
        355
```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 898 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...845
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
TTATTTCTTA TTATTGTAAG GATTTAGGCT ATTGAACTTT AGGAGTTTTA ATG ATA      56
                                                          Met Ile
                                                            1

TTA AGA GCG AGT GTG TTG AGC GCG TTA CTT CTT GTA GGC TTA GGG GCA     104
Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu Gly Ala
          5                  10                  15

GCC CCT AAA CAT TCA GTT TCA GCT AAT GAC AAA CGG ATG CAG GAT AAT     152
Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln Asp Asn
     20                  25                  30

TTA GTG AGC GTG ATT GAA AAA CAG ACC AAT AAA AAG GTG CGT ATT TTA     200
```

```
Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg Ile Leu
35                  40                  45                  50

GAA ATC AAA CCT TTA AAA TCT AGC CAG GAT TTA AAA ATG GTC GTT ATT      248
Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val Val Ile
                55                  60                  65

GAA GAT CCG GAC ACT AAA TAC AAT ATC CCG CTT GTG GTG AGT AAG GAT      296
Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser Lys Asp
            70                  75                  80

GGT AAT TTA ATC ATA GGG CTT AGC AAC ATA TTC TTT AGC AAT AAA AGC      344
Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn Lys Ser
        85                  90                  95

GAT GAT GTG CAA TTA GTT GCA GAA ACC AAT CAA AAA GTT CAA GCT CTT      392
Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln Ala Leu
    100                 105                 110

AAC GCC ACC CAA CAA AAT AGC GCG AAA TTG AAC GCT ATT TTT AAT GAA      440
Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe Asn Glu
115                 120                 125                 130

ATA CCG GCT GAT TAT GCG ATA GAG TTG CCC TCT ACT AAC GCT GCA AAT      488
Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala Ala Asn
                135                 140                 145

AAG GAT AAA ATC CTT TAT ATT GTC TCT GAT CCC ATG TGC CCA CAT TGC      536
Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro His Cys
            150                 155                 160

CAA AAA GAG CTC ACT AAA CTT AGG GAT CAT TTA AAA GAA AAC ACC GTG      584
Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn Thr Val
        165                 170                 175

AGA ATG GTC GTG GTG GGG TGG CTT GGG GTC AAT TCA GCT AAA AAA GCG      632
Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys Lys Ala
    180                 185                 190

GCT TTA ATC CAA GAA GAA ATG GCG AAA GCT AGG GCT AGG GGA GCG AGC      680
Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly Ala Ser
195                 200                 205                 210

GTG GAA GAT AAG ATC TCT ATT CTT GAA AAG ATT TAT TCC ACC CAA TAC      728
Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr Gln Tyr
                215                 220                 225

GAT ATT AAC GCT CAA AAA GAG CCT GAA GAT TTA CGC ACT AAA GTG GAA      776
Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys Val Glu
            230                 235                 240

AAT ACC ACT AAA AAG ATT TTT GAA TCT GGC GTG ATT AAG GGT GTG CCT      824
Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly Val Pro
        245                 250                 255

TTC TTA TAC CAT TAT AAG GCA TGATATAAGG TTGCTCTCAT GAAAAAACCC TATA    879
Phe Leu Tyr His Tyr Lys Ala
    260                 265
```

GGAAGATTTC TGATTATGC 898

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```
Met Ile Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu
 1               5                  10                  15
Gly Ala Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln
            20                  25                  30
Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg
        35                  40                  45
Ile Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val
    50                  55                  60
Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser
65                  70                  75                  80
Lys Asp Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn
                85                  90                  95
Lys Ser Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln
            100                 105                 110
Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe
        115                 120                 125
Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala
    130                 135                 140
Ala Asn Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro
145                 150                 155                 160
His Cys Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn
                165                 170                 175
Thr Val Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys
            180                 185                 190
Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly
        195                 200                 205
Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr
    210                 215                 220
Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys
225                 230                 235                 240
Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly
                245                 250                 255
Val Pro Phe Leu Tyr His Tyr Lys Ala
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 760 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...707
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```
TCTTTTAGAC GAAAACGCCA TGATTTTACA CTGGCAAAAA GAGGGCTTGC ATG CGT      56
                                                          Met Arg
                                                            1

AAA ATC TTG TTA TTG GGT CTG ATT TTA CAA GCG CTC TTC AGC GAA GAA     104
Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser Glu Glu
      5                  10                  15

GCC GCG CAA GAA TTG TTG CAA TGC TCT GCG ATT TTT GAA TCT AAA AAA     152
Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser Lys Lys
  20                  25                  30

GCC GAA TTG AAA GAC GAT TTG CGC CGA TTG AGT GAA AAA GAG CAG TCT     200
Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu Gln Ser
35                  40                  45                  50

TTA AGG ATC TTG CAA ACC GAA AAC GCC CGC CTT TTA GAT GAA AAA ACC     248
Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu Lys Thr
                55                  60                  65

GAT CTG TTG AAC CAA AAA GAA AAA GAA GTG GAA GAA AAA CTG AAA AAT     296
Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu Lys Asn
            70                  75                  80

TTA GCC GCT AAA GAA GAA GCC TTT AAA ACC TTA CAA ACG GAA GAA AAA     344
Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys
      85                  90                  95

AAA CGC CTT AAA AAT TTG ATA GAA GAA AAC GAA GGC ATT TTA AGA GAA     392
Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu
  100                 105                 110

ATC AAG CAG GCT AAA GAC AGC AAG ATT GGC GAG ACT TAT TCT AAA ATG     440
Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met
115                 120                 125                 130

AAA GAT TCT AAA TCG GCT CTG ATT TTA GAA AAT TTA CCC ACT CAA AAC     488
Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn
                135                 140                 145

GCA TTA GAA ATT TTA ATG GCG CTA AAA CCC CAA GAA CTC GGT AAA ATT     536
Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly Lys Ile
            150                 155                 160

TTA GCC AAA ATG GAT CCT AAA AAA GCG GCG GCT TTG ACA GAG TTG TGG     584
Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu Leu Trp
      165                 170                 175
```

```
CAA AAA CCC CCA AAA GAA AAT AAA GAA ATC CCA AAA ACC ACA GCA CCC      632
Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr Ala Pro
    180                 185                 190

ACG CCC CCT ATA GCA CCC ACG CCT TTA AAA GAG CCG ATG ATA AAA GAT      680
Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile Lys Asp
195                 200                 205                 210

CCT AAC ACC AAA GAG CCT GCA GGG GTA TGATGTTCAT TGTAGCGGTT TTGATGC    734
Pro Asn Thr Lys Glu Pro Ala Gly Val
                215

TGGCGTTTTT AATCTTTGTC CATGAA                                        760
```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```
Met Arg Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser
 1               5                  10                  15
Glu Glu Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser
            20                  25                  30
Lys Lys Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu
        35                  40                  45
Gln Ser Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu
    50                  55                  60
Lys Thr Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu
65                  70                  75                  80
Lys Asn Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu
                85                  90                  95
Glu Lys Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu
            100                 105                 110
Arg Glu Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser
        115                 120                 125
Lys Met Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr
    130                 135                 140
Gln Asn Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly
145                 150                 155                 160
Lys Ile Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu
                165                 170                 175
Leu Trp Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr
            180                 185                 190
Ala Pro Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile
        195                 200                 205
Lys Asp Pro Asn Thr Lys Glu Pro Ala Gly Val
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1340
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```
CTAAAGTGCG CTAAAATTCA CTTCAGTGAT ACAAAAAAGG AAATAAAATA ATG AAT      56
                                                        Met Asn
                                                          1

ATT CAA ATA AAG AAA AGG TTT TTA GCA AAT TTG TTG CTT TTT AGC CTG     104
Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe Ser Leu
          5                  10                  15

TTT TGC CTT AAG GCT GAA ACC CTT TCA GAA GAT CAT CAA ATC CTG TTG     152
Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile Leu Leu
     20                  25                  30

AGT TCA GAC GCT TTC CAT AGA GGG GAT TTT GCT GCC GCT CAA AAA GGC     200
Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln Lys Gly
35                   40                  45                  50

TAT ATG AAT CTC TAT AAG CAA ACC AAT AAG GTG GTG TAT GCT AAA GAA     248
Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala Lys Glu
                55                  60                  65

GCG GCC ATT TCA GCG GCG AGC TTA GGG GAT ATT AAA ACC GCT ATG CAT     296
Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala Met His
          70                  75                  80

TTA GCC ATG CTC TAT CAA AAA ATC ACC AAT AAT CGT AAT GAT GTT TCT     344
Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp Val Ser
     85                  90                  95

ATC AAT AAG ATT TTA GTG GAT GGC TAT GCG CAA ATG GGG CAG ATT GAT     392
Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln Ile Asp
100                 105                 110

AAG GCG ATT GAA TTG CTG CAC AAA ATC CGT AAA GAA GAA AAG ACC ATA     440
Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys Thr Ile
115                 120                 125                 130

GCC ACA GAC AAT GTG TTA GGG ACT TTG TAT TTG ACT CAA AAG CGT TTG     488
Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys Arg Leu
                135                 140                 145

GAT AAG GCT TTC CCA TTG TTG AAT AAG TTT TAT AAC CAA GTG CAT GAT     536
```

```
Asp Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln Val His Asp
            150                 155                 160

GAA GAC AGC CTA GAA AAA CTC ATT ACG ATC TAT TTT TTG CAA AAT CGT      584
Glu Asp Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu Gln Asn Arg
        165                 170                 175

AAA AAA GAG GGC TTG GAT TTG TTG CAA TCT CAT ATA GAC AGG TAT GGT      632
Lys Lys Glu Gly Leu Asp Leu Leu Gln Ser His Ile Asp Arg Tyr Gly
    180                 185                 190

TGC TCA GAG CAA TTG TGC CAA AAA GCG CTC AAC ACT TTC ACG CAA TTT      680
Cys Ser Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe Thr Gln Phe
195                 200                 205                 210

AAC GAG CTT GAT TTG GCT AAA ACG ACT TTT GCT CGT TTG TAT GAA AAA      728
Asn Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr Glu Lys
                215                 220                 225

AAC CCT ATT GTT CAA AAT GCT CAG TTT TAC ATA GGG GTA TTA ATC TTG      776
Asn Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu Ile Leu
            230                 235                 240

TTA AAA GAG TTT GAT AAG GCC CAG AAA ATC GCA GAA TTA TTC CCT TTT      824
Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe Pro Phe
        245                 250                 255

GAC AGG CGT TTG TTG TTA GAC TTA TAC ACC GCA CAA AAA AAA TTC GAT      872
Asp Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys Phe Asp
    260                 265                 270

CAA GCT TCC AAA CAA GCT TCT TTG ATC TAT CAA GAA AAA AAA GAC CCT      920
Gln Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Lys Lys Asp Pro
275                 280                 285                 290

AAA TTC TTA GGA TTA GAG GCC ATT TAT CAT TAT GAA AGC TTG AGT GCG      968
Lys Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu Ser Ala
                295                 300                 305

AAT AAG AAA AAG CTC ACC AAA GAA GAG ATG TTG CCT ATC ATT CAA AAA     1016
Asn Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile Gln Lys
            310                 315                 320

TTA GAG CAA GCC ACC AAA GAG CGC CAA GCA TGG CTC GCT AAA ACC AAA     1064
Leu Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys Thr Lys
        325                 330                 335

GAT AAA GAA GAC GCG CAA GAC GCT TTC TTT TAT AAT TTT TTA GGG TAT     1112
Asp Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu Gly Tyr
    340                 345                 350

TCC TTA ATA GAT TAT GAC ATG GAT ATT AAA AGG GGC ATG GAT TTT GTG     1160
Ser Leu Ile Asp Tyr Asp Met Asp Ile Lys Arg Gly Met Asp Phe Val
355                 360                 365                 370

AGG AAA GCC TTA GCG TTG GAT TCT GGA TCA GTG CTT TAT TTG GAT TCT     1208
Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu Asp Ser
                375                 380                 385
```

```
TTA GCA TGG GGT TAT TAC AAA TTA GGG AAT TGT TTG GAA GCT AAA AAA    1256
Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala Lys Lys
            390                 395                 400

ATC TTT TCT AGC ATC GCT AAA GAG TCT ATC CAA GCC GAA CCT GAA TTG    1304
Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro Glu Leu
        405                 410                 415

AAA GAA CAC AAT AAA ATC ATT CAA GAA TGC AAG AAA TAGGGATTTT AGAAAA  1356
Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys
    420                 425                 430

TTTACAAAAA AGCTTAGCCT TAAAAGAGGG CATGCTT                          1393
```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```
Met Asn Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe
 1               5                  10                  15
Ser Leu Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile
            20                  25                  30
Leu Leu Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln
        35                  40                  45
Lys Gly Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala
    50                  55                  60
Lys Glu Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala
65                  70                  75                  80
Met His Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp
                85                  90                  95
Val Ser Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln
            100                 105                 110
Ile Asp Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys
        115                 120                 125
Thr Ile Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys
    130                 135                 140
Arg Leu Asp Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln Val
145                 150                 155                 160
His Asp Glu Asp Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu Gln
                165                 170                 175
Asn Arg Lys Lys Glu Gly Leu Asp Leu Leu Gln Ser His Ile Asp Arg
            180                 185                 190
Tyr Gly Cys Ser Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe Thr
        195                 200                 205
Gln Phe Asn Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr
    210                 215                 220
Glu Lys Asn Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu
225                 230                 235                 240
Ile Leu Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe
```

```
                245                 250                 255
Pro Phe Asp Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys
            260                 265                 270
Phe Asp Gln Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Lys Lys
        275                 280                 285
Asp Pro Lys Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu
    290                 295                 300
Ser Ala Asn Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile
305                 310                 315                 320
Gln Lys Leu Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys
                325                 330                 335
Thr Lys Asp Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu
            340                 345                 350
Gly Tyr Ser Leu Ile Asp Tyr Asp Met Asp Ile Lys Arg Gly Met Asp
        355                 360                 365
Phe Val Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu
    370                 375                 380
Asp Ser Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala
385                 390                 395                 400
Lys Lys Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro
                405                 410                 415
Glu Leu Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1090 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1037
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```
TTACCCTAAA ACGCTATTTT TAAAATAATC CATTAAAATA AAGGCGAGGA ATG AAA      56
                                                        Met Lys
                                                          1

AGA TTT GTT TTG TTT TTA TTG TTC ATG TGC GTT TGC GTT CAA GCT TAC     104
Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln Ala Tyr
  5                  10                  15

GCC GAG CAA GAT TAC TTT TTT AGG GAT TTT AAA TCT AGA GAT TTG CCC     152
Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp Leu Pro
    20                  25                  30

CAA AAA CTC CAT CTT GAT AAA AAG CTC TCC CAA ACA ATA CAG CCA TGC     200
Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln Pro Cys
35                  40                  45                  50
```

```
ATG CAA CTT AAC GCA TCA AAA CAC TAC ACT TCT ACC GGG GTT AGA GAG      248
Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val Arg Glu
                55                  60                  65

CCT GAT AAA TGC ACA AAG AGT TTT AAA AAA TCC GCT CTC ATG TCC TAT      296
Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met Ser Tyr
            70                  75                  80

GAC TTA GCG CTA GGT TAT TTG GTG AGT AAG AAT AAG CAA TAC GGC TTA      344
Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr Gly Leu
        85                  90                  95

AAG GCT ATA GAA ATT TTA AAC GCT TGG GCT AAA GAG CTT CAA AGC GTG      392
Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln Ser Val
    100                 105                 110

GAT ACT TAT CAG AGC GAG GAT AAT ATC AAT TTT TAC ATG CCT TAT ATG      440
Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro Tyr Met
115                 120                 125                 130

AAC ATG GCT TAT TGG TTT GTC AAA AAG GCG TTT CCT AGC CCA GAA TAT      488
Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro Glu Tyr
                135                 140                 145

GAA GAT TTC ATT AAG CGG ATG CGC CAG TAT TCT CAA TCA GCT CTT AAC      536
Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala Leu Asn
            150                 155                 160

ACT AAC CAT GGG GCG TGG GGC ATT CTT TTT GAT GTG AGT TCT GCG CTA      584
Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser Ala Leu
        165                 170                 175

GCG TTA GAC GAT AAT GCC CTT TTG CAC AAT AGC GCT AAT CGG TGG CAG      632
Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg Trp Gln
    180                 185                 190

GAG TGG GTG TTT AAA GCC ATA GAT GAG AAT GGG GTT ATT GNT AGC GCG      680
Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa Ser Ala
195                 200                 205                 210

ATC ACT AGG AGC GAT ACG AGC GAT TAT CAT GGC GGC CCT ACA AAG GGC      728
Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr Lys Gly
                215                 220                 225

ATT AAG GGG ATA GCT TAT ACC AAT TTC GCG CTT CTT GCG CTA ACC ATA      776
Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu Thr Ile
            230                 235                 240

TCA GGC GAA TTG CTT TTT GAG AAC GGG TAT GAT TTG TGG GGT AGT GGA      824
Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly Ser Gly
        245                 250                 255

GCT GGG AAA AGG CTC TCT GTG GCG TAT AAC AAA GTT GCA ACA TGG ATT      872
Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr Trp Ile
    260                 265                 270

TTA AAC CCT GAA ACT TTC CCT TAT TTC CAG CCT AAC CTT ATC GGG GTG      920
Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile Gly Val
```

```
275                 280                 285                 290

CAT AAC AAC GCC TAT TTC ATT ATT TTA GCC AAG CAT TAT TCT AGC CCT     968
His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser Ser Pro
                295                 300                 305

AGT GCA AAT GAG CTT TTA AAG CAA GGC GAT TTA CAC GAA GAT GGT TTC    1016
Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp Gly Phe
            310                 315                 320

AGG CTG AAA CTC CGA TCG CCA TGAATTTTTC TGTATCCAAG GTTAGCCTTA AGGA  1071
Arg Leu Lys Leu Arg Ser Pro
        325

TGGCCATGCG CTTTAACCT                                              1090
```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
Met Lys Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln
 1               5                  10                  15
Ala Tyr Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp
            20                  25                  30
Leu Pro Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln
        35                  40                  45
Pro Cys Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val
    50                  55                  60
Arg Glu Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met
65                  70                  75                  80
Ser Tyr Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr
                85                  90                  95
Gly Leu Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln
            100                 105                 110
Ser Val Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro
        115                 120                 125
Tyr Met Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro
    130                 135                 140
Glu Tyr Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala
145                 150                 155                 160
Leu Asn Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser
                165                 170                 175
Ala Leu Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg
            180                 185                 190
Trp Gln Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa
        195                 200                 205
Ser Ala Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr
    210                 215                 220
Lys Gly Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu
```

```
225                 230                 235                 240
Thr Ile Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly
                245                 250                 255
Ser Gly Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr
            260                 265                 270
Trp Ile Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile
        275                 280                 285
Gly Val His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser
    290                 295                 300
Ser Pro Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp
305                 310                 315                 320
Gly Phe Arg Leu Lys Leu Arg Ser Pro
                325
```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...320
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```
TTAACGATCG CAAAAGCCGA TGAAAGTTTT GATGAAATCA TAAAAGGTGT  GTG AAT      56
                                                        Val Asn
                                                         1

TTT TTG AAA AAG CCA AAG TAT TAT AAA TTC ATA GAG GGG GCG AAT TAT      104
Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala Asn Tyr
          5                  10                  15

TTG AGC TTG GGG CTT TCT ATG GTG GTA GCG ATC CTT ATG GGC GTG GCT      152
Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly Val Ala
     20                  25                  30

ATA GGC TAT GGG CTT AAA AAA CTC ACT CAT ATT TCG TGG CTT TTT TGG      200
Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu Phe Trp
35                  40                  45                  50

CTT GGG GTT ATT TGG GGC GTC TTA GCG AGC TTT CTC AAT GTC TAT AAA      248
Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu Asn Val Tyr Lys
                55                  60                  65

GCT TAT AAA AAC ATG CAA AAA GAC TAT GAA GAA CTA GCC AAA GAC CCT      296
Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu Ala Lys Asp Pro
            70                  75                  80

AAA TAC ACA CAA AAT AAA ACA AAA TAAATCCAAT CAAATCCCAT GTGCCAAATC     350
Lys Tyr Thr Gln Asn Lys Thr Lys
```

85 90

CAATGCTTGC TTATTTTACT TTC 373

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```
Val Asn Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala
 1               5                  10                  15
Asn Tyr Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly
            20                  25                  30
Val Ala Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu
        35                  40                  45
Phe Trp Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu Asn Val
    50                  55                  60
Tyr Lys Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu Ala Lys
65                  70                  75                  80
Asp Pro Lys Tyr Thr Gln Asn Lys Thr Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...590
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```
TTGGTTGGTT GTTTTTATCA TAGAGTGTAA TTTAAAATAA GGATCATTTG ATG TTA      56
                                                        Met Leu
                                                          1

AAC AAG TTT AAA AAA ATC GTT GGC GTT AGT GTG TTA GTG GGC TGT TTA     104
Asn Lys Phe Lys Lys Ile Val Gly Val Ser Val Leu Val Gly Cys Leu
 5                  10                  15

GGG GTT TTG CAA GCT AAA AAC AGC TTA TTT GTC TTA CCT TAT GAG CAA     152
```

```
Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr Glu Gln
    20                  25                  30

AAA GAC GCT CTC AAT TCT TTA GTT TCT GGC ATT AGT AAC GCC AGA GAG      200
Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala Arg Glu
35                  40                  45                  50

AGC GTG AAA ATC GCT ATC TAT AGT TTC ACG CAC AGA GAT ATT GCA AGA      248
Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile Ala Arg
                55                  60                  65

GCG ATT AAA AGC GTA GCG AGT AGG GGG ATT AAG GTG CAA ATC ATT TAT      296
Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile Ile Tyr
            70                  75                  80

GAT TAT GAA AGC AAT CAT CAT AAC AAG CAA TCC ACT ATT GGC TAT CTG      344
Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly Tyr Leu
        85                  90                  95

GAC AAA TAC CCT AAC ACG AAA GTG TGC TTA TTG AAA GGG CTT AAG GCT      392
Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu Lys Ala
    100                 105                 110

AAA AAC GGG AAT TAT TAC GGC ATC ATG CAC CAA AAA GTA GCG ATC ATT      440
Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala Ile Ile
115                 120                 125                 130

GAT GAT AAG ATC GTG TTT TTA GGC TCA GCG AAT TGG AGC AAA AAC GCT      488
Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys Asn Ala
                135                 140                 145

TTT GAA AAC AAT TAT GAA GTG CTT TTA AAA ACC GAT GAC ACA GAA ACG      536
Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr Glu Thr
            150                 155                 160

ATC CTC AAA GCC AAG AGC TAT TAC CAA AAG ATG TTA GGG AGT TGC GTT      584
Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser Cys Val
        165                 170                 175

GGG TTT TAAAAGCCCT TTAGAAGTGG TAATTATACC CCACATAAAA GGCAAAGACC CT    642
Gly Phe
    180

A                                                                    643
```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```
Met Leu Asn Lys Phe Lys Lys Ile Val Gly Val Ser Val Leu Val Gly
 1               5                  10                  15
Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr
            20                  25                  30
Glu Gln Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala
        35                  40                  45
Arg Glu Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile
    50                  55                  60
Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile
65                  70                  75                  80
Ile Tyr Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly
                85                  90                  95
Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu
            100                 105                 110
Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala
        115                 120                 125
Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys
    130                 135                 140
Asn Ala Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr
145                 150                 155                 160
Glu Thr Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser
                165                 170                 175
Cys Val Gly Phe
            180
```

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...761
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```
TATAAGAGAG TATAATTCAA GGCTTAAAAT AACTCAAGTA AGGCTAGTGG ATG AAA      56
                                                          Met Lys
                                                            1

AAA GCG CTT TAT TTA GGG GCT GTT GCG TTT AGC GTT GCA TTC AGC ATG     104
Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe Ser Met
  5                  10                  15

GCA TCA GCC AAT GAG CCA AAA ATT GAT TTT AAC CCT CCC AAT TAT GTA     152
Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn Tyr Val
    20                  25                  30

GAA GAA ACC CCC TCT AAA GAA TTT ATC CCT GAA TTG AAC AAG TTA GGG     200
Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys Leu Gly
```

```
35                  40                  45                  50

AGT TTG TTT GGG CAG GGT GAG CGC CCC TTG TTT GCG GAC AGG AGG GCG      248
Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg Arg Ala
                55                  60                  65

ATG AAG CCT AAC GAT TTG ATC ACA ATC ATT GTT TCT GAA AAA GCG AGC      296
Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys Ala Ser
            70                  75                  80

GCG AAT TAT TCC AGC TCT AAA GAT TAT AAA AGC GCT TCA GGG GGT AAT      344
Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly Gly Asn
        85                  90                  95

TCC ACG CCC CCA AGA CTC ACT TAT AAC GGG CTA GAT GAA AGA AAG AAA      392
Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg Lys Lys
    100                 105                 110

AAA GAA GCG GAG TAT TTA GAC GAT AAG AAT AAT TAC AAT TTC ACC AAA      440
Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe Thr Lys
115                 120                 125                 130

TCC AGC AAT AAC ACG AAT TTT AAA GGC GGT GGC TCG CAA AAA AAG AGC      488
Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys Lys Ser
                135                 140                 145

GAA GAT TTA GAG ATT GTG TTG AGC GCT CGA ATC ATT AAG GTG CTA GAA      536
Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val Leu Glu
            150                 155                 160

AAC GGG AAT TAT TTC ATC TAT GGG AAT AAG GAA GTG CTA GTG GAT GGG      584
Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val Asp Gly
        165                 170                 175

GAA AAG CAA ATC CTT AAG GTG AGT GGG GTG ATC CGC CCT TAT GAT ATT      632
Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr Asp Ile
    180                 185                 190

GAA AGG AAT AAC ACC ATC CAA TCC AAG TTT TTA GCC GAC GCT AAG ATT      680
Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala Lys Ile
195                 200                 205                 210

GAA TAC ACG AAT TTA GGG CAT TTG AGC GAT TCC AAT AAG AAG AAA TTC      728
Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys Lys Phe
                215                 220                 225

GCT GCT GAT GCG ATG GAA ACC CAA ATG CCT TAT TAAAAAGAGC AAAGCCTAGC    781
Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr
        230                 235

ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGT                                 814
```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```
Met Lys Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe
 1               5                  10                  15
Ser Met Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn
            20                  25                  30
Tyr Val Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys
        35                  40                  45
Leu Gly Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg
    50                  55                  60
Arg Ala Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys
65                  70                  75                  80
Ala Ser Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly
                85                  90                  95
Gly Asn Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg
            100                 105                 110
Lys Lys Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe
        115                 120                 125
Thr Lys Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys
    130                 135                 140
Lys Ser Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val
145                 150                 155                 160
Leu Glu Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val
                165                 170                 175
Asp Gly Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr
            180                 185                 190
Asp Ile Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala
        195                 200                 205
Lys Ile Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys
    210                 215                 220
Lys Phe Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 850 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...797
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```
TTGGGTAAGA TTAGGAATTG ATTTTAAAGA AAAAGAAAGA AAGGAATTTA ATG AAA      56
```

```
                                                                  Met Lys
                                                                    1

AAA GGT AGT TTG GCA ATC GTT TTA GGA TCG CTA TTA GCG AGT GGG GCG      104
Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser Gly Ala
          5                  10                  15

TTT TAT ACG GCT CTA GCT GAT GGA ATG CCT GCA AAA CAG CAG CAC AAT      152
Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln His Asn
     20                  25                  30

AAT ACG GGC GAG TCA GTG GAG TTG CAT TTC CAC TAT CCT ATT AAA GGC      200
Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile Lys Gly
35                   40                  45                  50

AAG CAA GAG CCT AAA AAC AGC CAT TTA GTC GTT TTG ATC GAA CCT AAA      248
Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu Pro Lys
                55                  60                  65

ATA GAG ATC AAT AAA GTT ATC CCT GAA AGT TAT CAA AAA GAG TTT GAG      296
Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu Phe Glu
           70                  75                  80

AAG TCT TTG TTT CTC CAG TTG AGT AGT TTT TTA GAG AGA AAA GGC TAT      344
Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys Gly Tyr
      85                  90                  95

AGC GTT TCG CAA TTT AAA GAT GCT AGC GAA ATC CCT CAA GAC ATC AAA      392
Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp Ile Lys
 100                 105                 110

GAA AAA GCG TTG CTC GTT TTA CGC ATG GAT GGG AAT GTG GCT ATC TTG      440
Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala Ile Leu
115                 120                 125                 130

GAA GAT ATT GTA GAA GAG AGC GAT GCG CTT AGC GAA GAA AAA GTG ATA      488
Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys Val Ile
                135                 140                 145

GAC ATG TCT TCA GGG TAT TTG AAC TTG AAT TTT GTT GAG CCA AAA AGT      536
Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro Lys Ser
           150                 155                 160

GAA GAT ATT ATC CAT AGT TTT GGT ATT GAT GTT TCA AAG ATT AAG GCT      584
Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile Lys Ala
      165                 170                 175

GTG ATT GAA AGA GTG GAA TTG CGG CGC ACC AAT TCT GGA GGT TTT GTC      632
Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly Phe Val
 180                 185                 190

CCC AAA ACT TTT GTG CAT AGG ATT AAG GAA ACC GAT CAT GAT CAA GCC      680
Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp Gln Ala
195                 200                 205                 210

ATT AGA AAA ATC ATG AAT CAA GCC TAT CAC AAA GTG ATG GTG CAT ATT      728
Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val His Ile
                215                 220                 225
```

```
ACC AAA GAG TTA AGC AAA AAA CAC ATG GAA CAT TAT GAA AAA GTT TCT      776
Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys Val Ser
            230                 235                 240

AGT GAA ATG AAA AAA CGA AAG TAGTTTTTAA GAAACGAAAA GCTTAAAAAT CATT    831
Ser Glu Met Lys Lys Arg Lys
        245

GAGAGCTATT TTTAAAAAA                                                 850
```

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```
Met Lys Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser
 1               5                  10                  15
Gly Ala Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln
            20                  25                  30
His Asn Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile
        35                  40                  45
Lys Gly Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu
    50                  55                  60
Pro Lys Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu
65                  70                  75                  80
Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys
                85                  90                  95
Gly Tyr Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp
            100                 105                 110
Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala
        115                 120                 125
Ile Leu Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys
    130                 135                 140
Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro
145                 150                 155                 160
Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile
                165                 170                 175
Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly
            180                 185                 190
Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp
        195                 200                 205
Gln Ala Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val
    210                 215                 220
His Ile Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys
225                 230                 235                 240
Val Ser Ser Glu Met Lys Lys Arg Lys
                245
```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...788
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```
TACAAATAGG TATAATCACC AATTCCAATC ATTTAATCAA AGGGAGTTCT ATG AAA      56
                                                         Met Lys
                                                           1

AAT ACT TTC AAA GCG TTT GCC TTT TTA ATT GTA TTT TTT TCA AGC GCT     104
Asn Thr Phe Lys Ala Phe Ala Phe Leu Ile Val Phe Phe Ser Ser Ala
          5                  10                  15

TTA TTA GCG CAG GAT TTA AAA ATC GCT GCT GCT GCT AAT CTT ACA CGC     152
Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn Leu Thr Arg
     20                  25                  30

GCT TTA AAA GCC CTT GTT AAA GAA TTT CAA AAA GAA CAC CCC AAA GAC     200
Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His Pro Lys Asp
35                   40                  45                  50

ACT GTT AAT ATT AGC TTT AAT TCT TCA GGC AAA CTC TAC GCT CAA ATC     248
Thr Val Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr Ala Gln Ile
                55                  60                  65

ATT CAA AAC GCC CCT TTT GAT TTA TTC ATT TCA GCA GAT ATG ATT AGA     296
Ile Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp Met Ile Arg
           70                  75                  80

CCT AAA AAG CTT TAT GAT AAA AAA ATA ACC CCT TTT AAA GAA GAA GTC     344
Pro Lys Lys Leu Tyr Asp Lys Lys Ile Thr Pro Phe Lys Glu Glu Val
      85                  90                  95

TAT GCT AAA GGC GTG TTG GTT TTA TGG AGT GAA GAT CTA AAA ATG GAT     392
Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asp Leu Lys Met Asp
 100                 105                 110

TCT TTA GAA ATT CTT AAA AAT CCT AAA ATC AAG CGT ATC GCT ATG GCT     440
Ser Leu Glu Ile Leu Lys Asn Pro Lys Ile Lys Arg Ile Ala Met Ala
115                 120                 125                 130

AAT CCT AAA CTA GCC CCT TAT GGA AAA GCC AGC ATG GAA GTC TTA GAG     488
Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Glu
                135                 140                 145

AAT TTA AAA CTC ACT CCC AGT CTT AAA TCT AAA ATC GTT TAT GGC GCT     536
```

```
Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr Gly Ala
            150                 155                 160

TCT ATT TCT CAA GCC CAT CAA TTT GTC GCT ACT AAA AAC GCT CAA ATA      584
Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala Gln Ile
        165                 170                 175

GGC TTT GGA GCG TTA TCC TTG ATG GAT AAA AAA GAT AAA AAC CTC TCT      632
Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn Leu Ser
    180                 185                 190

TAT TTC ATC ATT GAT AAA GCC CTT TAT AAC CCT ATT GAA CAA GCC TTG      680
Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln Ala Leu
195                 200                 205                 210

ATT ATC ACT AAA AAT GGG GCT AAC AAC CCT TTA GCC AAA GTC TTT AAA      728
Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys
                215                 220                 225

GAT TTT TTA TTC AGC CCT AAA GCC AGA GCT ATT TTT AAA GAA TAC GGC      776
Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly
            230                 235                 240

TAT ATT GTG GAT TAAAACGCAT AAAAAAGGCG AGCAATGGAT CATGAGTTTT TGATT    833
Tyr Ile Val Asp
        245

ACCATGCG                                                             841
```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```
Met Lys Asn Thr Phe Lys Ala Phe Ala Phe Leu Ile Val Phe Phe Ser
 1               5                  10                  15
Ser Ala Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn Leu
            20                  25                  30
Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His Pro
        35                  40                  45
Lys Asp Thr Val Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr Ala
    50                  55                  60
Gln Ile Ile Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp Met
65                  70                  75                  80
Ile Arg Pro Lys Lys Leu Tyr Asp Lys Lys Ile Thr Pro Phe Lys Glu
                85                  90                  95
Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asp Leu Lys
            100                 105                 110
Met Asp Ser Leu Glu Ile Leu Lys Asn Pro Lys Ile Lys Arg Ile Ala
        115                 120                 125
```

```
Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val
    130                 135                 140
Leu Glu Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr
145                 150                 155                 160
Gly Ala Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala
                165                 170                 175
Gln Ile Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn
            180                 185                 190
Leu Ser Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln
        195                 200                 205
Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val
    210                 215                 220
Phe Lys Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu
225                 230                 235                 240
Tyr Gly Tyr Ile Val Asp
                245
```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1406
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```
AGCCATTTTA TGGCATTTAA AAAAGTTTAA AAATGTTTAA AAGGAATTTT ATG TTA      56
                                                        Met Leu
                                                          1

AGG CTT TTG ATA GGA CTT CTT CTA ATG AGT TTT ATA AGC TTG CAA TCA     104
Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu Gln Ser
          5                  10                  15

GCC TCT TGG CAA GAA CCC TTA AGA GTG AGT ATA GAA TTT GTG GAT TTG     152
Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val Asp Leu
     20                  25                  30

CCT AAA AAA ATC ATT CGT TTT CCG GCT CAT GAT TTG CAA GTG GGG GAG     200
Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val Gly Glu
35                  40                  45                  50

TTT GGT TTT GTC GTT ACT AAA CTT TCA GAT TAT GAA ATC GTT AAT TCT     248
Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val Asn Ser
                55                  60                  65

GAA GTG GTC ATT ATT GCC GTT GAA AAT GGC GTC GCA ACG GCT AAA TTC     296
Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala Lys Phe
```

```
                70                  75                  80

AGA GCG TTT GAG TCT ATG AAA CAA AGG CAT TTA CCC ACT CCA AGA ATG      344
Arg Ala Phe Glu Ser Met Lys Gln Arg His Leu Pro Thr Pro Arg Met
        85                  90                  95

GTC GCT AGA AAG GGT GAT TTA GTC TAT TTT AGG CAA TTC AAC AAC CAA      392
Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn Asn Gln
    100                 105                 110

GCG TTT TTA ATC GCT CCT AAT GAT GAA CTC TAT GAG CAA ATC AGA GCG      440
Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile Arg Ala
115                 120                 125                 130

ACT AAC ACC GAT ATT AAT TTT ATT AGT TCT GAT TTG TTG GTT ACT TTT      488
Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val Thr Phe
                135                 140                 145

TTG AAT GGG TTT GAC CCA AAA ATC GCT AAT TTA AGG AAA GCG TGC AAC      536
Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala Cys Asn
            150                 155                 160

GTT TAT AGC GTG GGG GTG ATT TAT ATT GTA ACC ACC AAC ACG CTC AAT      584
Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr Leu Asn
        165                 170                 175

ATT TTA AGT TGT GAG AGT TTT GAA ATT TTA GAA AAA AGA GAG CTG GAT      632
Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu Leu Asp
    180                 185                 190

ACA AGC GGC GTT ACT AAA ACT TCC ACG CCG TTT TTT TCT AGG GTT GAG      680
Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg Val Glu
195                 200                 205                 210

GGT ATT GAT GCA GGC ACG CTA GGG AAA CTT TTT TCA GGC AGT CAG TCT      728
Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser Gln Ser
                215                 220                 225

AAA AAT TAC TTC GCT TAC TAT GAC GCT TTA GTG AAG AAA GAA AAA CGC      776
Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu Lys Arg
            230                 235                 240

AAA GAA GTG AGG ATT AAA AAG AGG GAA GAA AAG ATT GAT TCT AGA GAA      824
Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser Arg Glu
        245                 250                 255

ATT AAA CGA GAA ATC AAG CAA GAG GCC ATT AAA GAG CCT AAA AAA GCC      872
Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys Lys Ala
    260                 265                 270

AAT CAA GGC ACA CAA AAC GCT CCT ACT TTA GAA GAG AAA AAC TAC CAA      920
Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn Tyr Gln
275                 280                 285                 290

AAA GCA GAG CGC AAA CTT GAT GCT AAA GAA GAA AGG CGT TAT TTG AGA      968
Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr Leu Arg
                295                 300                 305
```

```
GAT GAA AGG AAA AAA GCC AAA GCC ACC AAA AAG GCT ATG GAA TTT GAA    1016
Asp Glu Arg Lys Lys Ala Lys Ala Thr Lys Lys Ala Met Glu Phe Glu
            310                 315                 320

GAA AGA GAA AAA GAG CAT GAT GAA AGG GAC GAA CAA GAG ACT GAA GGA    1064
Glu Arg Glu Lys Glu His Asp Glu Arg Asp Glu Gln Glu Thr Glu Gly
        325                 330                 335

AGA AGA AAA GCT TTA GAA ATG GAT AAA GGC GAT AAA AAA GAA GAA AGA    1112
Arg Arg Lys Ala Leu Glu Met Asp Lys Gly Asp Lys Lys Glu Glu Arg
    340                 345                 350

GTC AAA CCC AAA GAA AAT GAG CGA GAA ATC AAG CAA GAA GCC ATT AAA    1160
Val Lys Pro Lys Glu Asn Glu Arg Glu Ile Lys Gln Glu Ala Ile Lys
355                 360                 365                 370

GAG CCA AGT GAT GGA AAT AAC GCC ACC CAA CAA GGC GAA AAA CAA AAC    1208
Glu Pro Ser Asp Gly Asn Asn Ala Thr Gln Gln Gly Glu Lys Gln Asn
                375                 380                 385

GCT CCT AAA GAG AAC AAC GCT CAA AAA GAA GAG AAT AAA CCA AAT TCT    1256
Ala Pro Lys Glu Asn Asn Ala Gln Lys Glu Glu Asn Lys Pro Asn Ser
            390                 395                 400

AAA GAA GAA AAA CGC CGC TTG AAA GAA GAA AAG AAA AAA GCC AAA GCC    1304
Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala
        405                 410                 415

GAA CAA AGA GCG AGA GAA TTT GAA CAA AGA GCG AGA GAG CAT CAA GAA    1352
Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu
    420                 425                 430

AGA GAT GAA AAA GAG CTT GAA GAG CGA AGA AAG GCG CTA GAA GCG GGT    1400
Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Ala Gly
435                 440                 445                 450

AAA AAA TAACATGTTA GACCAACAAC ACATCCAATA CTTTAAAAAC CTAGTAGGGG GA  1458
Lys Lys

G                                                                  1459
```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```
Met Leu Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu
 1               5                  10                  15
Gln Ser Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val
            20                  25                  30
```

```
Asp Leu Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val
        35                  40                  45
Gly Glu Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val
    50                  55                  60
Asn Ser Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala
65                  70                  75                  80
Lys Phe Arg Ala Phe Glu Ser Met Lys Gln Arg His Leu Pro Thr Pro
                85                  90                  95
Arg Met Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn
            100                 105                 110
Asn Gln Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile
        115                 120                 125
Arg Ala Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val
    130                 135                 140
Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala
145                 150                 155                 160
Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr
                165                 170                 175
Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu
            180                 185                 190
Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg
        195                 200                 205
Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser
    210                 215                 220
Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu
225                 230                 235                 240
Lys Arg Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser
                245                 250                 255
Arg Glu Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys
            260                 265                 270
Lys Ala Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn
        275                 280                 285
Tyr Gln Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr
    290                 295                 300
Leu Arg Asp Glu Arg Lys Lys Ala Lys Ala Thr Lys Lys Ala Met Glu
305                 310                 315                 320
Phe Glu Glu Arg Glu Lys Glu His Asp Glu Arg Asp Glu Gln Glu Thr
                325                 330                 335
Glu Gly Arg Arg Lys Ala Leu Glu Met Asp Lys Gly Asp Lys Lys Glu
            340                 345                 350
Glu Arg Val Lys Pro Lys Glu Asn Glu Arg Glu Ile Lys Gln Glu Ala
        355                 360                 365
Ile Lys Glu Pro Ser Asp Gly Asn Asn Ala Thr Gln Gln Gly Glu Lys
    370                 375                 380
Gln Asn Ala Pro Lys Glu Asn Asn Ala Gln Lys Glu Glu Asn Lys Pro
385                 390                 395                 400
Asn Ser Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala
                405                 410                 415
Lys Ala Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala Arg Glu His
            420                 425                 430
Gln Glu Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu
        435                 440                 445
Ala Gly Lys Lys
    450
```

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 74...943
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```
GGCCTATGAC GATTGTCTCG CTTTTAGAAA ACACTCTAAT CGCTTTTGAA AAACAACAAA      60
GGAAGGGATT TTA ATG AAA TTT TTA CGC TCT GTT TAT GCA TTT TGC TCC          109
               Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser
                1               5                  10

AGT TGG GTA GGG ACG ATT GTT ATT GTG CTG TTG GTT ATC TTT TTT ATC        157
Ser Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile
        15                  20                  25

GCG CAA GCC TTT ATC ATT CCC TCT CGC TCT ATG GTT GGC ACG CTC TAT        205
Ala Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr
    30                  35                  40

GAG GGC GAC ATG CTC TTT GTC AAA AAG TTT TCT TAC GGC ATA CCC ATT        253
Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile
45                  50                  55                  60

CCT AAA ATC CCA TGG ATT GAG CTT CCT GTT ATG CCT GAT TTT AAA AAT        301
Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn
                65                  70                  75

AAC GGA CAT TTG ATA GAG GGG GAT CGC CCT AAG CGT GGC GAA GTG GTG        349
Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val
            80                  85                  90

GTG TTT ATC CCT CCC CAT GAA AAA AAG TCT TAC TAT GTT AAA AGG AAT        397
Val Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn
        95                  100                 105

TTT GCC ATT GGA GGC GAT GAG GTG TTG TTC ACT AAT GAG GGT TTT TAT        445
Phe Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr
    110                 115                 120

TTG CAC CCT TTT GAG AGC GAC ACG GAC AAA AAT TAC ATC GCT AAA CAT        493
Leu His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His
125                 130                 135                 140

TAC CCT AAC GCC ATG ACA AAA GAA TTT ATG GGT AAA ATT TTT GTT TTA        541
Tyr Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu
                145                 150                 155

AAC CCT TAT AAA AAT GAG CAT CCG GGT ATC CAT TAC CAA AAA GAC AAT        589
```

```
Asn Pro Tyr Lys Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn
            160                 165                 170

GAA ACC TTC CAC TTA ATG GAG CAA TTA GCC ACT CAA GGC GCA GAA GCT      637
Glu Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala
        175                 180                 185

AAT ATC AGC ATG CAA CTC ATT CAA ATG GAG GGC GAA AAG GTG TTT TAT      685
Asn Ile Ser Met Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr
    190                 195                 200

AAG AAA ATC AAT GAC GAT GAA TTT TTC ATG ATC GGC GAC AAC AGA GAC      733
Lys Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp
205                 210                 215                 220

AAT TCT AGC GAC TCG CGC TTT TGG GGG AGT GTG GCT TAT AAA AAC ATC      781
Asn Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile
                225                 230                 235

GTG GGT TCG CCA TGG TTT GTT TAT TTC AGT TTG AGT TTA AAA AAT AGC      829
Val Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser
            240                 245                 250

CTA GAA ATG GAT GCA GAA AAT AAC CCT AAA AAA CGC TAT CTG GTG CGT      877
Leu Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg
        255                 260                 265

TGG GAA CGC ATG TTT AAA AGC GTT GGA GGC TTA GAA AAA ATC ATT AAA      925
Trp Glu Arg Met Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys
    270                 275                 280

AAA GAA AAC GCA ACG CAT TAAGGTTTTT TGTGCAATTT TTTGATTTCT CTTTAGAA    981
Lys Glu Asn Ala Thr His
285                 290

AGTTTTATTA CCAC                                                     995
```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```
Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser Ser Trp Val Gly
 1               5                  10                  15
Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile Ala Gln Ala Phe
            20                  25                  30
Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met
        35                  40                  45
Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro
    50                  55                  60
```

```
Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu
65                  70                  75                  80
Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro
                85                  90                  95
Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly
            100                 105                 110
Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe
        115                 120                 125
Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala
    130                 135                 140
Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys
145                 150                 155                 160
Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His
                165                 170                 175
Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met
            180                 185                 190
Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn
        195                 200                 205
Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp
    210                 215                 220
Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro
225                 230                 235                 240
Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu Glu Met Asp
                245                 250                 255
Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp Glu Arg Met
            260                 265                 270
Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys Glu Asn Ala
        275                 280                 285
Thr His
    290
```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 548...2419
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```
GATACAATTC CAAATTTAAA AAACAAACGA TTTAATTCAA ATTTAAGGAA AAATTTTGAT     60
TACAGTGGTT AAACGAAACG GGCGCATTGA GCCTTTGGAC ATTACCAAAA TCCAAAAATA    120
CACTAAGGAC GCTACGGACA ATTTAGAGGG CGTGAGCCAA AGTGAGCTGG AAGTGGATGC    180
GAGGTTGCAA TTCAGGGACA AGATCACTAC TGAAGAAATC CAACAAACTT TGATTAAAAC    240
CGCTGTGGAT AAGATAGATA TTGACACGCC TAATTGGAGT TTTGTCGCCT CAAGGCTTTT    300
TTTGTATGAT TTATACCATA AAGTAAGTGG TTTTACAGGG TATAGGCATT TGAAAGAGTA    360
TTTTGAAAAC GCTGAAGAAA AGGGCCGCAT CCTTAAGGGC TTTAAGGAAA AATTTGATCT    420
AGAGTTTTTA AATAGCCAGA TCAAGCCTGA AAGGGATTTC CAATTCAATT ATTTAGGGAT    480
```

```
TAAAACCTTG TATGATCGCT ATTTGTTAAA AGACGCTAAC AACAACCCTA TTGAATTGCC     540
CCAACAC ATG TTT ATG AGC ATT GCG ATG TTT TTA GCA CAA AAC GAA CAA       589
        Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln
         1               5                  10

GAA CCC AAT AAA ATC GCC TTA GAA TTT TAT GAA GTT TTG AGC AAG TTT       637
Glu Pro Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe
15                  20                  25                  30

GAA GCG ATG TGC GCG ACC CCC ACT CTA GCG AAC GCC CGC ACC ACC AAA       685
Glu Ala Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys
                35                  40                  45

CAC CAG CTC AGC TCA TGC TAT ATT GGC AGC ACG CCG GAT AAT ATT GAG       733
His Gln Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu
            50                  55                  60

GGG ATT TTT GAC AGC TAT AAG GAA ATG GCG CTG TTG TCC AAA TAC GGC       781
Gly Ile Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly
        65                  70                  75

GGA GGG ATT GGC TGG GAT TTT TCT TTG GTG CGC TCT ATT GGG AGT TAT       829
Gly Gly Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr
    80                  85                  90

ATT GAT GGG CAT AAA AAT GCG AGC GCT GGC ACG ATC CCT TTT TTA AAA       877
Ile Asp Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys
95                  100                 105                 110

ATC GCT AAC GAT GTG GCG ATT GCG GTG GAT CAA TTA GGC ACA CGA AAG       925
Ile Ala Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys
                115                 120                 125

GGC GCG ATT GCG GTG TAT TTG GAA ATT TGG CAC ATT GAT GTG ATG GAG       973
Gly Ala Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu
            130                 135                 140

TTC ATT GAT TTA AGG AAA AAT AGC GGC GAT GAA AGG CGA AGA GCG CAT      1021
Phe Ile Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His
        145                 150                 155

GAT TTA TTC CCG GCT CTT TGG GTG TGC GAT TTG TTT TTG AAA AGG GTT      1069
Asp Leu Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val
    160                 165                 170

TTA GAA GAT GCG ATG TGG ACT TTA TTT GAC CCT TAT GAG TGT AAG GAT      1117
Leu Glu Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp
175                 180                 185                 190

TTG ACT GAG CTT TAT GGG CAG GAT TTT GAA AAA CGC TAT TTA GAG TAT      1165
Leu Thr Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr
                195                 200                 205

GAA AAA GAT CCC AAG ATC ATT AAG GAA TAC ATT AAC GCT AAA GAT TTA      1213
Glu Lys Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu
            210                 215                 220

TGG AAA AAA ATC TTA ATG AAT TAT TTT GAA GCC GGT TTG CCT TTC TTA      1261
```

```
Trp Lys Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu
        225                 230                 235

GCC TTT AAA GAT AAC GCC AAT CGG TGC AAC CCA AAC GCT CAT GCA GGA    1309
Ala Phe Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly
    240                 245                 250

ATC ATT CGA TCC AGC AAT CTA TGC ACG GAG ATT TTC CAA AAT ACC GCG    1357
Ile Ile Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala
255                 260                 265                 270

CCT AAC CAC TAC TAC ATG CAA ATA GAA TAC ACC GAC GGC ACC ATA GAG    1405
Pro Asn His Tyr Tyr Met Gln Ile Glu Tyr Thr Asp Gly Thr Ile Glu
                275                 280                 285

TTT TTT GAA GAA AAA GAG TTG GTA ACG ACA GAT AGT AAT ATC ACT AAA    1453
Phe Phe Glu Glu Lys Glu Leu Val Thr Thr Asp Ser Asn Ile Thr Lys
            290                 295                 300

TGC GCT AAC AAG CTC ACT AGC ACC GAT ATT CTA AAG GGC AAG CCA ATC    1501
Cys Ala Asn Lys Leu Thr Ser Thr Asp Ile Leu Lys Gly Lys Pro Ile
        305                 310                 315

TAT ATC GCT ACT AAA GTC GCT AAA GAC GGG CAA ACG GCG GTG TGC AAT    1549
Tyr Ile Ala Thr Lys Val Ala Lys Asp Gly Gln Thr Ala Val Cys Asn
    320                 325                 330

CTG GCG AGC ATC AAT TTA AGC AAA ATC AAC ACT GAA GAA GAC ATT AAA    1597
Leu Ala Ser Ile Asn Leu Ser Lys Ile Asn Thr Glu Glu Asp Ile Lys
335                 340                 345                 350

AGG GTT GTG CCG ATC ATG GTC AGG CTT TTA GAC AAT GTG ATT GAT TTG    1645
Arg Val Val Pro Ile Met Val Arg Leu Leu Asp Asn Val Ile Asp Leu
                355                 360                 365

AAT TTC TAC CCT AAC CGC AAA GTC AAA GCC ACT AAT TTA CAA AAT AGG    1693
Asn Phe Tyr Pro Asn Arg Lys Val Lys Ala Thr Asn Leu Gln Asn Arg
            370                 375                 380

GCC ATA GGG TTA GGG GTT ATG GGT GAA GCG CAA ATG CTC GCA GAA CAC    1741
Ala Ile Gly Leu Gly Val Met Gly Glu Ala Gln Met Leu Ala Glu His
        385                 390                 395

CAA ATC GCT TGG GGG TCT AAA GAG CAT TTA GAA AAA ATT GAC GCT TTA    1789
Gln Ile Ala Trp Gly Ser Lys Glu His Leu Glu Lys Ile Asp Ala Leu
    400                 405                 410

ATG GAG CAA ATC AGC TAC CAT GCG ATT GAC ACG AGC GCG AAT TTA GCG    1837
Met Glu Gln Ile Ser Tyr His Ala Ile Asp Thr Ser Ala Asn Leu Ala
415                 420                 425                 430

AAA GAA AAA GGG GTT TAT AAG GAT TTT GAA AAT TCA GAA TGG AGT AAG    1885
Lys Glu Lys Gly Val Tyr Lys Asp Phe Glu Asn Ser Glu Trp Ser Lys
                435                 440                 445

GGG ATT TTC CCC ATT GAT AAA GCC AAT AAT GAA GCC TTA AAG CTC ACC    1933
Gly Ile Phe Pro Ile Asp Lys Ala Asn Asn Glu Ala Leu Lys Leu Thr
            450                 455                 460
```

```
GAA AAA GGG CTT TTT AAT CAC GCT TGC GAT TGG CAA GGT TTG AGG GAA    1981
Glu Lys Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu
        465                 470                 475

AAA GTC AAA GCC AAT GGC ATG CGT AAT GGC TAT TTA ATG GCG ATC GCT    2029
Lys Val Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala
    480                 485                 490

CCC ACA AGC TCC ATT TCT ATT TTA GTA GGC ACA ACC CAA ACG ATT GAA    2077
Pro Thr Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu
495                 500                 505                 510

CCC ATT TAT AAG AAA AAA TGG TTT GAA GAA AAT TTG AGC GGG CTT ATT    2125
Pro Ile Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile
                515                 520                 525

CCT GTT GTG GTG CCT AAT TTG AAT GTA GAA ACC TGG AAT TTT TAC ACA    2173
Pro Val Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr
            530                 535                 540

TCA GCC TAT GAT ATT GAC GCT AAA GAT TTG ATT AAA GCA GCG GCC GTG    2221
Ser Ala Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val
        545                 550                 555

CGC CAA AAG TGG ATT GAT CAA GGC CAA AGC CTT AAT GTG TTT TTA CGC    2269
Arg Gln Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg
    560                 565                 570

ATA GAA AAC GCC AGC GGT AAA ACC TTG CAT GAC ATC TAC ACG CTC GCT    2317
Ile Glu Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala
575                 580                 585                 590

TGG AAA TTA GGA CTC AAA TCC ACT TAT TAT TTG CGC AGC GAA AGC CCT    2365
Trp Lys Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro
                595                 600                 605

AGC ATA GAT GAA AAA AGC GTG TTG GAT CGA TCG GTG GAG TGT TTT AAT    2413
Ser Ile Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn
            610                 615                 620

TGC CAA TAATATAAGC TTAAATAAGC TAATCTTTGC TAAAATGAGA TTTAAAATTA TT  2471
Cys Gln

TA                                                                 2473
```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```
Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln Glu Pro
 1               5                  10                  15
Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe Glu Ala
            20                  25                  30
Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys His Gln
        35                  40                  45
Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu Gly Ile
    50                  55                  60
Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly Gly Gly
65                  70                  75                  80
Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr Ile Asp
                85                  90                  95
Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys Ile Ala
            100                 105                 110
Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys Gly Ala
        115                 120                 125
Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu Phe Ile
    130                 135                 140
Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His Asp Leu
145                 150                 155                 160
Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val Leu Glu
                165                 170                 175
Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp Leu Thr
            180                 185                 190
Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr Glu Lys
        195                 200                 205
Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu Trp Lys
    210                 215                 220
Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu Ala Phe
225                 230                 235                 240
Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly Ile Ile
                245                 250                 255
Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala Pro Asn
            260                 265                 270
His Tyr Tyr Met Gln Ile Glu Tyr Thr Asp Gly Thr Ile Glu Phe Phe
        275                 280                 285
Glu Glu Lys Glu Leu Val Thr Thr Asp Ser Asn Ile Thr Lys Cys Ala
    290                 295                 300
Asn Lys Leu Thr Ser Thr Asp Ile Leu Lys Gly Lys Pro Ile Tyr Ile
305                 310                 315                 320
Ala Thr Lys Val Ala Lys Asp Gly Gln Thr Ala Val Cys Asn Leu Ala
                325                 330                 335
Ser Ile Asn Leu Ser Lys Ile Asn Thr Glu Glu Asp Ile Lys Arg Val
            340                 345                 350
Val Pro Ile Met Val Arg Leu Leu Asp Asn Val Ile Asp Leu Asn Phe
        355                 360                 365
Tyr Pro Asn Arg Lys Val Lys Ala Thr Asn Leu Gln Asn Arg Ala Ile
    370                 375                 380
Gly Leu Gly Val Met Gly Glu Ala Gln Met Leu Ala Glu His Gln Ile
385                 390                 395                 400
Ala Trp Gly Ser Lys Glu His Leu Glu Lys Ile Asp Ala Leu Met Glu
                405                 410                 415
Gln Ile Ser Tyr His Ala Ile Asp Thr Ser Ala Asn Leu Ala Lys Glu
            420                 425                 430
Lys Gly Val Tyr Lys Asp Phe Glu Asn Ser Glu Trp Ser Lys Gly Ile
        435                 440                 445
Phe Pro Ile Asp Lys Ala Asn Asn Glu Ala Leu Lys Leu Thr Glu Lys
    450                 455                 460
```

```
Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu Lys Val
465                 470                 475                 480
Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala Pro Thr
                485                 490                 495
Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu Pro Ile
            500                 505                 510
Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile Pro Val
        515                 520                 525
Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr Ser Ala
    530                 535                 540
Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val Arg Gln
545                 550                 555                 560
Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg Ile Glu
                565                 570                 575
Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala Trp Lys
            580                 585                 590
Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro Ser Ile
        595                 600                 605
Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn Cys Gln
    610                 615                 620
```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 56...1390
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
GCAAAATTCT AGCCTTAAAT CTTTGATGAA ACGAAGTCAA ATTATAAGAT AAGGC ATG      58
                                                             Met
                                                              1

TTA AAA TTC CCT AAA ATG AGT TTA AGG ATT TTA ATG CTT TCT GTC ATC      106
Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val Ile
             5                  10                  15

ATA CTG GCC GCT GGT AAA GGC ACT CGC ATG CGT TCT AGC CTG CCT AAA      154
Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro Lys
        20                  25                  30

ACT TTA CAC ACC ATT TGT GGG GAG CCT ATG TTG TTT TAC ATT TTA GAA      202
Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu Glu
    35                  40                  45

ACG GCT TTT TCA ATC AGC GAT GAT GTG CAT CTT ATC TTA CAC CAC CAA      250
Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His Gln
```

```
50                  55                  60                  65

CAA GAA CGC ATT AAA GAA GCG GTG TTG GAG CGT TTT AAG GGC GTC ATT      298
Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val Ile
                70                  75                  80

TTT CAC ACT CAA ATT GTG GAA AAA TAT TCA GGG ACA GGT GGG GCT ATC      346
Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala Ile
            85                  90                  95

ATG CAA AAA GAT AAA ACG CCT ATT TCT ACG AAA CAT GAG CGG GTT TTG      394
Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val Leu
        100                 105                 110

ATT TTG AAT GCG GAC ATG CCT TTA ATC ACT AAA GAC GCT CTC GCC CCC      442
Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala Pro
    115                 120                 125

TTA TTA GAA AGC AAG AAT AAC GCT ATA GGC TTA CTC CAT TTA GCT GAC      490
Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala Asp
130                 135                 140                 145

CCT AAA GGT TAT GGG CGC GTT GTT TTA GAA AAC CAT CAG GTT AAA AAG      538
Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys Lys
                150                 155                 160

ATT GTA GAA GAA AAG GAC GCT AAT GAT GAA GAA AAA GAA ATT AAA AGC      586
Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys Ser
            165                 170                 175

GTG AAT GCT GGC GTG TAT GGG TTT GAA AGG GAT TTT TTA GAA AAA TAC      634
Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys Tyr
        180                 185                 190

TTA CCC AAG CTC CAT GAC CAA AAC GCC CAA AAA GAA TAC TAC CTC ACG      682
Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu Thr
    195                 200                 205

GAT TTA ATC GCT CTA GGG ATC AAT GAA AAC GAA ACA ATT GAC GCT ATT      730
Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala Ile
210                 215                 220                 225

TTC TTA AAA GAA GAG TGT TTT TTA GGG GTG AAT AGC CAA ACA GAA AGG      778
Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu Arg
                230                 235                 240

GCG AAA GCT GAA GAA ATC ATG CTA GAA AGA CTG CGC AAA AAC GCC ATG      826
Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala Met
            245                 250                 255

GAC TTG GGG GTA GTG ATG CAA TTG CCT AAT AGC ATT TAT TTA GAA AAA      874
Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu Lys
        260                 265                 270

GGC GTG AGT TTT AAG GGG GAG TGC GTT TTA GAG CAA GGG GTG CGT TTG      922
Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg Leu
    275                 280                 285
```

```
ATT GGG AAT TGT TTG ATA GAA AAC GCG CAT ATT AAG GCT TAT AGC GTG      970
Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser Val
290                 295                 300                 305

ATA GAA GAG AGC CAG ATT GTT AAT AGC AGT GTG GGG CCG TTT GCC CAT     1018
Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala His
                310                 315                 320

GCG CGC CCT AAA AGC GTG ATT TGT AAT AGC CAT GTG GGG AAT TTT GTA     1066
Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe Val
            325                 330                 335

GAG ACT AAA AAC GCT AAA CTT CAA GGC ACT AAA GCA GGG CAT TTG AGC     1114
Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu Ser
        340                 345                 350

TAT TTA GGG GAT TGT GAG ATA GGG AAA AAC ACA AAT GTA GGG GCT GGC     1162
Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala Gly
    355                 360                 365

GTG ATC ACT TGC AAT TAC GAT GGT AAA AAG AAA CAC CAA ACA ATC ATC     1210
Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile Ile
370                 375                 380                 385

GGT GAA AAT GTC TTT ATA GGG AGC GAT AGC CAG CTA GTC GCC CCC ATA     1258
Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro Ile
                390                 395                 400

AAT ATC GGC TCT AAT GTC TTA ATC GGC AGC GGC ACC ACT ATC ACT AAA     1306
Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr Lys
            405                 410                 415

GAC ATT CCT AGC GGT TCG TTG AGC CTT TCA CGC GCC CCT CAA ACC AAC     1354
Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr Asn
        420                 425                 430

ATT GAA AAC GGG TAT TTT AAG TTT TTT AAG AAA CCT TAATTTGTTT GAATAA   1406
Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro
    435                 440                 445

TGAAAAATCC TAAAATATTA ATCATTTACT TTAA                               1440
```

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```
Met Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val
 1               5                  10                  15
Ile Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro
```

```
            20                  25                  30
Lys Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu
        35                  40                  45
Glu Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His
    50                  55                  60
Gln Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val
65                  70                  75                  80
Ile Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala
                85                  90                  95
Ile Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val
            100                 105                 110
Leu Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala
        115                 120                 125
Pro Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala
    130                 135                 140
Asp Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys
145                 150                 155                 160
Lys Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys
                165                 170                 175
Ser Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys
            180                 185                 190
Tyr Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu
        195                 200                 205
Thr Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala
    210                 215                 220
Ile Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu
225                 230                 235                 240
Arg Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala
                245                 250                 255
Met Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu
            260                 265                 270
Lys Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg
        275                 280                 285
Leu Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser
    290                 295                 300
Val Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala
305                 310                 315                 320
His Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe
                325                 330                 335
Val Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu
            340                 345                 350
Ser Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala
        355                 360                 365
Gly Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile
    370                 375                 380
Ile Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro
385                 390                 395                 400
Ile Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr
                405                 410                 415
Lys Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr
            420                 425                 430
Asn Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 771 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 227...715
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```
GCAAAGATAA AAAACAAACG GGTTTTGGTG AAATTTTCTG GGGAAGCGTT AGCTGGNGGA     60
CAACCAGTTT GGGATTGACA TTCATGTGTT AGATCACATC GCTAAAGAGA TCAAAAGTTT    120
AGTGGAAAAC GATATTGAAG TGGGTATTGT GATTGGTGGA GGCAATATTA TTAGGGGGGT    180
TAGCGCGGCT CAAGGGGGGA TTATTAGGCG CACCAGTGGG GATTAT ATG GGC ATG       235
                                                  Met Gly Met
                                                   1

TTA GCC ACC GTG ATT AAT GCG GTA GCG ATG CAA GAA GCT TTA GAG CAT      283
Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His
     5                  10                  15

ATC GGC TTA GAC ACA AGG GTG CAG AGC GCG ATT GAA ATC AAA GAG ATT      331
Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile
20                  25                  30                  35

TGT GAA AGT TAC ATT TAC AGA AAA GCG ATC AGG CAT TTA GAA AAG GGT      379
Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly
                40                  45                  50

AGG GTG GTG ATT TTT GGC GCA GGC ACG GGA AAC CCG TTT TTC ACT ACG      427
Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr
            55                  60                  65

GAT ACG GCT GCC ACT TTA AGA GCG ATT GAA ATT GGA TCG GAT TTA ATC      475
Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile
        70                  75                  80

ATT AAA GCG ACT AAA GTG GAT GGC ATT TAC GAC AAA GAT CCT AAC AAG      523
Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys
    85                  90                  95

TTT AAA GAC GCT AAA AAA TTA GAC ACT TTA AGC TAT AAC GAT GCC TTG      571
Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn Asp Ala Leu
100                 105                 110                 115

ATA GGG GAT ATT GAA GTG ATG GAC GAT ACC GCT ATT TCT TTA GCT AAA      619
Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser Leu Ala Lys
                120                 125                 130

GAC AAT AAG CTC CCC ATT GTG GTG TGT AAC ATG TTC AAA AAA GGG AAT      667
Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys Lys Gly Asn
            135                 140                 145
```

```
TTA TTG CAA GTG ATC AAG CAC CAA CAA GGC GTA TTT TCT ATG GTA AAA T   716
Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser Met Val Lys
        150                 155                 160

AAGCCCTTTA ACATTGGATA GAACTCAAAA TAAAAGGATC AGTTTGAAAA AAGAG       771
```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```
Met Gly Met Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala
 1               5                  10                  15
Leu Glu His Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile
            20                  25                  30
Lys Glu Ile Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu
        35                  40                  45
Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe
    50                  55                  60
Phe Thr Thr Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser
65                  70                  75                  80
Asp Leu Ile Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp
                85                  90                  95
Pro Asn Lys Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn
            100                 105                 110
Asp Ala Leu Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser
        115                 120                 125
Leu Ala Lys Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys
    130                 135                 140
Lys Gly Asn Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser
145                 150                 155                 160
Met Val Lys
```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 56...607
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```
TCATGTAAAA TAAAGGGTTT TATTAAAGAT GAGAGATTGT TTTAAGGTTT GAATA ATG      58
                                                              Met
                                                               1

AGA GCT TTT TTA AAG ATT TTA ATG GTT TTG ATT TTT ATG AGC GTT GCT      106
Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val Ala
      5                  10                  15

TAT GCT AAA AAT CCT TCA ACG CTT TCT AAA GAA GAA GAG GTT TTG CAG      154
Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu Gln
  20                  25                  30

CAT TTG CAA AGT TTT AGC GCG CAT TTC AAG CAG GTT TTA AAA AAT GAA      202
His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn Glu
35                  40                  45

AAA CCT TTA GTT TAT TAC GGG GTT TTA AAG GCT AAA GCC CCT AAT TGG      250
Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn Trp
50                  55                  60                  65

GCT TTA TGG GTT TAT GAA AAG CCT TTA AAA AAA GAA ATT TAC ATG AAC      298
Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met Asn
                70                  75                  80

GAT AAA GAA GTG GTA ATT TAT GAG CCT AAT TTG TTT CAA GCG ACC ATC      346
Asp Lys Glu Val Val Ile Tyr Glu Pro Asn Leu Phe Gln Ala Thr Ile
            85                  90                  95

ACG CCC TTA AAA GAC AAG ACG GAT TTT TTC ACC ATT CTC AAG CGT TTA      394
Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Arg Leu
        100                 105                 110

AAA AAG CAA GAT GAC GGA TCT TTT AAA ACG ACT ATC AAC AAA ACC ACT      442
Lys Lys Gln Asp Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr Thr
    115                 120                 125

TAT CGT TTG GTT TTT AAA GAC GGC AAG CCT TTT TCA TTG GAA TTT AAA      490
Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe Lys
130                 135                 140                 145

GAT GGA ATG AAC AAT CTT GTA ACG ATC ACT TTT TCT CAA GCA GAA ATC      538
Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu Ile
                150                 155                 160

AAC CCC ACC ATT GCT AAT GAA ATC TTT GTT TTT AAG CCT AAA GAT GAA      586
Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp Glu
            165                 170                 175

AAC ATT GAT ATT GTG CGC CAA TGATTTTTAA TGATTCATTG CATCTTGTTA GCAA    641
Asn Ile Asp Ile Val Arg Gln
        180

AAGTTAGCTA AAATAGAC                                                  659
```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```
Met Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val
 1               5                  10                  15
Ala Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu
            20                  25                  30
Gln His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn
        35                  40                  45
Glu Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn
    50                  55                  60
Trp Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met
65                  70                  75                  80
Asn Asp Lys Glu Val Val Ile Tyr Glu Pro Asn Leu Phe Gln Ala Thr
                85                  90                  95
Ile Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Arg
            100                 105                 110
Leu Lys Lys Gln Asp Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr
        115                 120                 125
Thr Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe
    130                 135                 140
Lys Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu
145                 150                 155                 160
Ile Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp
                165                 170                 175
Glu Asn Ile Asp Ile Val Arg Gln
            180
```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 729...2981
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```
GAAACGATCG CAGAAAGCAA TGAAAGCACG GTAGTAGCGG AATTTCATAG CAGTAATGAA     60
AAAAAAGCGC TTATGAGAGC GAAGCAGAGC TAGAAAGGGC GTTTATTAAG CTTTTAGAAA    120
AACAAGGCTA TGAATTTAAA AAAATCCACA AAGAAGAAGA ATTAAAAGAC AATTTAAAAG    180
```

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AGCAGTTAGA AAAGCTTAAT GATCATTCTT TCACGCCTAA AGAATGGGAC ACTCTTTATT    240
CTCAATTCAT CGCTAATAAA AACGATGACT ATAAGGCTAA AACGAAAAAG ATCCAAGAAG    300
ATCCGATTTT TAATCTCACG CTAGAGAACG GGAAAACCAA AAACATTAAA ATCATTGATA    360
AGAAAAATAT CCATAGAAAC GCCTTGCAAG TGATCCACCA ATACAGCAAT AAAGGGGGGA    420
AGTATCAAAA CCGCTATGAT GTGAGTATCC TTGTGAATGG CTTGCCTTTA GTGCATGTGG    480
AATTGAAAAA AAGAGGCGTG GCGATCAGGG AGGCGTTCAA CCAGATCAAG CGCTATAAAA    540
GGGATAGTTT TAGCGCTGAA GACGGGCTTT TTGATTTTGT GCAGATTTTT GTCATCAGTA    600
ACGGCACGAG CTCTAAATAC TATTCAAACA CCACAAGAAT AGCCCAGCTG GAAAAAAACC    660
ATAAAGCCGA TACTTTTGAA TTCACGAATT ATTGGGCGGA TAGCAAGAAT CACAATATTG    720
AGGATTTA ATG GAT TTT GCT AAG GCG TTT TTT GCA AAG CGC AGC CTT TTG      770
         Met Asp Phe Ala Lys Ala Phe Phe Ala Lys Arg Ser Leu Leu
          1               5                  10

AAC GTT TTA ACG TGC TAT TGC GTT TTC ACA AGC GAA GAG GTT TTA TTG      818
Asn Val Leu Thr Cys Tyr Cys Val Phe Thr Ser Glu Glu Val Leu Leu
15                  20                  25                  30

GTG ATG CGG CCT TAT CAA ATC GTG GCG GCC GAA AGG ATT TTG GAA AAG      866
Val Met Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys
                35                  40                  45

ATC AAA ACC GCG CAA AAT AGT AAA ACG AAA AAT CAA AGC AAA GGC TAT      914
Ile Lys Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr
            50                  55                  60

ATC TGG CAC ACG ACA GGG AGC GGT AAA ACC CTA ACG AGC TTT AAA AGC      962
Ile Trp His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser
        65                  70                  75

GCA ACG TTG GCT AAA GAA TTA GAG AGC GTT TCA AAA GTC TTG TTC GTG     1010
Ala Thr Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val
    80                  85                  90

GTG GAC AGG AAG GAT TTG GAC TAT CAA ACC ATG AAA GAA TAC GAT AAA     1058
Val Asp Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys
95                  100                 105                 110

TTC CAA AAA GAT TGC GCT AAT TCC AAC ACA AGC ACT AAG ATT TTA AAA     1106
Phe Gln Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys
                115                 120                 125

GAA CAG CTT GAA GAT TCT AAC GCT AAA ATC ATT ATC ACC ACG ATC CAA     1154
Glu Gln Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln
            130                 135                 140

AAA TTA GAC AAA TTC GTT AAA TCC CAT AAA GGG CAT GCG ATT TTT AAT     1202
Lys Leu Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn
        145                 150                 155

GAA GAA GTT GTG ATG ATT TTT GAT GAA TGC CAC AGG AGT CAG TTA GGC     1250
Glu Glu Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly
    160                 165                 170

TCT ATG CAT CAA GCC ATC ACT AAA GCG TTT AAA AAA TAC CAC CTT TTT     1298
Ser Met His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe
175                 180                 185                 190

GGC TTT ACT GGC ACG CCC ATT TTT GCA GCT AAT TGC GAT AAA AAC AAC     1346
```

```
Gly Phe Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn
                195                 200                 205

CCT TTA GGC ACG ACA GAG CAA AAG TTT GGG AAA TGC CTC CAC CAA TAC    1394
Pro Leu Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr
            210                 215                 220

ACC ATT ATT GAT GCG ATC AGG GAT AAA AAC GTT TTG CCC TTT AGA GTG    1442
Thr Ile Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val
        225                 230                 235

GAA TAC CAC AAC ACC ATT AAA GCT AAA GAG GAC ATT AAG GAT AAT AAG    1490
Glu Tyr His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys
    240                 245                 250

GTT AGA GCG GTT GAT GAA AAA AAC GCC CTT TTG GAT ACT AGG AGG ATC    1538
Val Arg Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile
255                 260                 265                 270

AAA GAA ATC ACT AAA TGC ATT TTA GAG CGT TTC AAT CAA GCC ACT AAA    1586
Lys Glu Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys
                275                 280                 285

AAT AAA AAA TTC AAT TCC ATT CTG GCA TGC TCT AGC ATA GAA GCG CTG    1634
Asn Lys Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu
            290                 295                 300

AAA AAA TAC TAC CAA GCC TTT AAA GAA GAA AAA CAC GAT CTT AAA ATC    1682
Lys Lys Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile
        305                 310                 315

GCT GCC ATT TTT AGC TAT AGC GCT AAT GAG GAA ATT GAC ACG CTA GAA    1730
Ala Ala Ile Phe Ser Tyr Ser Ala Asn Glu Glu Ile Asp Thr Leu Glu
    320                 325                 330

GAT GAA AAC AAT GAA AGC GCT TGC CGG CTA GAC AAA AGC TCA AGG GAT    1778
Asp Glu Asn Asn Glu Ser Ala Cys Arg Leu Asp Lys Ser Ser Arg Asp
335                 340                 345                 350

TTT TTA GAG GGC GCG ATT GCG GAT TAT AAT GGG ATG TTT GGC GTT TCT    1826
Phe Leu Glu Gly Ala Ile Ala Asp Tyr Asn Gly Met Phe Gly Val Ser
                355                 360                 365

TTT GAC ACT TCG GAT CAA AAA TTC CAA AGT TAT TAC AAG GAT CTT TCT    1874
Phe Asp Thr Ser Asp Gln Lys Phe Gln Ser Tyr Tyr Lys Asp Leu Ser
            370                 375                 380

CAA AAA ATG AAA GAG CGT AAA ATC GAT CTT TTA ATG GTG GTG AAC ATG    1922
Gln Lys Met Lys Glu Arg Lys Ile Asp Leu Leu Met Val Val Asn Met
        385                 390                 395

TTT TTG ACC GGG TTT GAC GCT ACA AGG CTC AAC ACC CTT TGG GTG GAT    1970
Phe Leu Thr Gly Phe Asp Ala Thr Arg Leu Asn Thr Leu Trp Val Asp
    400                 405                 410

AAA AAT CTC AAA TAC CAT GGG CTA ATT CAA GCT TTT TCA CGC GCA AAC    2018
Lys Asn Leu Lys Tyr His Gly Leu Ile Gln Ala Phe Ser Arg Ala Asn
415                 420                 425                 430
```

```
CGC ATT TTA GAT AGC GTT AAA ACG CAT GGG AAT ATC GTG TGT TTT AGG     2066
Arg Ile Leu Asp Ser Val Lys Thr His Gly Asn Ile Val Cys Phe Arg
                435                 440                 445

GAT TTA GAA CAG GAT TTG AAT GAC GCT CTC ATG CTT TTT GGC AAC AAG     2114
Asp Leu Glu Gln Asp Leu Asn Asp Ala Leu Met Leu Phe Gly Asn Lys
            450                 455                 460

GAC GCT CAA TCT ATT GCG CTG TTA AGA AAA TAT GAA GAT TAT TTG AAA     2162
Asp Ala Gln Ser Ile Ala Leu Leu Arg Lys Tyr Glu Asp Tyr Leu Lys
        465                 470                 475

GGC TAC ACG GAT AAC AAC AAA GAA TAC GAG GGC TAT GAG GGT TTG ATT     2210
Gly Tyr Thr Asp Asn Asn Lys Glu Tyr Glu Gly Tyr Glu Gly Leu Ile
    480                 485                 490

AAA AGG CTT TTA ACC GAA TTC CCA TTA AAA GAG CCA ATC GTT TCA GAA     2258
Lys Arg Leu Leu Thr Glu Phe Pro Leu Lys Glu Pro Ile Val Ser Glu
495                 500                 505                 510

AGC CAG AAA AAG GAT TTT ATT AAG CTT TTT GGC AAG ATT TTG AAA TTA     2306
Ser Gln Lys Lys Asp Phe Ile Lys Leu Phe Gly Lys Ile Leu Lys Leu
                515                 520                 525

GAA AAT ATT TTA AAC AGC TTT GAA AAT TTC AAA AAA GAC GAT TAC ATC     2354
Glu Asn Ile Leu Asn Ser Phe Glu Asn Phe Lys Lys Asp Asp Tyr Ile
            530                 535                 540

AAT CCC AGG GAT TTT CAA GAC TAT CAA AGC AAA TAC CTT GAT TTT TAC     2402
Asn Pro Arg Asp Phe Gln Asp Tyr Gln Ser Lys Tyr Leu Asp Phe Tyr
        545                 550                 555

GAT GCA ATG AGA TCA GAA AAA GGG AAG GAT AAA GAA GAG ATT AAT GAT     2450
Asp Ala Met Arg Ser Glu Lys Gly Lys Asp Lys Glu Glu Ile Asn Asp
    560                 565                 570

GAT TTG ATT TTT GAA ATT GAA CTC ATC AAA CAA GTG GAA GTC AAT ATT     2498
Asp Leu Ile Phe Glu Ile Glu Leu Ile Lys Gln Val Glu Val Asn Ile
575                 580                 585                 590

GAC TAT ATT TTG AAT TTG ATT GAA GAG TTC GCT AAA GAG CAT GGG GTG     2546
Asp Tyr Ile Leu Asn Leu Ile Glu Glu Phe Ala Lys Glu His Gly Val
                595                 600                 605

GAA ATC CAA GGC GTT AAA ACC AAA ATA GAG CCA ATC ATC AAC TCC AGC     2594
Glu Ile Gln Gly Val Lys Thr Lys Ile Glu Pro Ile Ile Asn Ser Ser
            610                 615                 620

ATA GAG TTA AGG AAT AAA AAA GAT TTG ATC ATG GAT TTC ATT GAC AAA     2642
Ile Glu Leu Arg Asn Lys Lys Asp Leu Ile Met Asp Phe Ile Asp Lys
        625                 630                 635

TAC AAC AAA GAC CAA GAA GTC CAT GCG CAT TTT CAA GAT TAT ATC CAC     2690
Tyr Asn Lys Asp Gln Glu Val His Ala His Phe Gln Asp Tyr Ile His
    640                 645                 650

CAA AAA AGA GAA GAG GAA TTC CAA AAT ATC ATA GAA GAA AAC CGC TTG     2738
Gln Lys Arg Glu Glu Glu Phe Gln Asn Ile Ile Glu Glu Asn Arg Leu
```

```
655                 660                 665                 670

AAT GAA GAA AAA GCC TAT TCG TTC ATG CAG CAT GCC TTT AAA GGG GGC    2786
Asn Glu Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly
                675                 680                 685

GAA ATC AGT TTT AGT GGG ACG GAA TTC CCT AAA ATC ATT GAA GAA AAA    2834
Glu Ile Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys
            690                 695                 700

CCC TCC ATG TTT GGT AAA AAT TCG CGC TAT CAA GAG GTG AAA GAA AAA    2882
Pro Ser Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys
        705                 710                 715

GTC GCT GCA AGC CTT TCT CGT TTT TTC CAC CGC TTT TGT GAT CTC ACT    2930
Val Ala Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr
    720                 725                 730

AGC GCT ATA TTT AAG AAA AAT GAG GTT AAA AAA GAT GAG GTT AAT GAA    2978
Ser Ala Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu
735                 740                 745                 750

AAA TAGTTCATGA ACGCTTTTGC ATTAAGGCTC AAAAAAAGCG CCGTTTAATG GATT    3035
Lys
```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```
Met Asp Phe Ala Lys Ala Phe Phe Ala Lys Arg Ser Leu Leu Asn Val
 1               5                  10                  15
Leu Thr Cys Tyr Cys Val Phe Thr Ser Glu Glu Val Leu Leu Val Met
            20                  25                  30
Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys Ile Lys
        35                  40                  45
Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr Ile Trp
    50                  55                  60
His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser Ala Thr
65                  70                  75                  80
Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val Val Asp
                85                  90                  95
Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys Phe Gln
            100                 105                 110
Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys Glu Gln
        115                 120                 125
Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln Lys Leu
    130                 135                 140
```

Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn Glu Glu
145 150 155 160
Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly Ser Met
165 170 175
His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe Gly Phe
180 185 190
Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn Pro Leu
195 200 205
Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr Thr Ile
210 215 220
Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val Glu Tyr
225 230 235 240
His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys Val Arg
245 250 255
Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile Lys Glu
260 265 270
Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys Asn Lys
275 280 285
Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu Lys Lys
290 295 300
Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile Ala Ala
305 310 315 320
Ile Phe Ser Tyr Ser Ala Asn Glu Glu Ile Asp Thr Leu Glu Asp Glu
325 330 335
Asn Asn Glu Ser Ala Cys Arg Leu Asp Lys Ser Ser Arg Asp Phe Leu
340 345 350
Glu Gly Ala Ile Ala Asp Tyr Asn Gly Met Phe Gly Val Ser Phe Asp
355 360 365
Thr Ser Asp Gln Lys Phe Gln Ser Tyr Tyr Lys Asp Leu Ser Gln Lys
370 375 380
Met Lys Glu Arg Lys Ile Asp Leu Leu Met Val Val Asn Met Phe Leu
385 390 395 400
Thr Gly Phe Asp Ala Thr Arg Leu Asn Thr Leu Trp Val Asp Lys Asn
405 410 415
Leu Lys Tyr His Gly Leu Ile Gln Ala Phe Ser Arg Ala Asn Arg Ile
420 425 430
Leu Asp Ser Val Lys Thr His Gly Asn Ile Val Cys Phe Arg Asp Leu
435 440 445
Glu Gln Asp Leu Asn Asp Ala Leu Met Leu Phe Gly Asn Lys Asp Ala
450 455 460
Gln Ser Ile Ala Leu Leu Arg Lys Tyr Glu Asp Tyr Leu Lys Gly Tyr
465 470 475 480
Thr Asp Asn Asn Lys Glu Tyr Glu Gly Tyr Glu Gly Leu Ile Lys Arg
485 490 495
Leu Leu Thr Glu Phe Pro Leu Lys Glu Pro Ile Val Ser Glu Ser Gln
500 505 510
Lys Lys Asp Phe Ile Lys Leu Phe Gly Lys Ile Leu Lys Leu Glu Asn
515 520 525
Ile Leu Asn Ser Phe Glu Asn Phe Lys Lys Asp Asp Tyr Ile Asn Pro
530 535 540
Arg Asp Phe Gln Asp Tyr Gln Ser Lys Tyr Leu Asp Phe Tyr Asp Ala
545 550 555 560
Met Arg Ser Glu Lys Gly Lys Asp Lys Glu Glu Ile Asn Asp Asp Leu
565 570 575
Ile Phe Glu Ile Glu Leu Ile Lys Gln Val Glu Val Asn Ile Asp Tyr
580 585 590
Ile Leu Asn Leu Ile Glu Glu Phe Ala Lys Glu His Gly Val Glu Ile
595 600 605

```
Gln Gly Val Lys Thr Lys Ile Glu Pro Ile Ile Asn Ser Ser Ile Glu
    610                 615                 620
Leu Arg Asn Lys Lys Asp Leu Ile Met Asp Phe Ile Asp Lys Tyr Asn
625                 630                 635                 640
Lys Asp Gln Glu Val His Ala His Phe Gln Asp Tyr Ile His Gln Lys
                645                 650                 655
Arg Glu Glu Glu Phe Gln Asn Ile Ile Glu Glu Asn Arg Leu Asn Glu
            660                 665                 670
Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly Glu Ile
        675                 680                 685
Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys Pro Ser
    690                 695                 700
Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys Val Ala
705                 710                 715                 720
Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr Ser Ala
                725                 730                 735
Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu Lys
            740                 745                 750
```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 850 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 68...799
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```
ACCACTATTG TAGAAAAATA ACAAGAGGGT TTGCAAAAAC TCTCATTAAA AACAAGGAGC     60
AAAAAAG ATG AAA AAG GCG GGC TTT CTT TTT TTA GCG GTA ATG GCT ATC      109
        Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile
         1               5                   10

GTT GTT ATG AGT TTA AAC GCT AAA GAT CCG AAT GTG TTG CGT AAG ATT      157
Val Val Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile
15                  20                  25                  30

GTT TTT GAG AAA TGT CTG CCT AAT TAT GAG AAA AAT CAG AAT CCT TCG      205
Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser
                35                  40                  45

CCA TGC ATA GAA GTC AAA CCC GAT GCC GGC TAT GTG GTT TTA AAA GAT      253
Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp
            50                  55                  60

ATT AAC GGC CCG TTG CAA TAT TTG TTG ATG CCA ACA ACT CAC ATT AGC      301
Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser
        65                  70                  75
```

```
GGT ATT GAA AGC CCT TTG TTA CTT GAT CCT TCT ACG CCT AAC TTT TTT      349
Gly Ile Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe
    80                  85                  90

TAT TTA TCC TGG CAA GCG CGT GAT TTT ATG AGT AAA AAA TAC GGC CAA      397
Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln
95                  100                 105                 110

CCC ATT CCT GAT TAT GCG ATT TCT TTG ACG ATT AAC TCT AGC AAA GGG      445
Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly
                115                 120                 125

CGA TCG CAA AAC CAT TTT CAT ATC CAT ATC TCT TGC ATT AGT CTT GAA      493
Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu
            130                 135                 140

GCA CGC AAA CAG CTG GAT AAT AAC CTA AAA AAA ATC AAC AGC CGT TGG      541
Ala Arg Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp
        145                 150                 155

TCG CCA TTA CCG GGC GGT TTG AAT GGG CAT AAA TAC TTG GCG CGT CGG      589
Ser Pro Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg
    160                 165                 170

GTA ACA GAG AGC GAG TTA GTG CAA AAA AGC CCG TTT GTC ATG CTT AAT      637
Val Thr Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn
175                 180                 185                 190

AAA GAA GTG CCT AAT GCG TAC AAA CGC ATG GGG GAC TAT GGC TTA GCG      685
Lys Glu Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala
                195                 200                 205

GTG GTG CAA CAA AGC GAT AAC TCC TTT GTC TTA TTA GCG ACA CAA TTT      733
Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe
            210                 215                 220

AAC CCA TTG ACT TTA AAT CGC GCT TCA GCC GAA GAG ATT CAA GAT CAT      781
Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His
        225                 230                 235

GAA TGC GCG ATT TTG CAC TAAAGCGAGT TAGATTCTTA AGCTTGAGCG ATAACCTT    837
Glu Cys Ala Ile Leu His
    240

TAAAAAGCGT TAT                                                      850
```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```
Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile Val Val
 1               5                  10                  15
Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val Phe
            20                  25                  30
Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys
        35                  40                  45
Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn
    50                  55                  60
Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile
65                  70                  75                  80
Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu
                85                  90                  95
Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile
            100                 105                 110
Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser
        115                 120                 125
Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg
    130                 135                 140
Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro
145                 150                 155                 160
Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr
                165                 170                 175
Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu
            180                 185                 190
Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val
        195                 200                 205
Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro
    210                 215                 220
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys
225                 230                 235                 240
Ala Ile Leu His
```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 57...929
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```
GTCCTATTTT TTCATTCATT CAACGAATTT AAAAATTACA ATAAAGAGTT ATAGTT ATG     59
                                                                 Met
                                                                  1

AAA CGA AGG GAT TTT ATT AAA ACG ACT ACT TTA GGC GCT ACA GGT GCT     107
Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly Ala
```

```
                5                   10                  15

GTT TTA GGA GCA CAG ATT TTG CAG GCA GAA GAA AGT AAA GGG AGT GTT      155
Val Leu Gly Ala Gln Ile Leu Gln Ala Glu Glu Ser Lys Gly Ser Val
        20                  25                  30

GCA AAA TAT AAA ATA GAA GCT CAA TAC AGC ATT GAT TTT GAT TCT GCA      203
Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser Ala
    35                  40                  45

GAA CAC ACT TCA CTT TTC ATT CCC ATG CCG AGT GTT GTA GCG AGC AAT      251
Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser Asn
50                  55                  60                  65

GTG CAT TTA CAA GGC AAT CAT GCT AGC TAT AAA AGC ATG CTC AAT TTT      299
Val His Leu Gln Gly Asn His Ala Ser Tyr Lys Ser Met Leu Asn Phe
                70                  75                  80

GGA GTG CCT TAT TTG CAA GTG GAT TTT TTA AAA AGC ACT CAA AAA AAG      347
Gly Val Pro Tyr Leu Gln Val Asp Phe Leu Lys Ser Thr Gln Lys Lys
            85                  90                  95

CAA GTC CAT TTG TCT TAT GAG ATC GCT AGC TAT CAA TTG AAT GAG CGT      395
Gln Val His Leu Ser Tyr Glu Ile Ala Ser Tyr Gln Leu Asn Glu Arg
        100                 105                 110

TTG TTT GAA ACG AGC GAT TTT GTA GCA ATG GGG CGT TAT GAA AGA GAC      443
Leu Phe Glu Thr Ser Asp Phe Val Ala Met Gly Arg Tyr Glu Arg Asp
    115                 120                 125

GAT GCG AGC GTG GCT AAC ATT GCC AAC CAG CTT AAG GGA ACA ACC CCT      491
Asp Ala Ser Val Ala Asn Ile Ala Asn Gln Leu Lys Gly Thr Thr Pro
130                 135                 140                 145

AAA GAA AGC GTT CGC AAT TTT TAT GCG TTC ATC AAG CAT GAG ATG CCT      539
Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met Pro
                150                 155                 160

AAG AGA CAG AAG GCT TTA GAG GGT AAA GAA AAT TTA CCT AAG CGT GAG      587
Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg Glu
            165                 170                 175

AGT TTG CCC TGG TTT GCA ACC ATT TCA AAA GAG AGC ATG TTT GTG TCC      635
Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val Ser
        180                 185                 190

TTA TGC CAT GCG TGC GGG ATT AAA AGC GCT GAA GTG CAA GGC TTG AAA      683
Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu Lys
    195                 200                 205

CTG GGT CAA AAC AGC GTG GTG AAA AAC GCT CCT AGA GTG GAA GTG TAT      731
Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val Tyr
210                 215                 220                 225

TTG AAA GAT TCA TTT CTA GCG TTT GAT TTT CAA AAT AAT CAC AAG GAA      779
Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys Glu
                230                 235                 240
```

```
GTT TTT ATC CCG TTG AAT CGT CAT AAA GAC ATG CAG TTA GAT TCT GCC      827
Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser Ala
            245                 250                 255

TTA TTG GCG ACT TTT GGC GAT GCT TTT GCC CTT GTG GAT GGT AGG GAT      875
Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg Asp
        260                 265                 270

TTA GGC AAT TAC GAG AGC AAA CTT TTT GAA AAA AGA GTG TCC TAT ACG      923
Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr Thr
    275                 280                 285

ATT GTC TAAAGGCATG AAATCTAGGA ATATTCCTTG ATAGCGGGCT TTCCTTTTTA GG   981
Ile Val
290
```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```
Met Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly
 1               5                  10                  15
Ala Val Leu Gly Ala Gln Ile Leu Gln Ala Glu Glu Ser Lys Gly Ser
            20                  25                  30
Val Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser
        35                  40                  45
Ala Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser
    50                  55                  60
Asn Val His Leu Gln Gly Asn His Ala Ser Tyr Lys Ser Met Leu Asn
65                  70                  75                  80
Phe Gly Val Pro Tyr Leu Gln Val Asp Phe Leu Lys Ser Thr Gln Lys
                85                  90                  95
Lys Gln Val His Leu Ser Tyr Glu Ile Ala Ser Tyr Gln Leu Asn Glu
            100                 105                 110
Arg Leu Phe Glu Thr Ser Asp Phe Val Ala Met Gly Arg Tyr Glu Arg
        115                 120                 125
Asp Asp Ala Ser Val Ala Asn Ile Ala Asn Gln Leu Lys Gly Thr Thr
    130                 135                 140
Pro Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met
145                 150                 155                 160
Pro Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg
                165                 170                 175
Glu Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val
            180                 185                 190
Ser Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu
        195                 200                 205
Lys Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val
    210                 215                 220
```

```
Tyr Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys
225                 230                 235                 240
Glu Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser
                245                 250                 255
Ala Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg
            260                 265                 270
Asp Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr
        275                 280                 285
Thr Ile Val
    290
```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 686 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 82...633
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```
TGTGATTAAA CAAAATCAAA AACTTTTTAA CTATAATCAA ACCTAAATTA AAGTTCAAGG     60
AGTGGCATTT TGTTTAAAAG A ATG GTT TTA ATC GCT CTT TTA GGG GTG TTT     111
                       Met Val Leu Ile Ala Leu Leu Gly Val Phe
                        1               5                  10

TCA AGC GTT TCA TTA AGC GCT AAG AGT CTT TTA AGA GAT GAT GGG ATT     159
Ser Ser Val Ser Leu Ser Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile
                15                  20                  25

TTA GTC TCT GAT TTA AAG GGC ATG AAA TCA GAA CTA TCT GAT GCT CCT     207
Leu Val Ser Asp Leu Lys Gly Met Lys Ser Glu Leu Ser Asp Ala Pro
            30                  35                  40

GCT TGG GTT TTT GAA GAC GCT AAA GCC CCC TAC GAA GAA ATG GGC GTG     255
Ala Trp Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val
        45                  50                  55

GCG TAT ATC CCT GTT AAT AAT AAA TAT TTA GGG ATT GAG CAA GCG ACC     303
Ala Tyr Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr
    60                  65                  70

TTA AAC GCT AAA TTG AGT CTG ATC GTG GTT TTT CAT GAA ATC ATG ATG     351
Leu Asn Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met
75                  80                  85                  90

AAG TAT AAA AAA CGC TTC ATG GAG CAA TTC CAT GAG TCC GAG CAG ACG     399
Lys Tyr Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr
                95                  100                 105
```

```
ACT ACG AAT ATC AGT TAC GCT ATC TAT AAT TAT CTA GCG ACT AAG ATC      447
Thr Thr Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile
            110                 115                 120

CAG GTA TCC AAC ACC TAC ACG AAT TTA AAA TCG GAG GTG GCG GTG GTG      495
Gln Val Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val
        125                 130                 135

AAA ATC AAG CTA GTG GGT TGT CAG ATT GAG CAA ATC AAA AGG TAT TTA      543
Lys Ile Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu
    140                 145                 150

AAA GCG AGC GTT GAA AAC CTT AAC GAT AAT GAA ATC GCT TAC ATC GCT      591
Lys Ala Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala
155                 160                 165                 170

AAG GTC GCT CAA AAA GAA TTT GGT AGC GTT TGT GCG TTA AGG TAGTTTTAT    642
Lys Val Ala Gln Lys Glu Phe Gly Ser Val Cys Ala Leu Arg
                175                 180

AGCATTCTAG CGAGCATGTT TAAGGCATGC TCTACGCTTT TATT                     686
```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
Met Val Leu Ile Ala Leu Leu Gly Val Phe Ser Ser Val Ser Leu Ser
 1               5                  10                  15
Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile Leu Val Ser Asp Leu Lys
            20                  25                  30
Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp Val Phe Glu Asp
        35                  40                  45
Ala Lys Ala Pro Tyr Glu Glu Met Gly Val Ala Tyr Ile Pro Val Asn
    50                  55                  60
Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn Ala Lys Leu Ser
65                  70                  75                  80
Leu Ile Val Val Phe His Glu Ile Met Met Lys Tyr Lys Lys Arg Phe
                85                  90                  95
Met Glu Gln Phe His Glu Ser Glu Gln Thr Thr Thr Asn Ile Ser Tyr
            100                 105                 110
Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile Gln Val Ser Asn Thr Tyr
        115                 120                 125
Thr Asn Leu Lys Ser Glu Val Ala Val Val Lys Ile Lys Leu Val Gly
    130                 135                 140
Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu Lys Ala Ser Val Glu Asn
145                 150                 155                 160
Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala Lys Val Ala Gln Lys Glu
                165                 170                 175
Phe Gly Ser Val Cys Ala Leu Arg
```

180

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 112...252
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
ATGCCTGCCA TTTCATAGCC TAAATTTTCT TTAGAGCCGA ATTGATAAGC GGCTTTTAAG     60
ACTTCTTTTT GCTTAGCGTT AAAATCTTTA ATATTGTCGC AATTGGTCAT C ATG ACT     117
                                                          Met Thr
                                                           1

TTA GTA ACG GGC GAT TTG GGC TTG TTT TTA ACC CCT TTA GCG GGC TTA      165
Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala Gly Leu
          5                  10                  15

GGC TCT GTT TTA GTG GGG CTT TCT GTT GCG GCT AAA CTT AAA GAT GCA      213
Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys Asp Ala
    20                  25                  30

CTT AAG GCT GTG CCT AGC CAT AAG GCT TTA AAG ATG GTG TGAGTGAGTG GG    264
Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
35                  40                  45

GTTAAATGTT TCAAAACGCC TACCTTTTGT ATTAAGAAAT AAACTA                   310
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
Met Thr Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala
 1               5                  10                  15
Gly Leu Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys
            20                  25                  30
Asp Ala Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
```

35 40 45

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 145...579
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```
GCGTTCAATA GAATGCTTTA GTTAGGAAGC TCCTTGCTTT AGCAAGGNGT GGTTTCACTG      60
AAAGAGAGTA AGAAATTTGA AGAAAGGGTT TATCTTTTTT TAGATGAATT TGTGCGTTTT     120
GGTAAATTGC CTTTTTTATT AGAA ATG CCA GCA TTA AGT AGG AGC TAT GGT         171
                          Met Pro Ala Leu Ser Arg Ser Tyr Gly
                           1               5

GTG GTT TTA ATT TTT ATC ACG CAA TCC AAC GCT CTT ATT GAA AAA TAT       219
Val Val Leu Ile Phe Ile Thr Gln Ser Asn Ala Leu Ile Glu Lys Tyr
10                  15                  20                  25

TAC GGC AGA GAA GAT GCA AGA ATT GTT AAT AGC ACC GTG GCT TAC AAA       267
Tyr Gly Arg Glu Asp Ala Arg Ile Val Asn Ser Thr Val Ala Tyr Lys
                30                  35                  40

ATA ATT TTC AAA ATG GAT GAT TTA GAA TAC GCT AAA CAG GTG AGC GAA       315
Ile Ile Phe Lys Met Asp Asp Leu Glu Tyr Ala Lys Gln Val Ser Glu
            45                  50                  55

GAA GTC GGT AAG ATG ACT AGA AAA ACA CGA AGC CAC TCT ACA GAA AAA       363
Glu Val Gly Lys Met Thr Arg Lys Thr Arg Ser His Ser Thr Glu Lys
        60                  65                  70

GGA CAA CTC ATT ACC GGA GGG ACT TCT AGT ATA GGT AAA GAG GCG TGG       411
Gly Gln Leu Ile Thr Gly Gly Thr Ser Ser Ile Gly Lys Glu Ala Trp
    75                  80                  85

GAC TTA TTG AGC GCG CAA GAT ATT ATG AAT ATT GAT AAA GAT GAA GTG       459
Asp Leu Leu Ser Ala Gln Asp Ile Met Asn Ile Asp Lys Asp Glu Val
90                  95                  100                 105

ATC GTT TTA GTA AGC GGT CAT AAG GCT AAA CCC TTA AAA TTA AAA GCG       507
Ile Val Leu Val Ser Gly His Lys Ala Lys Pro Leu Lys Leu Lys Ala
                110                 115                 120

AAT TAT TAT TTC AAA AAC AAA GAA TTA CTC TCT CGT ATT AAC TGG GAA       555
Asn Tyr Tyr Phe Lys Asn Lys Glu Leu Leu Ser Arg Ile Asn Trp Glu
            125                 130                 135
```

```
GTC AAG CCC AAT GAA GAA GTG TTT TGATGGATTA AAAAAGTTTG CATGAGTATT     609
Val Lys Pro Asn Glu Glu Val Phe
        140                 145

TTTTAATTGC TTTTTTAAAA AT                                            631
```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```
Met Pro Ala Leu Ser Arg Ser Tyr Gly Val Val Leu Ile Phe Ile Thr
 1               5                  10                  15
Gln Ser Asn Ala Leu Ile Glu Lys Tyr Tyr Gly Arg Glu Asp Ala Arg
            20                  25                  30
Ile Val Asn Ser Thr Val Ala Tyr Lys Ile Ile Phe Lys Met Asp Asp
        35                  40                  45
Leu Glu Tyr Ala Lys Gln Val Ser Glu Glu Val Gly Lys Met Thr Arg
    50                  55                  60
Lys Thr Arg Ser His Ser Thr Glu Lys Gly Gln Leu Ile Thr Gly Gly
65                  70                  75                  80
Thr Ser Ser Ile Gly Lys Glu Ala Trp Asp Leu Leu Ser Ala Gln Asp
                85                  90                  95
Ile Met Asn Ile Asp Lys Asp Glu Val Ile Val Leu Val Ser Gly His
            100                 105                 110
Lys Ala Lys Pro Leu Lys Leu Lys Ala Asn Tyr Tyr Phe Lys Asn Lys
        115                 120                 125
Glu Leu Leu Ser Arg Ile Asn Trp Glu Val Lys Pro Asn Glu Glu Val
    130                 135                 140
Phe
145
```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 106...237
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```
TAAGGGCTTA CGCATAAAAT CGCATCCGCG CCGATTTTTT GAGCGAACTT TGCTAAAGAA      60
AGGGACTCGC TCGTGGCGTT ACTGCCCACG CCGGCTAACA CTTTC ATG CGC GAA TTT    117
                                                  Met Arg Glu Phe
                                                   1

GAG GGC GTT TTA GTG TTT TTG CAA GTT TCT ATG GCG ATT TCA ATG CAA      165
Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala Ile Ser Met Gln
 5                  10                  15                  20

CGC ATG TGC TCT TTG TGG GTG AGC GTG GCG GAT TCT CCT GTC GTG CCA      213
Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser Pro Val Val Pro
                25                  30                  35

ACA GGC ACG CAT GCG TCC ATG CCC TGAAAAATTT GGCGCTTGAT CAAGGTTTCA     267
Thr Gly Thr His Ala Ser Met Pro
            40

TAAGCGGCCT CATCAACGCT CAA                                           290
```

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```
Met Arg Glu Phe Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala
 1               5                  10                  15
Ile Ser Met Gln Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser
            20                  25                  30
Pro Val Val Pro Thr Gly Thr His Ala Ser Met Pro
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 58...369
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```
AAAGAAGGTT TGAAAAGCTT TTTTAAAAGG CTTTTGAAGT ATTTGGGGTA GGCTTGA ATG     60
                                                                 Met
                                                                  1

AAA GTG CAA AAT TTT ATC CAT TTT TCT GTT GTG GTA GGG TTT TTT TTG      108
Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe Leu
              5                  10                  15

GGG TTA GTG TTT TCG GTG TTG AAA TTC AAT GAG CCA GAG AGC ATT TTA      156
Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile Leu
         20                  25                  30

TTA TGG ACG GTG TTA TCC ACG CTT GGG GGG TAC TTG ATT GCG TTG TTG      204
Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu Leu
     35                  40                  45

TTT GCG TCT ATT TTT ATC GCT TGC ACG GAT TTG GAT ATT TGT CTT TTT      252
Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu Phe
50                  55                  60                  65

GAC AAA AAA GGC ACT GAA GAG AGT TTG CTT CGT TTC AAC CAT GAG TTT      300
Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu Phe
                 70                  75                  80

AAA AAC AGA GAA AAA GAA GTG GCT AGT ATT TTA GAA TAC ATT AGA AGT      348
Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg Ser
             85                  90                  95

TAT GAT TTT GAT GAT GGA AAA TAGAATGCCC AAAGGAATTC AAAAAACTGA AACA    403
Tyr Asp Phe Asp Asp Gly Lys
        100

AGCGAAAAAA ATATAGAA                                                 421
```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```
Met Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe
 1               5                  10                  15
Leu Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile
            20                  25                  30
Leu Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu
        35                  40                  45
Leu Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu
    50                  55                  60
Phe Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu
65                  70                  75                  80
Phe Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg
```

```
                85                  90                  95
Ser Tyr Asp Phe Asp Asp Gly Lys
            100
```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 670 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...617
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```
GTTTAGAAAA GCGTTTGAAC GCTATAAAAA ATGCAGAGTG GCTTTAAGGC ATG AAA      56
                                                         Met Lys
                                                           1

AAG ATT GCA TTT TTT ATT TTT GTC ATT TTG TTT TCG GTA GGG ATT TAT     104
Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly Ile Tyr
          5                  10                  15

TTA ATT TGG CAT GTT TTA TTG GAA AAA GCC CTA GAA TTG AAA TTA GCA     152
Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys Leu Ala
     20                  25                  30

ACC TCA GCT AAT GAT TTG CTT TTA AAA TTG TTG GCA ATT CTT GGC GTT     200
Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu Gly Val
35                  40                  45                  50

TTT TCA ATG TTA GTG CTT TTT CAA GGC ATT ATT TCT TCG TAT AAG AAG     248
Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr Lys Lys
                55                  60                  65

CGC CAA CTC AAA CGC ATT TTA CAA AAA ATA GAC GCC ATG AAC GGC TTT     296
Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn Gly Phe
            70                  75                  80

GAA TTT GAA GAA TAT TCC AAA ATC TTT TTC ACT TCA AAG GGT TTT GAA     344
Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly Phe Glu
        85                  90                  95

GTG AGC ATC ACG CAA AAA AGC GGC GAT TAT GGA GCG GAT TTG ATT ATA     392
Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu Ile Ile
    100                 105                 110

GAA AAA GAC GGC ATC AAG TGG GCG GTT CAA GTC AAA CGC TAC TCG CAT     440
Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr Ser His
115                 120                 125                 130
```

```
AAA GTT TCG CCC AAA GCC ATT CAA GAG GTG GTC TCT TCT AAA GCT TAT      488
Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys Ala Tyr
                135                 140                 145

TAC GCT TGC GAA AAA GCT TGC GTG ATC ACC AAC AGC TAT TTC ACG CAA      536
Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe Thr Gln
            150                 155                 160

GCC GCT CAA AAA CTG GCT CAA GCT AAC GAA GTG CTC TTG ATT GAC AGA      584
Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile Asp Arg
        165                 170                 175

GAC GAA TGG GTC AGG TTT TTG AAC GAA AAG AGA TGAACCGATC CCATCAGATC    637
Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
    180                 185

GTTTGTTCTC AAGTTCTTTT AAAATTTTGT CGT                                 670
```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```
Met Lys Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly
 1               5                  10                  15
Ile Tyr Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys
            20                  25                  30
Leu Ala Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu
        35                  40                  45
Gly Val Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr
    50                  55                  60
Lys Lys Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn
65                  70                  75                  80
Gly Phe Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly
                85                  90                  95
Phe Glu Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu
            100                 105                 110
Ile Ile Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr
        115                 120                 125
Ser His Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys
    130                 135                 140
Ala Tyr Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe
145                 150                 155                 160
Thr Gln Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile
                165                 170                 175
Asp Arg Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 125...538
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```
CAAAGAGTGG GATAAAATCA CAGAAATTTG TAAGAGAGCG CTAGCTTTAA GATAACAAAA     60
AGATCATGGC ATTTTGTATT TGCTTAATAA CACTATAATA AAATTTTTAA TAAGGAGATA    120
CATC ATG TTA GAA AAT GTC AAA AAG TCC TTT TTT AGG GTT TTG TGC TTG     169
     Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu
      1               5                  10                  15

GGT GCG TTG TGT TTA GGG GGG CTA ATG GCA GAG CAA GAC CCT AAA GAG      217
Gly Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu
                20                  25                  30

CTT GTG GGT TTG GGG GCA AAG AGC TAC AAA GAG AAA GAT TTC ACT CAA      265
Leu Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln
            35                  40                  45

GCG AAG AAA TAT TTT GAG AAA GCG TGC GAT TTG AAA GAA AAT AGC GGG      313
Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly
        50                  55                  60

TGT TTT AAT TTA GGG GTG CTT TAT TAT CAA GGG CAA GGG GTG GAA AAG      361
Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys
    65                  70                  75

AAC TTG AAA AAA GCC GCC TCC TTT TAC GCT AAA GCT TGC GAT TTG AAT      409
Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn
80                  85                  90                  95

TAC AGC AAT GGG TGT CAT TTG CTA GGG AAT TTA TAT TAC AGC GGG CAA      457
Tyr Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln
                100                 105                 110

GGC GTG TCC CAA AAC ACC AAT AAA GCC CTA CAA TAC TAC TCT AAA GCG      505
Gly Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala
            115                 120                 125

TGC GAT TTG AAA TAC GCT GAA GGG TGC GCG ACT TAGGGGGGAT TTATCATGAT   558
Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
        130                 135

GGTAAAGTGG TAACTAGGGA TTTTAAAAAA GCGGTGGAAT AT                      600
```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```
Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu Gly
 1               5                  10                  15
Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu
            20                  25                  30
Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln Ala
        35                  40                  45
Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys
    50                  55                  60
Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys Asn
65                  70                  75                  80
Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn Tyr
                85                  90                  95
Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly
            100                 105                 110
Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys
        115                 120                 125
Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 59...826
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```
TTTTAAGATT GGTAGCCATT GGCATTATGT TTGATCTTAT TAAAGCAGAG GAGTAACA      58

ATG GGA TAC GCA AGC AAA TTA GCC TTG AAG ATT TGT TTG GCA AGT TTA      106
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
 1               5                  10                  15

TGT TTA TTT AGC GCT CTT GGT GCA GAA CAC CTT GAA CAA AAA AGG AAC      154
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn
```

```
                20                  25                  30

TAT ATT TAT AAM GGG GAG GAA GCC TAT AAT AAT AAG GAA TAT GAG CGG      202
Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg
            35                  40                  45

GCG GCT TCT TTT TAT AAG AGC GCG ATT AAA AAT GGC GAG CCG CTT GCT      250
Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala
        50                  55                  60

TAT GTT CTT TTA GGG ATC ATG TAT GAA AAT GGT AGG GGT GTG CCT AAA      298
Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys
 65                  70                  75                  80

GAT GAA AAG AAA GCG GCT GAA TAT TTT CAA AAA GCG GTT GAT AAC GAT      346
Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp
                85                  90                  95

ATA CCT AGA GGG TAT AAC AAT TTA GGC GTG ATG TAT AAA GAG GGT AGA      394
Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg
            100                 105                 110

GGT GTG CCT AAA GAT GAA AAG AAA GCC GTG GAG TAT TTT AGA ATA GCT      442
Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala
        115                 120                 125

ACC GAG AAG GGC TAT ACT AAC GCC TAT ATA AAC TTA GGC ATC ATG TAT      490
Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr
    130                 135                 140

ATG GAG GGT AGG GGA GTT CCA AGC AAC TAT GTG AAA GCG ACA GAG TGC      538
Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys
145                 150                 155                 160

TTT AGA AAA GCG ATG CAT AAG GGT AAT GTA GAA GCT TAT ATC CTT TTA      586
Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu
                165                 170                 175

GGG GAT ATT TAT TAT AGT GGG AAT GAT CAA TTG GGT ATT GAG CCA GAC      634
Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp
            180                 185                 190

AAA GAT AAG GCG ATT GTC TAT TAT AAA ATG GCG GCT GAT ATG AGC TCT      682
Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser
        195                 200                 205

TCT AGA GCT TAT GAA GGG TTA GCA GAG TCT TAT CAG TAT GGG TTA GGC      730
Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly
    210                 215                 220

GTG GAA AAA GAT AAG AAA AAG GCT GAA GAA TAC ATG CAA AAA GCA TGC      778
Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys
225                 230                 235                 240

GAT TTT GAC ATT GAT AAA AAT TGT AAG AAA AAG AAC ACT TCA AGC CGA      826
Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg
                245                 250                 255
```

TAACTCTCAA ACTTGGGCTT GATTAGGATT TTTGTTTTAT TTTAAGTAGC ATG 879

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
 1               5                  10                  15
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn
            20                  25                  30
Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg
        35                  40                  45
Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala
    50                  55                  60
Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys
65                  70                  75                  80
Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp
                85                  90                  95
Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg
            100                 105                 110
Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala
        115                 120                 125
Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr
    130                 135                 140
Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys
145                 150                 155                 160
Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu
                165                 170                 175
Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp
            180                 185                 190
Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser
        195                 200                 205
Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly
    210                 215                 220
Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys
225                 230                 235                 240
Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 66...269
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```
TGGGGGTTGT GGTTGCTCAT GTTCGCATGG GTAGTAAGGT ATAGGAGTAT TTAAAAGGCA     60
AGGTC ATG AAT AGT TCT AAT CTC AAA AAT TGG CTA TTC CCT ACC ATT TGC    110
      Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys
       1               5                  10                  15

TTT TTT TTA TTT TGT TAT ATT TTA ATT TTT TTA ATG TTC TTT ATG TTT      158
Phe Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe
                20                  25                  30

AAA AGT TTG CAA TCG CAA TCG TTT GGC TCT GTG GCA GAA ACC GGA AAA      206
Lys Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys
            35                  40                  45

AAA CCC ATC ACC ACC ACC AAG AAA TTT GGT AAG GAA TTG CAA AAA CAG      254
Lys Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln
        50                  55                  60

ATT TCA AAA ATC CAT TAACTTTTTT TCTTTTTTGC CGATACTTGC TGTAATGGAA T   310
Ile Ser Lys Ile His
    65

GAATATCAA                                                           319
```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```
Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys Phe
 1               5                  10                  15
Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe Lys
            20                  25                  30
Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys Lys
        35                  40                  45
Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln Ile
    50                  55                  60
Ser Lys Ile His
65
```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 66...1058
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```
AAAAACTAGA GAGTGTTATA AGAAAAACAG AAGAGTGGAT GTCAAATTAA TGAAGTAATT      60
CTAGG ATG AAA AGG CTT TTT TTT ATC CCT TTT ATC GCT CCC TTT TTT CTC     110
      Met Lys Arg Leu Phe Phe Ile Pro Phe Ile Ala Pro Phe Phe Leu
       1               5                  10                  15

AAT GGG GAG CCT TCA GCG TTT GAT TTG CAA AGT GGG GCT ACC AAA AAA       158
Asn Gly Glu Pro Ser Ala Phe Asp Leu Gln Ser Gly Ala Thr Lys Lys
                  20                  25                  30

GAA CTC AAG CAG TTG CAA ATC AAT AGT AAG AAT TTT TCT AAT ATT TTG       206
Glu Leu Lys Gln Leu Gln Ile Asn Ser Lys Asn Phe Ser Asn Ile Leu
              35                  40                  45

ACC AAA ATC CAT TCG CAA GTA GAG GCT AAC ACT CAA GCT CAA GAG GGT       254
Thr Lys Ile His Ser Gln Val Glu Ala Asn Thr Gln Ala Gln Glu Gly
          50                  55                  60

TTG AGA AGC GTT TAT GAG GGG CAG GCT AAT AAG ATT AAA GAT CTC AAT       302
Leu Arg Ser Val Tyr Glu Gly Gln Ala Asn Lys Ile Lys Asp Leu Asn
      65                  70                  75

AAC GCT ATC CTT TCC CAA GAA GAA TCC TTA CGA GCC TTA AAA GCT TCG       350
Asn Ala Ile Leu Ser Gln Glu Glu Ser Leu Arg Ala Leu Lys Ala Ser
80                  85                  90                  95

CAA GAA GTG CAG GCT AAC ACG CTT AAG CAG CAA TCG CAA ACT TTA GAG       398
Gln Glu Val Gln Ala Asn Thr Leu Lys Gln Gln Ser Gln Thr Leu Glu
                  100                 105                 110

GAT TTG AGG AAT GAG ATT CAC GCT AAC CAG CAA GCT ATC CAG CAG TTA       446
Asp Leu Arg Asn Glu Ile His Ala Asn Gln Gln Ala Ile Gln Gln Leu
              115                 120                 125

GAC AAG CAA AAT AAA GAG ATG AGT GAA TTA TTG ACC AAG TTA AGC CAG       494
Asp Lys Gln Asn Lys Glu Met Ser Glu Leu Leu Thr Lys Leu Ser Gln
          130                 135                 140

GAT TTG GTT TCA CAA ATC GCC TTA ATC CAA AAA GCT CTC AAA GAA CAA       542
Asp Leu Val Ser Gln Ile Ala Leu Ile Gln Lys Ala Leu Lys Glu Gln
      145                 150                 155

GAG GAA AAA GCT GAA AAG CCG CTC AAA TCA AAC GCT CCG GCT AAT AAA       590
```

```
Glu Glu Lys Ala Glu Lys Pro Leu Lys Ser Asn Ala Pro Ala Asn Lys
160                 165                 170                 175

ACC CCC TCT TTG AAA GCC GAA TCC CCA AAA AAT CAA GAG GGA AAA ACT      638
Thr Pro Ser Leu Lys Ala Glu Ser Pro Lys Asn Gln Glu Gly Lys Thr
                180                 185                 190

CAA GAA AAG GCG AAA ATT GAG TTT GAT AAA GAC TTG TCT AAG CAA AAA      686
Gln Glu Lys Ala Lys Ile Glu Phe Asp Lys Asp Leu Ser Lys Gln Lys
            195                 200                 205

GAG ATC TTT CAA GAA GCT CTG TCT TTT TTT AAA AAT AAA TCC TAT GCA      734
Glu Ile Phe Gln Glu Ala Leu Ser Phe Phe Lys Asn Lys Ser Tyr Ala
        210                 215                 220

GAA GCC AAA GAG CGT TTG TTG TGG TTA GAA GCC AAT AGT TAC AGA CTT      782
Glu Ala Lys Glu Arg Leu Leu Trp Leu Glu Ala Asn Ser Tyr Arg Leu
    225                 230                 235

TAT TAT GTG CGT TAT GTT CTT GGA GAA GTG GCT TAT GGG GAA AAG AGA      830
Tyr Tyr Val Arg Tyr Val Leu Gly Glu Val Ala Tyr Gly Glu Lys Arg
240                 245                 250                 255

TAC AGA GAA GCG ATC AAG TAT TAC AAA GAG AGC GCT CTT TTA AAC AAA      878
Tyr Arg Glu Ala Ile Lys Tyr Tyr Lys Glu Ser Ala Leu Leu Asn Lys
                260                 265                 270

AAA GCG TCT TAC ATG CCT GTG CTT TTG TGG CAT ACG GCA TGG TCG TTT      926
Lys Ala Ser Tyr Met Pro Val Leu Leu Trp His Thr Ala Trp Ser Phe
            275                 280                 285

AAA AAA ATC AAA GAC GAT CAA AAC TAT TAT AAA TTT TTA AAC ACT TTG      974
Lys Lys Ile Lys Asp Asp Gln Asn Tyr Tyr Lys Phe Leu Asn Thr Leu
        290                 295                 300

CAA CAC TTG TAT CCT TCA AGC GAA CAA GCT AAA ATG GCG CAA AAA ATC     1022
Gln His Leu Tyr Pro Ser Ser Glu Gln Ala Lys Met Ala Gln Lys Ile
    305                 310                 315

TTA GAA AAC AAG GAG AAA CAC CAC CAT GCA AAA CCA TGATTTAGAG TCAATC  1074
Leu Glu Asn Lys Glu Lys His His His Ala Lys Pro
320                 325                 330

AAACAAGCCG CTTTGATTGA ATATGAAGTG AGAGAACA                          1112
```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```
Met Lys Arg Leu Phe Phe Ile Pro Phe Ile Ala Pro Phe Phe Leu Asn
 1               5                  10                  15
Gly Glu Pro Ser Ala Phe Asp Leu Gln Ser Gly Ala Thr Lys Lys Glu
            20                  25                  30
Leu Lys Gln Leu Gln Ile Asn Ser Lys Asn Phe Ser Asn Ile Leu Thr
        35                  40                  45
Lys Ile His Ser Gln Val Glu Ala Asn Thr Gln Ala Gln Glu Gly Leu
    50                  55                  60
Arg Ser Val Tyr Glu Gly Gln Ala Asn Lys Ile Lys Asp Leu Asn Asn
65                  70                  75                  80
Ala Ile Leu Ser Gln Glu Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln
                85                  90                  95
Glu Val Gln Ala Asn Thr Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp
            100                 105                 110
Leu Arg Asn Glu Ile His Ala Asn Gln Gln Ala Ile Gln Gln Leu Asp
        115                 120                 125
Lys Gln Asn Lys Glu Met Ser Glu Leu Leu Thr Lys Leu Ser Gln Asp
    130                 135                 140
Leu Val Ser Gln Ile Ala Leu Ile Gln Lys Ala Leu Lys Glu Gln Glu
145                 150                 155                 160
Glu Lys Ala Glu Lys Pro Leu Lys Ser Asn Ala Pro Ala Asn Lys Thr
                165                 170                 175
Pro Ser Leu Lys Ala Glu Ser Pro Lys Asn Gln Glu Gly Lys Thr Gln
            180                 185                 190
Glu Lys Ala Lys Ile Glu Phe Asp Lys Asp Leu Ser Lys Gln Lys Glu
        195                 200                 205
Ile Phe Gln Glu Ala Leu Ser Phe Phe Lys Asn Lys Ser Tyr Ala Glu
    210                 215                 220
Ala Lys Glu Arg Leu Leu Trp Leu Glu Ala Asn Ser Tyr Arg Leu Tyr
225                 230                 235                 240
Tyr Val Arg Tyr Val Leu Gly Glu Val Ala Tyr Gly Glu Lys Arg Tyr
                245                 250                 255
Arg Glu Ala Ile Lys Tyr Tyr Lys Glu Ser Ala Leu Leu Asn Lys Lys
            260                 265                 270
Ala Ser Tyr Met Pro Val Leu Leu Trp His Thr Ala Trp Ser Phe Lys
        275                 280                 285
Lys Ile Lys Asp Asp Gln Asn Tyr Tyr Lys Phe Leu Asn Thr Leu Gln
    290                 295                 300
His Leu Tyr Pro Ser Ser Glu Gln Ala Lys Met Ala Gln Lys Ile Leu
305                 310                 315                 320
Glu Asn Lys Glu Lys His His His Ala Lys Pro
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...483
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```
AACAAATGCG AGTTTCAAAT ATTTTGTAGG ATTTTAGGAA AGAAATAGGT T ATG AAT      57
                                                          Met Asn
                                                           1

ATA TCG GTT AAC CCC TAT TTA ATG GCG GTC GTT TTT GTG GTG TTT GTG      105
Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val Phe Val
          5                  10                  15

TTA TTG TTA TGG GCG ATG AAT GTT TGG GTG TAT AGG CCT TTG TTG GCT      153
Leu Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu Leu Ala
     20                  25                  30

TTT ATG GAT AAC AGA CAG GCA GAG ATA AAG GAT AGC TTG GCT AAA ATC      201
Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala Lys Ile
35                   40                  45                  50

AAA ACG GAT AAT GCC CAA AGT GTG GAG ATT GGC CAT CAA ATT GAG GCT      249
Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile Glu Ala
                55                  60                  65

CTT CTT AAA GAA GCG GCT GAA AAA CGC AGA GAA ATA ATA GCA GAA GCG      297
Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala Glu Ala
           70                  75                  80

ATT CAA AAA GCC ACA GAG TCC TAT GAC GCT GTG ATC AAG CAA AAA GAG      345
Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln Lys Glu
        85                  90                  95

AAC GAA CTC AAT CAA GAG TTT GAA GCG TTT GCG AAG CAA TTA CAA AAT      393
Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu Gln Asn
    100                 105                 110

GAA AAG CAA GCG CTA AAA GAG CAG TTG CAA GCG CAA ATG CCG GTA TTT      441
Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro Val Phe
115                 120                 125                 130

GAA GAC GAG TTA AAC AAG CGT GTG GCT ATG GGT TTA GGG AGT TGATGAATG    492
Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser
                135                 140

TTTGTAGTTA AAATGGTGTT AGGGTTTTTG ATCCTTTTA                           531
```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```
Met Asn Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val
 1               5                  10                  15
Phe Val Leu Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu
            20                  25                  30
Leu Ala Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala
        35                  40                  45
Lys Ile Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile
    50                  55                  60
Glu Ala Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala
65                  70                  75                  80
Glu Ala Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln
                85                  90                  95
Lys Glu Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu
            100                 105                 110
Gln Asn Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro
        115                 120                 125
Val Phe Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5832 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 387...5777
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

```
AAGCTTGATA TGGAGCATTT TGATCGCTTG ACCATGCTCA ATAGAGAAGA ATTGTTGCGC     60
GTTACTCGCT CCTTTCTCAA GCGATTTTAG AAGAGCCTTT CAGCCATAAC GGCAAGGATT    120
ATAAAGAAGG CGATCAAATC CCTAAAGAAG AAATCGCTTC AATCAACCGC TTCACTTTGG    180
CTAGTTTGGT CAAAAAGTAT TCTAAAGAAG TGCAAAACCA CTATGAAATC ACTAAAAACA    240
ATTTCTTAGA GCAAAAGAAA GTTTTGGGCG AAGAGCATGA AGAAAAGCTT TCTATTTTAG    300
AAAAAGATGA TATTTTGCCT AATGGCGTGA TCAAAAAAGT CAAGCTCTAT ATCGCTACAA    360
AACGAAAGCT TAAAGTGGGC GATAAA ATG GCA GGA AGG CAT GGG AAT AAA GGG      413
                             Met Ala Gly Arg His Gly Asn Lys Gly
                              1               5

ATT GTG TCT AAT ATC GTG CCG GTT GCG GAT ATG CCT TAT ACC GCT GAT      461
Ile Val Ser Asn Ile Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp
10                  15                  20                  25

GGC GAG CCT GTA GAT ATT GTT TTA AAC CCT TTA GGC GTG CCA AGC CGC      509
Gly Glu Pro Val Asp Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg
                30                  35                  40

ATG AAT ATC GGG CAG ATT TTA GAA ATG CAT TTA GGC TTA GTG GGG AAA      557
Met Asn Ile Gly Gln Ile Leu Glu Met His Leu Gly Leu Val Gly Lys
```

```
                45                  50                  55

GAA TTT GGG AAG CAA ATC GCT CGC ATG CTA GAG GAT AAA ACC AAA GAT      605
Glu Phe Gly Lys Gln Ile Ala Arg Met Leu Glu Asp Lys Thr Lys Asp
        60                  65                  70

TTT GCC AAA GAA TTG CGT GCT AAA ATG CTA GAA AWC GCT AAC GCT ATT      653
Phe Ala Lys Glu Leu Arg Ala Lys Met Leu Glu Xaa Ala Asn Ala Ile
    75                  80                  85

AAT GAA AAA GAC CCC TTG ACA ATC CAT GCG CTT GAG AAT TGT TCT GAT      701
Asn Glu Lys Asp Pro Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp
90                  95                  100                 105

GAA GAG CTT TTG GAA TAC GCA AAA GAT TGG AGC AAG GGC GTT AAG ATG      749
Glu Glu Leu Leu Glu Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met
                110                 115                 120

GCT ATC CCT GTG TTT GAA GGC ATC TCG CAA GAA AAA TTT TAT AAG CTA      797
Ala Ile Pro Val Phe Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu
            125                 130                 135

TTT GAA TTA GCT AAG ATC GCT ATG GAT GGC AAA ATG GAT CTG TAT GAC      845
Phe Glu Leu Ala Lys Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp
        140                 145                 150

GGA CGC ACA GGC GAG AAA ATG AGG GAG CGC GTG AAT GTG GGC TAC ATG      893
Gly Arg Thr Gly Glu Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met
    155                 160                 165

TAT ATG ATC AAA CTC CAC CAT TTA GTG GAT GAA AAA GTC CAT GCC AGA      941
Tyr Met Ile Lys Leu His His Leu Val Asp Glu Lys Val His Ala Arg
170                 175                 180                 185

AGC ACA GGC CCT TAT AGC TTA GTA ACG CAC CAG CCC GTG GGG GGT AAA      989
Ser Thr Gly Pro Tyr Ser Leu Val Thr His Gln Pro Val Gly Gly Lys
                190                 195                 200

GCG CTC TTT GGG GGT CAA AGG TTT GGG GAA ATG GAA GTG TGG GCC TTG     1037
Ala Leu Phe Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu
            205                 210                 215

GAA GCT TAT GGC GCA GCG CAC ACT CTA AAA GAA ATG CTC ACC ATT AAA     1085
Glu Ala Tyr Gly Ala Ala His Thr Leu Lys Glu Met Leu Thr Ile Lys
        220                 225                 230

TCC GAT GAT ATT AGA GGC AGA GAG AAC GCT TAT AGG GCT ATC GCT AAA     1133
Ser Asp Asp Ile Arg Gly Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys
    235                 240                 245

GGT GAG CAA GTG GGC GAG AGT GAA ATC CCT GAG ACT TTC TAT GTT TTG     1181
Gly Glu Gln Val Gly Glu Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu
250                 255                 260                 265

ACT AAA GAA TTG CAA TCG CTC GCT TTG GAT ATT AAT ATT TTT GGG GAC     1229
Thr Lys Glu Leu Gln Ser Leu Ala Leu Asp Ile Asn Ile Phe Gly Asp
                270                 275                 280
```

```
GAT GTG GAT GAG GAT GGA GCA CCT AAA CCC ATT GTC ATT AAA GAA GAT    1277
Asp Val Asp Glu Asp Gly Ala Pro Lys Pro Ile Val Ile Lys Glu Asp
            285                 290                 295

GAC AGG CCT AAA GAC TTT AGC TCT TTC CAG CTC ACA CTA GCT AGC CCT    1325
Asp Arg Pro Lys Asp Phe Ser Ser Phe Gln Leu Thr Leu Ala Ser Pro
        300                 305                 310

GAA AAA ATC CAT TCT TGG AGT TAT GGG GAA GTT AAA AAG CCA GAA ACG    1373
Glu Lys Ile His Ser Trp Ser Tyr Gly Glu Val Lys Lys Pro Glu Thr
    315                 320                 325

ATC AAT TAT CGC ACC CTA AAA CCT GAA CGA GAC GGC TTG TTT TGC ATG    1421
Ile Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Cys Met
330                 335                 340                 345

AAA ATC TTT GGC CCC ACT AAA GAT TAT GAA TGC TTG TGC GGC AAA TAC    1469
Lys Ile Phe Gly Pro Thr Lys Asp Tyr Glu Cys Leu Cys Gly Lys Tyr
                350                 355                 360

AAA AAG CCT CGC TTC AAA GAC ATT GGC ACA TGC GAA AAA TGC GGC GTG    1517
Lys Lys Pro Arg Phe Lys Asp Ile Gly Thr Cys Glu Lys Cys Gly Val
            365                 370                 375

GCG ATC ACG CAC TCC AAA GTC AGG CGT TTT AGA ATG GGG CAT ATT GAA    1565
Ala Ile Thr His Ser Lys Val Arg Arg Phe Arg Met Gly His Ile Glu
        380                 385                 390

TTG GCC ACT CCT GTA GCG CAT ATC TGG TAT GTT AAT TCC TTG CCT AGC    1613
Leu Ala Thr Pro Val Ala His Ile Trp Tyr Val Asn Ser Leu Pro Ser
    395                 400                 405

CGT ATC GGC ACG CTT TTA GGC GTT AAG ATG AAA GAC TTA GAG CGC GTG    1661
Arg Ile Gly Thr Leu Leu Gly Val Lys Met Lys Asp Leu Glu Arg Val
410                 415                 420                 425

TTG TAT TAT GAA GCT TAT ATC GTT AAA GAA CCA GGC GAA GCC GCT TAT    1709
Leu Tyr Tyr Glu Ala Tyr Ile Val Lys Glu Pro Gly Glu Ala Ala Tyr
                430                 435                 440

GAC AAT GAA GGC ACT AAG CTT GTG ATG AAA TAC GAT ATT TTG AAT GAA    1757
Asp Asn Glu Gly Thr Lys Leu Val Met Lys Tyr Asp Ile Leu Asn Glu
            445                 450                 455

GAG CAG TAT CAA AAT ATC TCA CGA AGA TAC GAA GAC AGG GGC TTT GTA    1805
Glu Gln Tyr Gln Asn Ile Ser Arg Arg Tyr Glu Asp Arg Gly Phe Val
        460                 465                 470

GCG CAA ATG GGC GGT GAA GCG ATC AAG GAT TTG TTA GAA GAA ATT GAT    1853
Ala Gln Met Gly Gly Glu Ala Ile Lys Asp Leu Leu Glu Glu Ile Asp
    475                 480                 485

TTG ATC ACC TTA TTG CAG AGT TTG AAA GAA GAA GTG AAA GAC ACC AAT    1901
Leu Ile Thr Leu Leu Gln Ser Leu Lys Glu Glu Val Lys Asp Thr Asn
490                 495                 500                 505

TCT GAT GCG AAA AAG AAA AAA CTC ATT AAG CGT TTG AAA GTG GTA GAA    1949
Ser Asp Ala Lys Lys Lys Lys Leu Ile Lys Arg Leu Lys Val Val Glu
```

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                    510                 515                 520

AGC TTT TTA AAT TCT GGT AAT AGG CCT GAA TGG ATG ATG CTC ACG GTT    1997
Ser Phe Leu Asn Ser Gly Asn Arg Pro Glu Trp Met Met Leu Thr Val
            525                 530                 535

TTA CCG GTA TTG CCA CCG GAT TTA AGG CCT TTA GTC GCG CTA GAT GGC    2045
Leu Pro Val Leu Pro Pro Asp Leu Arg Pro Leu Val Ala Leu Asp Gly
        540                 545                 550

GGG AAG TTT GCA GTC AGC GAT GTG AAT GAA TTG TAT CGT CGT GTC ATC    2093
Gly Lys Phe Ala Val Ser Asp Val Asn Glu Leu Tyr Arg Arg Val Ile
    555                 560                 565

AAT CGT AAC CAA CGC TTG AAA CGC TTA ATG GAG CTT GGA GCG CCA GAA    2141
Asn Arg Asn Gln Arg Leu Lys Arg Leu Met Glu Leu Gly Ala Pro Glu
570                 575                 580                 585

ATC ATT GTG CGC AAT GAA AAA AGG ATG TTG CAA GAA GCC GTG GAT GTG    2189
Ile Ile Val Arg Asn Glu Lys Arg Met Leu Gln Glu Ala Val Asp Val
                590                 595                 600

CTT TTT GAT AAC GGC CGC AGC ACT AAT GCG GTT AAA GGG GCT AAC AAA    2237
Leu Phe Asp Asn Gly Arg Ser Thr Asn Ala Val Lys Gly Ala Asn Lys
            605                 610                 615

CGC CCT TTA AAA TCG CTC AGT GAA ATC ATT AAA GGC AAG CAG GGG CGT    2285
Arg Pro Leu Lys Ser Leu Ser Glu Ile Ile Lys Gly Lys Gln Gly Arg
        620                 625                 630

TTC AGG CAA AAC CTT TTA GGT AAG CGC GTG GAT TTT TCA GGC AGA AGC    2333
Phe Arg Gln Asn Leu Leu Gly Lys Arg Val Asp Phe Ser Gly Arg Ser
    635                 640                 645

GTG ATT GTG GTT GGG CCT AAT CTC AAA ATG GAT GAA TGC GGG TTG CCT    2381
Val Ile Val Val Gly Pro Asn Leu Lys Met Asp Glu Cys Gly Leu Pro
650                 655                 660                 665

AAA AAC ATG GCG TTA GAA CTC TTC AAA CCG CAT TTG TTA TCC AAG CTT    2429
Lys Asn Met Ala Leu Glu Leu Phe Lys Pro His Leu Leu Ser Lys Leu
                670                 675                 680

GAA GAG AGA GGC TAT GCC ACC ACG CTC AAA CAG GCT AAA CGC ATG ATT    2477
Glu Glu Arg Gly Tyr Ala Thr Thr Leu Lys Gln Ala Lys Arg Met Ile
            685                 690                 695

GAG CAA AAA AGC AAT GAA GTA TGG GAG TGC TTG CAA GAA ATC ACA GAG    2525
Glu Gln Lys Ser Asn Glu Val Trp Glu Cys Leu Gln Glu Ile Thr Glu
        700                 705                 710

GGG TAT CCG GTG CTA CTC AAC CGC GCT CCT ACC TTG CAC AAG CAA TCC    2573
Gly Tyr Pro Val Leu Leu Asn Arg Ala Pro Thr Leu His Lys Gln Ser
    715                 720                 725

ATT CAA GCG TTC CAT CCA AAG CTG ATT GAC GGC AAA GCG ATC CAA TTG    2621
Ile Gln Ala Phe His Pro Lys Leu Ile Asp Gly Lys Ala Ile Gln Leu
730                 735                 740                 745
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```
CAC CCG TTA GTG TGT TCA GCG TTC AAC GCC GAT TTT GAC GGG GAC CAA     2669
His Pro Leu Val Cys Ser Ala Phe Asn Ala Asp Phe Asp Gly Asp Gln
                750                 755                 760

ATG GCG GTG CAT GTG CCT TTA AGC CAG GAA GCG ATC GCT GAA TGC AAG     2717
Met Ala Val His Val Pro Leu Ser Gln Glu Ala Ile Ala Glu Cys Lys
            765                 770                 775

GTG CTG ATG CTA AGC TCT ATG AAT ATC CTT TTG CCT GCT AGC GGT AAG     2765
Val Leu Met Leu Ser Ser Met Asn Ile Leu Leu Pro Ala Ser Gly Lys
        780                 785                 790

GCC GTA GCC ATT CCT AGC CAA GAT ATG GTT TTA GGG CTT TAT TAT CTT     2813
Ala Val Ala Ile Pro Ser Gln Asp Met Val Leu Gly Leu Tyr Tyr Leu
    795                 800                 805

TCT TTA GAA AAG AGC GGG GTC AAG GGC GAG CAT AAG CTT TTT TCT AGC     2861
Ser Leu Glu Lys Ser Gly Val Lys Gly Glu His Lys Leu Phe Ser Ser
810                 815                 820                 825

GTG AAT GAA ATC ATC ACC GCC ATT GAC ACG AAA GAA TTA GAC ATC CAC     2909
Val Asn Glu Ile Ile Thr Ala Ile Asp Thr Lys Glu Leu Asp Ile His
                830                 835                 840

GCA AAG ATT AGG GTT TTA GAT CAA GGG AAT ATT ATC GCT ACG AGT GCA     2957
Ala Lys Ile Arg Val Leu Asp Gln Gly Asn Ile Ile Ala Thr Ser Ala
            845                 850                 855

GGG CGC ATG ATC ATT AAG TCC ATT TTG CCT GAT TTT ATC CCT ACG GAT     3005
Gly Arg Met Ile Ile Lys Ser Ile Leu Pro Asp Phe Ile Pro Thr Asp
        860                 865                 870

TTG TGG AAC AGA CCC ATG AAG AAA AAA GAT ATT GGC GTG CTT GTG GAT     3053
Leu Trp Asn Arg Pro Met Lys Lys Lys Asp Ile Gly Val Leu Val Asp
    875                 880                 885

TAT GTG CAT AAA GTT GGC GGT ATC GGT ATT ACT GCA ACC TTT TTG GAT     3101
Tyr Val His Lys Val Gly Gly Ile Gly Ile Thr Ala Thr Phe Leu Asp
890                 895                 900                 905

AAT TTA AAA ACG CTT GGC TTT AGG TAT GCG ACT AAG GCT GGT ATT TCT     3149
Asn Leu Lys Thr Leu Gly Phe Arg Tyr Ala Thr Lys Ala Gly Ile Ser
                910                 915                 920

ATC TCT ATG GAG GAT ATT ATC ACG CCA AAA GAC AAG CAA AAA ATG GTG     3197
Ile Ser Met Glu Asp Ile Ile Thr Pro Lys Asp Lys Gln Lys Met Val
            925                 930                 935

GAA AAA GCC AAA GTA GAG GTT AAA AAA ATC CAG CAA CAA TAC GAT CAA     3245
Glu Lys Ala Lys Val Glu Val Lys Lys Ile Gln Gln Gln Tyr Asp Gln
        940                 945                 950

GGG CTG CTC ACT GAC CAA GAG CGT TAC AAT AAG ATC ATT GAC ACT TGG     3293
Gly Leu Leu Thr Asp Gln Glu Arg Tyr Asn Lys Ile Ile Asp Thr Trp
    955                 960                 965

ACT GAA GTC AAT GAC AAA ATG AGT AAA GAA ATG ATG ACC GCT ATC GCG     3341
Thr Glu Val Asn Asp Lys Met Ser Lys Glu Met Met Thr Ala Ile Ala
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970                 975                 980                 985

CAA GAT AAA GAG GGC TTT AAC TCT ATT TAT ATG ATG GCA GAT AGC GGC    3389
Gln Asp Lys Glu Gly Phe Asn Ser Ile Tyr Met Met Ala Asp Ser Gly
                990                 995                1000

GCA AGG GGT AGC GCG GCG CAA ATC CGT CAG CTT TCA GCG ATG AGG GGT    3437
Ala Arg Gly Ser Ala Ala Gln Ile Arg Gln Leu Ser Ala Met Arg Gly
           1005                1010                1015

CTT ATG ACA AAG CCG GAC GGC AGT ATC ATT GAA ACG CCC ATT ATT TCT    3485
Leu Met Thr Lys Pro Asp Gly Ser Ile Ile Glu Thr Pro Ile Ile Ser
       1020                1025                1030

AAC TTT AAA GAG GGG TTG AAT GTC TTA GAA TAC TTC AAT TCC ACG CAT    3533
Asn Phe Lys Glu Gly Leu Asn Val Leu Glu Tyr Phe Asn Ser Thr His
   1035                1040                1045

GGC GCT AGA AAG GGC TTA GCG GAT ACA GCG CTA AAA ACA GCC AAT GCG    3581
Gly Ala Arg Lys Gly Leu Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala
1050                1055                1060                1065

GGG TAT TTG ACC AGA AAG CTC ATT GAT GTT TCG CAA AAT GTC AAG GTG    3629
Gly Tyr Leu Thr Arg Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val
                1070                1075                1080

GTG TCT GAT GAT TGC GGC ACG CAT GAA GGG ATT GAA ATC ACG GAT ATT    3677
Val Ser Asp Asp Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile
           1085                1090                1095

GCG GTG GGG AGT GAG CTG ATT GAA CCT TTA GAA GAG CGT ATT TTT GGG    3725
Ala Val Gly Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly
       1100                1105                1110

CGC GTT TTA TTA GAA GAT GTG ATC GAT CCC ATT ACG AAT GAA ATC TTG    3773
Arg Val Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu
   1115                1120                1125

CTT TAT GCG GAC ACT TTG ATT GAT GAA GAG GGT GCT AAA AAG GTG GTT    3821
Leu Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val
1130                1135                1140                1145

GAA GCC GGG ATT AAA TCC ATT ACG ATC CGC ACC CCA GTA ACT TGT AAA    3869
Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys Lys
                1150                1155                1160

GCG CCA AAG GGC GTG TGC GCG AAA TGC TAT GGC TTG AAT TTG GGC GAA    3917
Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Gly Glu
           1165                1170                1175

GGC AAG ATG AGT TAT CCG GGT GAA GCG GTG GGC GTG GTA GCC GCG CAA    3965
Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val Ala Ala Gln
       1180                1185                1190

TCT ATT GGG GAG CCT GGA ACG CAG CTC ACT TTA AGG ACT TTC CAT GTG    4013
Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg Thr Phe His Val
   1195                1200                1205
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GGC GGG ACA GCG AGC AGG AGT CAG GAT GAG CGC GAA ATC GTA GCG AGC 4061
Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg Glu Ile Val Ala Ser
1210 1215 1220 1225

AAA GAA GGT TTT GTG CGT TTT TAC AAC CTT AGG ACT TAC ACG AAT AAA 4109
Lys Glu Gly Phe Val Arg Phe Tyr Asn Leu Arg Thr Tyr Thr Asn Lys
1230 1235 1240

GAG GGT AAA AAC ATT ATC GCT AAC CGC CGT AAC GCT TCT ATT TTA GTG 4157
Glu Gly Lys Asn Ile Ile Ala Asn Arg Arg Asn Ala Ser Ile Leu Val
1245 1250 1255

GTA GAG CCT AAG ATT AAA GCG CCT TTT GAT GGG GAA TTA CGC ATT GAA 4205
Val Glu Pro Lys Ile Lys Ala Pro Phe Asp Gly Glu Leu Arg Ile Glu
1260 1265 1270

ACG GTT TAT GAA GAA GTC GTT GTG AGC GTG AAA AAT GGC GAT CAA GAA 4253
Thr Val Tyr Glu Glu Val Val Val Ser Val Lys Asn Gly Asp Gln Glu
1275 1280 1285

GCT AAA TTT GTT TTA AGG AGA AGC GAT ATT GTC AAG CCA AGC GAA TTA 4301
Ala Lys Phe Val Leu Arg Arg Ser Asp Ile Val Lys Pro Ser Glu Leu
1290 1295 1300 1305

GCC GGC GTT GGC GGT AAG ATT GAG GGG AAA GTG TAT TTG CCT TAT GCT 4349
Ala Gly Val Gly Gly Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala
1310 1315 1320

AGT GGG CAT AAG GTG CAT AAG GGG GGA AGT ATC GCT GAT ATT ATC CAA 4397
Ser Gly His Lys Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln
1325 1330 1335

GAG GGC TGG AAT GTG CCT AAT CGC ATC CCT TAT GCG AGC GAA TTG CTA 4445
Glu Gly Trp Asn Val Pro Asn Arg Ile Pro Tyr Ala Ser Glu Leu Leu
1340 1345 1350

GTC AAG GAT AAT GAC CCT ATT GCG CAA GAT GTG TAT GCC AAA GAA AAA 4493
Val Lys Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys
1355 1360 1365

GGC GTA ATC AAA TAC TAT GTT TTA GAG GCT AAC CAT TTA GAG CGC ACC 4541
Gly Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr
1370 1375 1380 1385

CAT GGG ATC AAA AAG GGC GAT ATG GTG AGT GAA AAA GGC TTG TTT GCG 4589
His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe Ala
1390 1395 1400

GTG ATA GCT GAT GAT AAT GGT AGG GAA GCC GCT CGC CAT TAT ATC GCT 4637
Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr Ile Ala
1405 1410 1415

AGG GGT TCT GAG ATC TTG ATT GAT GAT AAT AGT GAA GTG AGC ACT AAT 4685
Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val Ser Thr Asn
1420 1425 1430

AGC GTG ATT TCT AAA CCC ACG ACT AAC ACT TTC AAA ACG ATT GCC ACA 4733
Ser Val Ile Ser Lys Pro Thr Thr Asn Thr Phe Lys Thr Ile Ala Thr

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    1435                1440                1445

 TGG GAT CCT TAC AAC ACC CCT ATC ATT GCG GAC TTT AAA GGT AAG GTG     4781
 Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp Phe Lys Gly Lys Val
1450                1455                1460                1465

 GGT TTT GTG GAT GTT ATC GCA GGG GTT ACG GTC GCT GAA AAA GAA GAC     4829
 Gly Phe Val Asp Val Ile Ala Gly Val Thr Val Ala Glu Lys Glu Asp
                1470                1475                1480

 GAA AAT ACC GGT ATC ACA AGC TTA GTG GTG AAT GAT TAC ATT CCA AGC     4877
 Glu Asn Thr Gly Ile Thr Ser Leu Val Val Asn Asp Tyr Ile Pro Ser
            1485                1490                1495

 GGA TAC AAA CCA AGC TTG TTT TTA GAG GGG GCT AAT GGC GAA GAG ATG     4925
 Gly Tyr Lys Pro Ser Leu Phe Leu Glu Gly Ala Asn Gly Glu Glu Met
        1500                1505                1510

 CGT TAT TTC CTA GAG CCA AAA ACC TCT ATC GCC ATT AGC GAT GGC TCT     4973
 Arg Tyr Phe Leu Glu Pro Lys Thr Ser Ile Ala Ile Ser Asp Gly Ser
    1515                1520                1525

 AGC GTG GAG CAA GCT GAA GTG TTA GCG AAA ATC CCT AAA GCG ACC GTT     5021
 Ser Val Glu Gln Ala Glu Val Leu Ala Lys Ile Pro Lys Ala Thr Val
1530                1535                1540                1545

 AAA TCT AGG GAT ATT ACC GGG GGT CTC CCA AGG GTT TCG GAA CTC TTT     5069
 Lys Ser Arg Asp Ile Thr Gly Gly Leu Pro Arg Val Ser Glu Leu Phe
                1550                1555                1560

 GAA GCG AGA AAA CCC AAG CCT AAA GAT GTG GCG ATC CTT TCT GAA GTT     5117
 Glu Ala Arg Lys Pro Lys Pro Lys Asp Val Ala Ile Leu Ser Glu Val
            1565                1570                1575

 GAT GGG ATT GTG AGT TTT GGC AAA CCC ATT CGC AAT AAA GAA CAC ATC     5165
 Asp Gly Ile Val Ser Phe Gly Lys Pro Ile Arg Asn Lys Glu His Ile
        1580                1585                1590

 ATC GTA ACT TCT AAA GAT GGC CGT TCC ATG GAT TAT TTT GTG GAT AAA     5213
 Ile Val Thr Ser Lys Asp Gly Arg Ser Met Asp Tyr Phe Val Asp Lys
    1595                1600                1605

 GGC AAG CAA ATT TTA GTG CAT GCC GAT GAA TTT GTG CAT GCG GGA GAA     5261
 Gly Lys Gln Ile Leu Val His Ala Asp Glu Phe Val His Ala Gly Glu
1610                1615                1620                1625

 GCG ATG ACG GAC GGA GTA ATT TCA AGC CAT GAT ATT TTA AGG ATC AGT     5309
 Ala Met Thr Asp Gly Val Ile Ser Ser His Asp Ile Leu Arg Ile Ser
                1630                1635                1640

 GGC GAA AAA GAG CTT TAT AAA TAC ATT GTG AGC GAA GTC CAG CAA GTG     5357
 Gly Glu Lys Glu Leu Tyr Lys Tyr Ile Val Ser Glu Val Gln Gln Val
            1645                1650                1655

 TAT CGC AGG CAG GGG GTG AGC ATT GCG GAC AAG CAC ATT GAA ATC ATT     5405
 Tyr Arg Arg Gln Gly Val Ser Ile Ala Asp Lys His Ile Glu Ile Ile
        1660                1665                1670
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GTT TCT CAA ATG CTA AGA CAG GTG CGT ATT TTA GAC AGC GGG GAT AGC     5453
Val Ser Gln Met Leu Arg Gln Val Arg Ile Leu Asp Ser Gly Asp Ser
   1675                1680                1685

AAG TTT ATT GAA GGG GAT TTA GTC AGT AAA AAA CTT TTC AAA GAA GAA     5501
Lys Phe Ile Glu Gly Asp Leu Val Ser Lys Lys Leu Phe Lys Glu Glu
1690                1695                1700                1705

AAC GCT CGT GTG ATC GCT TTA AAA GGC GAG CCA GCG ATT GCT GAA CCG     5549
Asn Ala Arg Val Ile Ala Leu Lys Gly Glu Pro Ala Ile Ala Glu Pro
                1710                1715                1720

GTG CTT TTA GGG ATC ACT AGA GCG GCT ATT GGG AGC GAT AGC ATC ATC     5597
Val Leu Leu Gly Ile Thr Arg Ala Ala Ile Gly Ser Asp Ser Ile Ile
           1725                1730                1735

TCA GCG GCC TCT TTC CAA GAA ACG ACT AAA GTT TTA ACA GAA GCC AGT     5645
Ser Ala Ala Ser Phe Gln Glu Thr Thr Lys Val Leu Thr Glu Ala Ser
       1740                1745                1750

ATC GCT ATG AAA AAA GAC TTT TTA GAG GAT TTG AAA GAG AAT GTG GTG     5693
Ile Ala Met Lys Lys Asp Phe Leu Glu Asp Leu Lys Glu Asn Val Val
   1755                1760                1765

TTG GGG AGG ATG ATC CCT GTG GGA ACA GGC ATG TAT AAG AAT AAA AAA     5741
Leu Gly Arg Met Ile Pro Val Gly Thr Gly Met Tyr Lys Asn Lys Lys
1770                1775                1780                1785

ATC GTG TTA AGA GCG CTT GAG GAT AAC TCT AAA TTT TGATATGAAA AATCGG  5793
Ile Val Leu Arg Ala Leu Glu Asp Asn Ser Lys Phe
                1790                1795

TTAAGATTTT TAAAAGAAAA ATTAGGGTAA AATGGGGGA                         5832
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(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1797 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

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Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile Val Pro
 1               5                  10                  15
Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp Ile Val
            20                  25                  30
Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln Ile Leu
        35                  40                  45
Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln Ile Ala
    50                  55                  60
Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu Arg Ala
65                  70                  75                  80
Lys Met Leu Glu Xaa Ala Asn Ala Ile Asn Glu Lys Asp Pro Leu Thr
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                    85                  90                  95
Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu Tyr Ala
                100                 105                 110
Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe Glu Gly
            115                 120                 125
Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu Ala Lys Ile Ala
    130                 135                 140
Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg Thr Gly Glu Lys Met
145                 150                 155                 160
Arg Glu Arg Val Asn Val Gly Tyr Met Tyr Met Ile Lys Leu His His
                165                 170                 175
Leu Val Asp Glu Lys Val His Ala Arg Ser Thr Gly Pro Tyr Ser Leu
            180                 185                 190
Val Thr His Gln Pro Val Gly Gly Lys Ala Leu Phe Gly Gly Gln Arg
        195                 200                 205
Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Ala Ala His
    210                 215                 220
Thr Leu Lys Glu Met Leu Thr Ile Lys Ser Asp Asp Ile Arg Gly Arg
225                 230                 235                 240
Glu Asn Ala Tyr Arg Ala Ile Ala Lys Gly Glu Gln Val Gly Glu Ser
                245                 250                 255
Glu Ile Pro Glu Thr Phe Tyr Val Leu Thr Lys Glu Leu Gln Ser Leu
            260                 265                 270
Ala Leu Asp Ile Asn Ile Phe Gly Asp Asp Val Asp Glu Asp Gly Ala
        275                 280                 285
Pro Lys Pro Ile Val Ile Lys Glu Asp Asp Arg Pro Lys Asp Phe Ser
    290                 295                 300
Ser Phe Gln Leu Thr Leu Ala Ser Pro Glu Lys Ile His Ser Trp Ser
305                 310                 315                 320
Tyr Gly Glu Val Lys Lys Pro Glu Thr Ile Asn Tyr Arg Thr Leu Lys
                325                 330                 335
Pro Glu Arg Asp Gly Leu Phe Cys Met Lys Ile Phe Gly Pro Thr Lys
            340                 345                 350
Asp Tyr Glu Cys Leu Cys Gly Lys Tyr Lys Lys Pro Arg Phe Lys Asp
        355                 360                 365
Ile Gly Thr Cys Glu Lys Cys Gly Val Ala Ile Thr His Ser Lys Val
    370                 375                 380
Arg Arg Phe Arg Met Gly His Ile Glu Leu Ala Thr Pro Val Ala His
385                 390                 395                 400
Ile Trp Tyr Val Asn Ser Leu Pro Ser Arg Ile Gly Thr Leu Leu Gly
                405                 410                 415
Val Lys Met Lys Asp Leu Glu Arg Val Leu Tyr Tyr Glu Ala Tyr Ile
            420                 425                 430
Val Lys Glu Pro Gly Glu Ala Ala Tyr Asp Asn Glu Gly Thr Lys Leu
        435                 440                 445
Val Met Lys Tyr Asp Ile Leu Asn Glu Glu Gln Tyr Gln Asn Ile Ser
    450                 455                 460
Arg Arg Tyr Glu Asp Arg Gly Phe Val Ala Gln Met Gly Gly Glu Ala
465                 470                 475                 480
Ile Lys Asp Leu Leu Glu Glu Ile Asp Leu Ile Thr Leu Leu Gln Ser
                485                 490                 495
Leu Lys Glu Glu Val Lys Asp Thr Asn Ser Asp Ala Lys Lys Lys Lys
            500                 505                 510
Leu Ile Lys Arg Leu Lys Val Val Glu Ser Phe Leu Asn Ser Gly Asn
        515                 520                 525
Arg Pro Glu Trp Met Met Leu Thr Val Leu Pro Val Leu Pro Pro Asp
    530                 535                 540
Leu Arg Pro Leu Val Ala Leu Asp Gly Gly Lys Phe Ala Val Ser Asp
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545 550 555 560
Val Asn Glu Leu Tyr Arg Arg Val Ile Asn Arg Asn Gln Arg Leu Lys
565 570 575
Arg Leu Met Glu Leu Gly Ala Pro Glu Ile Ile Val Arg Asn Glu Lys
580 585 590
Arg Met Leu Gln Glu Ala Val Asp Val Leu Phe Asp Asn Gly Arg Ser
595 600 605
Thr Asn Ala Val Lys Gly Ala Asn Lys Arg Pro Leu Lys Ser Leu Ser
610 615 620
Glu Ile Ile Lys Gly Lys Gln Gly Arg Phe Arg Gln Asn Leu Leu Gly
625 630 635 640
Lys Arg Val Asp Phe Ser Gly Arg Ser Val Ile Val Val Gly Pro Asn
645 650 655
Leu Lys Met Asp Glu Cys Gly Leu Pro Lys Asn Met Ala Leu Glu Leu
660 665 670
Phe Lys Pro His Leu Leu Ser Lys Leu Glu Glu Arg Gly Tyr Ala Thr
675 680 685
Thr Leu Lys Gln Ala Lys Arg Met Ile Glu Gln Lys Ser Asn Glu Val
690 695 700
Trp Glu Cys Leu Gln Glu Ile Thr Glu Gly Tyr Pro Val Leu Leu Asn
705 710 715 720
Arg Ala Pro Thr Leu His Lys Gln Ser Ile Gln Ala Phe His Pro Lys
725 730 735
Leu Ile Asp Gly Lys Ala Ile Gln Leu His Pro Leu Val Cys Ser Ala
740 745 750
Phe Asn Ala Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu
755 760 765
Ser Gln Glu Ala Ile Ala Glu Cys Lys Val Leu Met Leu Ser Ser Met
770 775 780
Asn Ile Leu Leu Pro Ala Ser Gly Lys Ala Val Ala Ile Pro Ser Gln
785 790 795 800
Asp Met Val Leu Gly Leu Tyr Tyr Leu Ser Leu Glu Lys Ser Gly Val
805 810 815
Lys Gly Glu His Lys Leu Phe Ser Ser Val Asn Glu Ile Ile Thr Ala
820 825 830
Ile Asp Thr Lys Glu Leu Asp Ile His Ala Lys Ile Arg Val Leu Asp
835 840 845
Gln Gly Asn Ile Ile Ala Thr Ser Ala Gly Arg Met Ile Ile Lys Ser
850 855 860
Ile Leu Pro Asp Phe Ile Pro Thr Asp Leu Trp Asn Arg Pro Met Lys
865 870 875 880
Lys Lys Asp Ile Gly Val Leu Val Asp Tyr Val His Lys Val Gly Gly
885 890 895
Ile Gly Ile Thr Ala Thr Phe Leu Asp Asn Leu Lys Thr Leu Gly Phe
900 905 910
Arg Tyr Ala Thr Lys Ala Gly Ile Ser Ile Ser Met Glu Asp Ile Ile
915 920 925
Thr Pro Lys Asp Lys Gln Lys Met Val Glu Lys Ala Lys Val Glu Val
930 935 940
Lys Lys Ile Gln Gln Gln Tyr Asp Gln Gly Leu Leu Thr Asp Gln Glu
945 950 955 960
Arg Tyr Asn Lys Ile Ile Asp Thr Trp Thr Glu Val Asn Asp Lys Met
965 970 975
Ser Lys Glu Met Met Thr Ala Ile Ala Gln Asp Lys Glu Gly Phe Asn
980 985 990
Ser Ile Tyr Met Met Ala Asp Ser Gly Ala Arg Gly Ser Ala Ala Gln
995 1000 1005
Ile Arg Gln Leu Ser Ala Met Arg Gly Leu Met Thr Lys Pro Asp Gly

1010 1015 1020
Ser Ile Ile Glu Thr Pro Ile Ile Ser Asn Phe Lys Glu Gly Leu Asn
025 1030 1035 1040
Val Leu Glu Tyr Phe Asn Ser Thr His Gly Ala Arg Lys Gly Leu Ala
1045 1050 1055
Asp Thr Ala Leu Lys Thr Ala Asn Ala Gly Tyr Leu Thr Arg Lys Leu
1060 1065 1070
Ile Asp Val Ser Gln Asn Val Lys Val Val Ser Asp Asp Cys Gly Thr
1075 1080 1085
His Glu Gly Ile Glu Ile Thr Asp Ile Ala Val Gly Ser Glu Leu Ile
1090 1095 1100
Glu Pro Leu Glu Glu Arg Ile Phe Gly Arg Val Leu Leu Glu Asp Val
105 1110 1115 1120
Ile Asp Pro Ile Thr Asn Glu Ile Leu Leu Tyr Ala Asp Thr Leu Ile
1125 1130 1135
Asp Glu Glu Gly Ala Lys Lys Val Val Glu Ala Gly Ile Lys Ser Ile
1140 1145 1150
Thr Ile Arg Thr Pro Val Thr Cys Lys Ala Pro Lys Gly Val Cys Ala
1155 1160 1165
Lys Cys Tyr Gly Leu Asn Leu Gly Glu Gly Lys Met Ser Tyr Pro Gly
1170 1175 1180
Glu Ala Val Gly Val Val Ala Ala Gln Ser Ile Gly Glu Pro Gly Thr
185 1190 1195 1200
Gln Leu Thr Leu Arg Thr Phe His Val Gly Gly Thr Ala Ser Arg Ser
1205 1210 1215
Gln Asp Glu Arg Glu Ile Val Ala Ser Lys Glu Gly Phe Val Arg Phe
1220 1225 1230
Tyr Asn Leu Arg Thr Tyr Thr Asn Lys Glu Gly Lys Asn Ile Ile Ala
1235 1240 1245
Asn Arg Arg Asn Ala Ser Ile Leu Val Val Glu Pro Lys Ile Lys Ala
1250 1255 1260
Pro Phe Asp Gly Glu Leu Arg Ile Glu Thr Val Tyr Glu Glu Val Val
265 1270 1275 1280
Val Ser Val Lys Asn Gly Asp Gln Glu Ala Lys Phe Val Leu Arg Arg
1285 1290 1295
Ser Asp Ile Val Lys Pro Ser Glu Leu Ala Gly Val Gly Gly Lys Ile
1300 1305 1310
Glu Gly Lys Val Tyr Leu Pro Tyr Ala Ser Gly His Lys Val His Lys
1315 1320 1325
Gly Gly Ser Ile Ala Asp Ile Ile Gln Glu Gly Trp Asn Val Pro Asn
1330 1335 1340
Arg Ile Pro Tyr Ala Ser Glu Leu Leu Val Lys Asp Asn Asp Pro Ile
345 1350 1355 1360
Ala Gln Asp Val Tyr Ala Lys Glu Lys Gly Val Ile Lys Tyr Tyr Val
1365 1370 1375
Leu Glu Ala Asn His Leu Glu Arg Thr His Gly Ile Lys Lys Gly Asp
1380 1385 1390
Met Val Ser Glu Lys Gly Leu Phe Ala Val Ile Ala Asp Asp Asn Gly
1395 1400 1405
Arg Glu Ala Ala Arg His Tyr Ile Ala Arg Gly Ser Glu Ile Leu Ile
1410 1415 1420
Asp Asp Asn Ser Glu Val Ser Thr Asn Ser Val Ile Ser Lys Pro Thr
425 1430 1435 1440
Thr Asn Thr Phe Lys Thr Ile Ala Thr Trp Asp Pro Tyr Asn Thr Pro
1445 1450 1455
Ile Ile Ala Asp Phe Lys Gly Lys Val Gly Phe Val Asp Val Ile Ala
1460 1465 1470
Gly Val Thr Val Ala Glu Lys Glu Asp Glu Asn Thr Gly Ile Thr Ser

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       1475                1480                1485
Leu Val Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe
   1490                1495                1500
Leu Glu Gly Ala Asn Gly Glu Glu Met Arg Tyr Phe Leu Glu Pro Lys
505                 1510                1515                1520
Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu Val
               1525                1530                1535
Leu Ala Lys Ile Pro Lys Ala Thr Val Lys Ser Arg Asp Ile Thr Gly
           1540                1545                1550
Gly Leu Pro Arg Val Ser Glu Leu Phe Glu Ala Arg Lys Pro Lys Pro
       1555                1560                1565
Lys Asp Val Ala Ile Leu Ser Glu Val Asp Gly Ile Val Ser Phe Gly
   1570                1575                1580
Lys Pro Ile Arg Asn Lys Glu His Ile Ile Val Thr Ser Lys Asp Gly
585                 1590                1595                1600
Arg Ser Met Asp Tyr Phe Val Asp Lys Gly Lys Gln Ile Leu Val His
               1605                1610                1615
Ala Asp Glu Phe Val His Ala Gly Glu Ala Met Thr Asp Gly Val Ile
           1620                1625                1630
Ser Ser His Asp Ile Leu Arg Ile Ser Gly Glu Lys Glu Leu Tyr Lys
       1635                1640                1645
Tyr Ile Val Ser Glu Val Gln Gln Val Tyr Arg Arg Gln Gly Val Ser
   1650                1655                1660
Ile Ala Asp Lys His Ile Glu Ile Ile Val Ser Gln Met Leu Arg Gln
665                 1670                1675                1680
Val Arg Ile Leu Asp Ser Gly Asp Ser Lys Phe Ile Glu Gly Asp Leu
               1685                1690                1695
Val Ser Lys Lys Leu Phe Lys Glu Glu Asn Ala Arg Val Ile Ala Leu
           1700                1705                1710
Lys Gly Glu Pro Ala Ile Ala Glu Pro Val Leu Leu Gly Ile Thr Arg
       1715                1720                1725
Ala Ala Ile Gly Ser Asp Ser Ile Ile Ser Ala Ala Ser Phe Gln Glu
   1730                1735                1740
Thr Thr Lys Val Leu Thr Glu Ala Ser Ile Ala Met Lys Lys Asp Phe
745                 1750                1755                1760
Leu Glu Asp Leu Lys Glu Asn Val Val Leu Gly Arg Met Ile Pro Val
               1765                1770                1775
Gly Thr Gly Met Tyr Lys Asn Lys Lys Ile Val Leu Arg Ala Leu Glu
           1780                1785                1790
Asp Asn Ser Lys Phe
       1795
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(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 65...640
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

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TAAGCGATTT GCTCTGTGTG GTGATTGACC CTAGGATTGA TTTTGAAAAG CGTTGAGGGT      60
AGGA ATG AAA ACT GAG ATG AAA TCT TCT TTA AAA CTT TTT ATG CGG CCT      109
     Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro
      1               5                  10                  15

TTG TTG GTG GTT TTA GCG TTC ATG TTG TTG TAT GCT TTA GTG CAT GCT      157
Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala
                  20                  25                  30

GCG CTT GGT TTT TAT GTA AAA AAA GAC AGC GCT CCA ATA AGC CCA AAT      205
Ala Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn
             35                  40                  45

GTA GAA AAA ACC GAG ACA GAG CGT CAA AAC GGC GTG CTT TCG CCC AAA      253
Val Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys
         50                  55                  60

CAA GAA GAA GCC AAC GCA ACC ACA ACT GCC ACA GAA GAA AGC CCC ACC      301
Gln Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr
     65                  70                  75

AAA GAC ACA GCG CCG CCT TTA GAC ACA GCC GCG CAA AAA CAA GAA ACT      349
Lys Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr
80                  85                  90                  95

AAA CAA GAG CAA GAA AAA GAA AAC GAG CCT AAA CAA GAT AGC GTC CCG      397
Lys Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro
                 100                 105                 110

CCC GTT CAA AAC AAT CAA AAA ACC CCT ACA ACC CCC TTA ATG GGA AAA      445
Pro Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys
             115                 120                 125

AAA CCT TTA GAG TAT AAA GTC GCA GTC AGT GGC GTG AAT GTG CGC GCT      493
Lys Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala
         130                 135                 140

TTT CCC AGC ACA AAA GGT AAA ATC TTG GGA TTG CTT TTA AAA AAT AAA      541
Phe Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys
     145                 150                 155

AGC GTG AAA GTT TTA GAA ATC CAA AAC GAT TGG GCT GAA ATT GAA TTT      589
Ser Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe
160                 165                 170                 175

TCT CAC GAA ACA AAG GGC TAT GTG TTT TTA AAA CTT TTA AAA AAG GCT      637
Ser His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala
                 180                 185                 190

GAA TGAAAGAATA ATGAAATTAA AATCTTTTGG GGTTTTTGGA AATCCCATTA           690
Glu
```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```
Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro Leu
 1               5                  10                  15
Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala Ala
            20                  25                  30
Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn Val
        35                  40                  45
Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys Gln
    50                  55                  60
Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr Lys
65                  70                  75                  80
Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr Lys
                85                  90                  95
Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro Pro
            100                 105                 110
Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys Lys
        115                 120                 125
Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala Phe
    130                 135                 140
Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys Ser
145                 150                 155                 160
Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe Ser
                165                 170                 175
His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala Glu
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 66...1502
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```
TTATGACTTT TACTAAACCT TTTTTTAAGC TATAATCCAA AAATCTAAAA TAAAAAGGAA     60
TAAGC ATG AAA AAA TCC CTT TGT CTG TCT TTC TTT CTG ACT TTC TCT AAC   110
      Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn
```

```
      1               5                  10                  15

CCT CTT CAA GCC CTT GTG ATC GAG CTT TTA GAA GAA ATC AAA ACT TCG      158
Pro Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser
                20                  25                  30

CCG CAT AAA GGC ACT TTT AAG GCT AAA GTC CTT GAT TCT AAA AAA CCA      206
Pro His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Lys Pro
            35                  40                  45

AGA CAA GTT TTA GGC GTT TAT AAT ATC TCC CCA CAC AAA AAA CTC ACG      254
Arg Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr
        50                  55                  60

CTC ACT ATC ACC CAC ATA TCC ACT GCA ATC GTC TAT CAA CCC CTT GAT      302
Leu Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp
    65                  70                  75

GAA AAA CTT TCT TTA GAA ACA ACC TTA AAC CCT AAC CGC CCT ACT ATC      350
Glu Lys Leu Ser Leu Glu Thr Thr Leu Asn Pro Asn Arg Pro Thr Ile
80                  85                  90                  95

CCT AGA AAC ACC CAG ATT GTT TTT TCT TCA AAA GAA TTG AAA GAG TCG      398
Pro Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Ser
                100                 105                 110

CAC CCG CAC CAA ATG CCT TCT TTA AAC GCG CCC ATG CAA AAA CCA CAA      446
His Pro His Gln Met Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln
            115                 120                 125

AAC AAA CCC CAT TCA TCG CAA CAA CCT TCT CAA AAC TTT TCT TAC CCA      494
Asn Lys Pro His Ser Ser Gln Gln Pro Ser Gln Asn Phe Ser Tyr Pro
        130                 135                 140

GAG CCC AAA CTA GGC TCT AAA AAC TCT AAA AAC AGC CTT TTA CAG CCT      542
Glu Pro Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro
    145                 150                 155

TTA GCA ATT CCT AGC AAA ATA AGT CCC ACT AAC GAA ACT CAA ACG CCA      590
Leu Ala Ile Pro Ser Lys Ile Ser Pro Thr Asn Glu Thr Gln Thr Pro
160                 165                 170                 175

ACA AAC GAC ACT AAA CCC CCT TTA AAG CAT TCT TCA GAA GAT CAA GAA      638
Thr Asn Asp Thr Lys Pro Pro Leu Lys His Ser Ser Glu Asp Gln Glu
                180                 185                 190

AGC AAC CTC TTT ATA ACG CCA CCC ACT GAA AAA ACG CTC CCT AAC AAC      686
Ser Asn Leu Phe Ile Thr Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn
            195                 200                 205

ACC TCT AAC GCT GAT ATT AGT GAA AAC AAT GAA AGC AAT GAG AAT AAA      734
Thr Ser Asn Ala Asp Ile Ser Glu Asn Asn Glu Ser Asn Glu Asn Lys
        210                 215                 220

GAT AAT GTG GAA AAA CAA GCC ATT AGA GAT GCT AAT ATT AAA GAA TTT      782
Asp Asn Val Glu Lys Gln Ala Ile Arg Asp Ala Asn Ile Lys Glu Phe
    225                 230                 235
```

```
GCA TGC GGG AAG TGG GTC TAT GAC GAT GAA AAT TTA CAA GCC TAC CGC      830
Ala Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg
240                 245                 250                 255

CCA AGC ATT TTA AAA CGC GTT GAT GAA GAC AAA CAA ACT GCA ACA GAT      878
Pro Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp
                260                 265                 270

ATT ACC CCT TGC GAT TAC AGC ACC GCT GAA AAT AAA AGC GGT AAA ATC      926
Ile Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile
            275                 280                 285

ATT ACC CCC TAT ACT AAA ATC TCC GTT CAT AAA ACA GAG CCT TTA GAA      974
Ile Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu
        290                 295                 300

GAG CCA CAA ACT TTT GAA GCT AAA AAT AAT TTC GCC ATT CTT CAA GCC     1022
Glu Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala
    305                 310                 315

AGA AGC TCT ACA GAA AAA TGC AAA AGG GCT AGA GCA AGA AAA GAC GGC     1070
Arg Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly
320                 325                 330                 335

ACG ACT AGG CAA TGC TAT CTA ATA GAA GAG CCT TTA AAA CAA GCA TGG     1118
Thr Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp
                340                 345                 350

GAG AGT GAG TAT GAA ATC ACC ACG CAA TTA GTG AAA GCC ATT TAT GAG     1166
Glu Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu
            355                 360                 365

CGC CCC AAA CAA GAC GAT CAA GTA GAG CCG ACT TTT TAT GAA ACC AGC     1214
Arg Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser
        370                 375                 380

GAA TTG GCT TAT TCT TCC ACA CGA AAA AGC GAA ATA ACG CAC AAT GAA     1262
Glu Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu
    385                 390                 395

TTG AAT TTG AAT GAA AAA TTC ATG GAA TTT GTG GAA GTG TAT GAG GGG     1310
Leu Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly
400                 405                 410                 415

CAT TAT TTA AAC GAT ATA ATT AAA GAG AGC AGT GAA TAT AAA GAA TGG     1358
His Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp
                420                 425                 430

GTT AAA AAC CAT GTG CGC TTT AAA GAA GGG GTG TGC ATG GCT TTA GAA     1406
Val Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu
            435                 440                 445

ATA GAA GAA CAG CCA CGA GCT AAA AGC ACG CCT TTG AGT ATT GAA AAC     1454
Ile Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn
        450                 455                 460

TCT CGT GTG GTA TGT GTC AAA AAG GGG AAT TAT TTA TTC AAC GAA GTT T   1503
Ser Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
```

465 470 475

AAGATGGTGG CTTGAGGCGG AATCGAACCA CCGACACGAA GATTTTC 1550

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 479 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro
1 5 10 15
Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser Pro
20 25 30
His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Lys Pro Arg
35 40 45
Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr Leu
50 55 60
Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp Glu
65 70 75 80
Lys Leu Ser Leu Glu Thr Thr Leu Asn Pro Asn Arg Pro Thr Ile Pro
85 90 95
Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Ser His
100 105 110
Pro His Gln Met Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln Asn
115 120 125
Lys Pro His Ser Ser Gln Gln Pro Ser Gln Asn Phe Ser Tyr Pro Glu
130 135 140
Pro Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro Leu
145 150 155 160
Ala Ile Pro Ser Lys Ile Ser Pro Thr Asn Glu Thr Gln Thr Pro Thr
165 170 175
Asn Asp Thr Lys Pro Pro Leu Lys His Ser Ser Glu Asp Gln Glu Ser
180 185 190
Asn Leu Phe Ile Thr Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn Thr
195 200 205
Ser Asn Ala Asp Ile Ser Glu Asn Asn Glu Ser Asn Glu Asn Lys Asp
210 215 220
Asn Val Glu Lys Gln Ala Ile Arg Asp Ala Asn Ile Lys Glu Phe Ala
225 230 235 240
Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg Pro
245 250 255
Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp Ile
260 265 270
Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile Ile
275 280 285
Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu Glu
290 295 300
Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala Arg
305 310 315 320
Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly Thr

```
                325                 330                 335
Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu
            340                 345                 350
Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg
        355                 360                 365
Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu
    370                 375                 380
Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu Leu
385                 390                 395                 400
Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His
                405                 410                 415
Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val
            420                 425                 430
Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu Ile
        435                 440                 445
Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn Ser
    450                 455                 460
Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
465                 470                 475
```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 68...568
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```
TGTAAAATAG GGATTTGCTA GGCCTTTAGT CGTTAAAAGG TAATTATCAT TAAGGAGTTT     60
TTTAATC ATG GCA GAT ATT CAA AGG CGT GAT TTT TTA GGA ATG AGC CTT      109
        Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu
         1               5                   10

GCT AGT GTT ACA GCT ATA GGG GCT ATA GCG AGT CTG GTA GCG ATG AAA      157
Ala Ser Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys
15                  20                  25                  30

AAG ACT TGG GAT CCG CTT CCA AGC GTT GTT TCA GCC GGT TTT ACG ACC      205
Lys Thr Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr
                35                  40                  45

ATA GAT GTG GCG AAT ATG CAA GAA GGG CAG TTT TCC ACC GTG GAA TGG      253
Ile Asp Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp
            50                  55                  60

CGT GGG AAA CCG GTC TAT ATC CTC AAG CGT TCT AAA AAA GAG GGC TTT      301
Arg Gly Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe
```

```
        65                  70                  75

AAT GAA AAG CGC GAT TTT AAA GTT GGC GAG AGC GTT TTT ACC ACA GCC      349
Asn Glu Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala
    80                  85                  90

ATT CAA ATT TGC ACG CAT TTA GGG TGT ATC CCC ACT TAT CAA GAT GAA      397
Ile Gln Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu
95                  100                 105                 110

GAA AAA GGC TTT TTA TGC CCA TGC CAT GGG GGG CGT TTC ACT TCT GAT      445
Glu Lys Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp
                115                 120                 125

GGC GTG AAT ATT GCC GGC ACT CCC CCT CCA CGC CCT TTT GAT ATC CCG      493
Gly Val Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro
            130                 135                 140

CCT TTT AAA ATT GAA GGC ACT AAG ATC ACT TTT GGT GAA GCC GGG GCT      541
Pro Phe Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala
        145                 150                 155

GAA TAC AAG AAA ATG ATG GCT AAA GCG TAAGGAGAGT TTAATGGCAG AGATAAA    595
Glu Tyr Lys Lys Met Met Ala Lys Ala
    160                 165

AAAAGCGAAA AATTTAGGCG AATGG                                          620
```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```
Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu Ala Ser
 1               5                  10                  15
Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys Lys Thr
            20                  25                  30
Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr Ile Asp
        35                  40                  45
Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp Arg Gly
    50                  55                  60
Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe Asn Glu
65                  70                  75                  80
Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala Ile Gln
                85                  90                  95
Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu Glu Lys
            100                 105                 110
Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp Gly Val
        115                 120                 125
Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro Pro Phe
```

```
    130                 135                 140
Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala Glu Tyr
145                 150                 155                 160
Lys Lys Met Met Ala Lys Ala
                165
```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...1167
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```
TTATAATCAA AGCTATTTTA AAAGCTGAAT AGCTATAGTT ATTAGGATGC G ATG TCA      57
                                                          Met Ser
                                                           1

AAA AGA ATG AAG TGT TTT AGT CAA AAA TGG TTG GTT TTT TTT GTT ACC      105
Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe Val Thr
          5                  10                  15

CTT TTA TTG GCT TCT TTA GGC CAT GCG AAA ATG GCT TTT GAA TCC GAT      153
Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu Ser Asp
    20                  25                  30

ATT GAC ACC AAA GCG CTA GAG GCT TTT GGG GTT AAT GCG GGC TTT TTA      201
Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly Phe Leu
35                  40                  45                  50

TCC CAA ATG CCC AAC GCT TTA AAA AAA ATG AAT AAA GAA GAA GAA TGG      249
Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu Glu Trp
                55                  60                  65

AAG AGA CTT GTC AAA AGA TTT GAT GTG AAT TAC CAG TTC ATC CCC ATC      297
Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile Pro Ile
            70                  75                  80

ATT AAA AAC ATG CTC ATA GAA GCG AGC GTG CCG CAA GAA TTT TTA TTT      345
Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe Leu Phe
        85                  90                  95

TTA GCC ATG GCC GAG TCT AAA TTT TCA TCA AGG GCT TAT AGC AGG AAA      393
Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser Arg Lys
    100                 105                 110

AAA GCG GTA GGG ATT TGG CAA TTC ATG CCA AGC ACG GCT AAA GAA TTA      441
```

```
Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys Glu Leu
115                 120                 125                 130

GGG CTT AAG GTC AAT CAT TAC ATT GAT GAA AGA AGA GAT CCC ATT AAA      489
Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro Ile Lys
                135                 140                 145

AGC ACT CAA GCG GCG ATC ACT TAT TTG AAA CGG CTC TAC AAG CAA ACC      537
Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys Gln Thr
            150                 155                 160

GGA GAG TGG TAT TTG GTC GCT ATG GCG TAT AAT TAC GGC TTA CGC AAG      585
Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu Arg Lys
        165                 170                 175

GTT CAA AAC GCT ATT AAA GCC GCC GGC ACT TCG GAC ATT AAA ATT TTG      633
Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys Ile Leu
    180                 185                 190

TTG GAT GAA GAT AAG AAA TAC CTC CCT AAA GAA ACA CGA GAG TAT ATC      681
Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu Tyr Ile
195                 200                 205                 210

CGC TCC ATT CTA AGC CTA GCG TTA AAA TTC AAC AGC CTA GAC AAC CTC      729
Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp Asn Leu
                215                 220                 225

AAA GAT AAA GAA TAT CTG CTC AAT CGT GGG GCG AGG GTG AGT TTA GTG      777
Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser Leu Val
            230                 235                 240

GGC GTC CCG TTT AAA AGG CGT GCT TCT TTA GTC CAA GTA GCC AAA AAT      825
Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala Lys Asn
        245                 250                 255

TTG AAT TTG AGT TTG GAA ACC TTA AAA TCC TAC AAC CAC CAA TTC CGT      873
Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln Phe Arg
    260                 265                 270

TAT AAC ATT CTG CCT TCT AAA GAC CCC ACT TAT ACC ATT TAT ATC CCT      921
Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr Ile Pro
275                 280                 285                 290

TAT GAA AAA CTC GCT CTT TTC AAA CAA CGC CAG ATC AAA CAA AAT AAA      969
Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln Asn Lys
                295                 300                 305

AAC ATT CAA GCC AGT TCA AAA AGC CCT TTT ATC ACC CAT GTG GTC TTA     1017
Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val Val Leu
            310                 315                 320

CCT AAA GAA ACC CTA TCT TCT ATC GCT AAA CGC TAT CAA GTC AGT ATT     1065
Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val Ser Ile
        325                 330                 335

TCC AAT ATC CAA TTA GCC AAT GAT CTC AAA GAT TCT AAT ATT TTT ATC     1113
Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile Phe Ile
    340                 345                 350
```

```
CAC CAG CGT TTA ATC ATC CCC ACC AAC AAA AAA TTA CTC GCT ACA AGG     1161
His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala Thr Arg
355                 360                 365                 370

GAA TTT TAATGGGTTT GGCGTTGGAA AAAGTTTGTT TTTTAGGCGT TATTTTTTTG AT  1219
Glu Phe

TA                                                                 1221
```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```
Met Ser Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe
 1               5                  10                  15
Val Thr Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu
            20                  25                  30
Ser Asp Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly
        35                  40                  45
Phe Leu Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu
    50                  55                  60
Glu Trp Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile
65                  70                  75                  80
Pro Ile Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe
                85                  90                  95
Leu Phe Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser
            100                 105                 110
Arg Lys Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys
        115                 120                 125
Glu Leu Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro
    130                 135                 140
Ile Lys Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys
145                 150                 155                 160
Gln Thr Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu
                165                 170                 175
Arg Lys Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys
            180                 185                 190
Ile Leu Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu
        195                 200                 205
Tyr Ile Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp
    210                 215                 220
Asn Leu Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser
225                 230                 235                 240
Leu Val Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala
                245                 250                 255
Lys Asn Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln
            260                 265                 270
Phe Arg Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr
```

```
        275                 280                 285
Ile Pro Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln
    290                 295                 300
Asn Lys Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val
305                 310                 315                 320
Val Leu Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val
                325                 330                 335
Ser Ile Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile
            340                 345                 350
Phe Ile His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala
        355                 360                 365
Thr Arg Glu Phe
    370
```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...510
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```
AAATGAGCTA AAATGAGCGT TTCATTTGAC AAATAAAGGG ATTGA ATG GCT TTT AAG     57
                                                  Met Ala Phe Lys
                                                   1

GTG GTG CAA ATT TGC GGA GGG CTT GGG AAT CAA ATG TTT CAA TAC GCT     105
Val Val Gln Ile Cys Gly Gly Leu Gly Asn Gln Met Phe Gln Tyr Ala
 5                  10                  15                  20

TTC GCT AAA AGT TTG CAA AAA CAC TCT AAT ACG CCT GTG CTG TTA GAT     153
Phe Ala Lys Ser Leu Gln Lys His Ser Asn Thr Pro Val Leu Leu Asp
                25                  30                  35

ATC ACT TCT TTT GAT TGG AGC GAT AGG AAA ATG CAA TTA GAA CTT TTC     201
Ile Thr Ser Phe Asp Trp Ser Asp Arg Lys Met Gln Leu Glu Leu Phe
            40                  45                  50

CCT ATT GAT TTG CCC TAT GCG AGC GCG AAA GAA ATC GCT ATA GCT AAA     249
Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile Ala Ile Ala Lys
        55                  60                  65

ATG CAA CAC CTC CCC AAG CTA GTA AGA GAC GCG CTC AAA TGC ATG GGA     297
Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu Lys Cys Met Gly
    70                  75                  80

TTT GAT AGG GTG AGT CAA GAA ATC GTT TTT GAA TAC GAG CCT AAA TTG     345
```

```
Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr Glu Pro Lys Leu
85                  90                  95                  100

CTA AAG CCA AGC CGC TTG ACT TAT TTT TTT GGC TAT TTC CAA GAT CCA      393
Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr Phe Gln Asp Pro
                105                 110                 115

CGA TAC TTT GAT GCT ATA TCC CCT TTA ATC AAG CAA ACC TTC ACT CTA      441
Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln Thr Phe Thr Leu
            120                 125                 130

CCC CCC CCC CCC CCG AAA ATA ATA AGA ATA ATA ATA AAA AAG AGG AAG      489
Pro Pro Pro Pro Pro Lys Ile Ile Arg Ile Ile Ile Lys Lys Arg Lys
        135                 140                 145

AAT ATC AGT GCA AGC TTT CTT TGATTTTAGC CGCTAAAAAC AGCGTGTTTG TGCA    544
Asn Ile Ser Ala Ser Phe Leu
    150                 155

TATAAGAAGA GGGGATT                                                  561
```

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
Met Ala Phe Lys Val Val Gln Ile Cys Gly Gly Leu Gly Asn Gln Met
 1               5                  10                  15
Phe Gln Tyr Ala Phe Ala Lys Ser Leu Gln Lys His Ser Asn Thr Pro
            20                  25                  30
Val Leu Leu Asp Ile Thr Ser Phe Asp Trp Ser Asp Arg Lys Met Gln
        35                  40                  45
Leu Glu Leu Phe Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile
    50                  55                  60
Ala Ile Ala Lys Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu
65                  70                  75                  80
Lys Cys Met Gly Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr
                85                  90                  95
Glu Pro Lys Leu Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr
            100                 105                 110
Phe Gln Asp Pro Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln
        115                 120                 125
Thr Phe Thr Leu Pro Pro Pro Pro Pro Lys Ile Ile Arg Ile Ile Ile
    130                 135                 140
Lys Lys Arg Lys Asn Ile Ser Ala Ser Phe Leu
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 86...1201
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
GGTTATTATA GTATAATATT GTCAAAAAAT AAATTCAACT TTGGATTAAA TTGATTAAAA      60
ACCTATTTTA GGGAAACCGC TTAAA ATG AGT ATT ATT ATT CCT ATT GTC ATC      112
                            Met Ser Ile Ile Ile Pro Ile Val Ile
                             1               5

GCT TTT GAT AAT CAC TAT GCC ATG CCG GCT GGC GTG AGC TTG TAT TCC      160
Ala Phe Asp Asn His Tyr Ala Met Pro Ala Gly Val Ser Leu Tyr Ser
10                  15                  20                  25

ATG CTA GCT TGC GCT AAA ACA GAA CAC CCC CAA TCA CAA AAT GAT AGT      208
Met Leu Ala Cys Ala Lys Thr Glu His Pro Gln Ser Gln Asn Asp Ser
                30                  35                  40

GAA AAA CTT TTT TAT AAG ATC CAC TGC CTG GTG GAT AAC TTA AGC CTT      256
Glu Lys Leu Phe Tyr Lys Ile His Cys Leu Val Asp Asn Leu Ser Leu
            45                  50                  55

GAA AAC CAG AGC AAA CTA AAA GAG ACT CTA GCC CCC TTT AGC GCT TTT      304
Glu Asn Gln Ser Lys Leu Lys Glu Thr Leu Ala Pro Phe Ser Ala Phe
        60                  65                  70

TCG AGC CTA GAA TTT TTA GAC ATT TCA ACC CCC AAT CTT CAC GCC ACT      352
Ser Ser Leu Glu Phe Leu Asp Ile Ser Thr Pro Asn Leu His Ala Thr
    75                  80                  85

CCA ATA GAA CCC TCT GCG ATT GAT AAA ATC AAT GAA GCT TTT TTG CAA      400
Pro Ile Glu Pro Ser Ala Ile Asp Lys Ile Asn Glu Ala Phe Leu Gln
90                  95                  100                 105

CTC AAT ATT TAC GCT AAG ACT CGC TTT TCT AAA ATG GTC ATG TGC CGC      448
Leu Asn Ile Tyr Ala Lys Thr Arg Phe Ser Lys Met Val Met Cys Arg
                110                 115                 120

TTG TTT TTG GCT TCT TTA TTC CCA CAA TAC GAC AAA ATC ATC ATG TTT      496
Leu Phe Leu Ala Ser Leu Phe Pro Gln Tyr Asp Lys Ile Ile Met Phe
            125                 130                 135

GAT GCA GAC ACT TTG TTT TTA AAC GAT GTG AGC GAG AGC TTT TTC ATC      544
Asp Ala Asp Thr Leu Phe Leu Asn Asp Val Ser Glu Ser Phe Phe Ile
        140                 145                 150

CCA CTA GAT GGC TAT TAT TTT GGA GCG GCT AAA GAT TTT GCT TCC GAT      592
```

```
Pro Leu Asp Gly Tyr Tyr Phe Gly Ala Ala Lys Asp Phe Ala Ser Asp
    155                 160                 165

AAA AGC CCT AAA CAT TTT CAA ATA GTG CGA GAA AAA GAC CCT CGT CAA      640
Lys Ser Pro Lys His Phe Gln Ile Val Arg Glu Lys Asp Pro Arg Gln
170                 175                 180                 185

GCC TTT TCC CTT TAT GAG CAT TAC CTT AAT GAA AGC GAT ATG CAA ATC      688
Ala Phe Ser Leu Tyr Glu His Tyr Leu Asn Glu Ser Asp Met Gln Ile
                190                 195                 200

ATC TAT GAA AGC AAT TAT AAC GCC GGG TTT TTA GTC GTG AAT TTA AAG      736
Ile Tyr Glu Ser Asn Tyr Asn Ala Gly Phe Leu Val Val Asn Leu Lys
            205                 210                 215

CTG TGG CGT GCT GAT CAT TTA GAA GAG CGC TTA CTC AAT TTA ACC CAT      784
Leu Trp Arg Ala Asp His Leu Glu Glu Arg Leu Leu Asn Leu Thr His
        220                 225                 230

CAA AAA GGC CAG TGC GTG TTT TAC CCT GAA CAG GAC CTT TTA ACG CTC      832
Gln Lys Gly Gln Cys Val Phe Tyr Pro Glu Gln Asp Leu Leu Thr Leu
    235                 240                 245

GCA TGC TAT CAA AAA GTT TTA ATC TTG CCT TAT ATT TAT AAC ACC CAC      880
Ala Cys Tyr Gln Lys Val Leu Ile Leu Pro Tyr Ile Tyr Asn Thr His
250                 255                 260                 265

CCT TTC ATG GCC AAT CAA AAA CGC TTC ATC CCT GAC AAA AAA GAA ATC      928
Pro Phe Met Ala Asn Gln Lys Arg Phe Ile Pro Asp Lys Lys Glu Ile
                270                 275                 280

GTC ATG CTG CAT TTT TAT TTT GTA GGA AAA CCT TGG GTT TTA CCT ACT      976
Val Met Leu His Phe Tyr Phe Val Gly Lys Pro Trp Val Leu Pro Thr
            285                 290                 295

TTT TCA TAT TCT AAA GAA TGG CAT GAG ACT CTT TTA AAA ACC CCT TTT     1024
Phe Ser Tyr Ser Lys Glu Trp His Glu Thr Leu Leu Lys Thr Pro Phe
        300                 305                 310

TAT GCT GAA TAT TCC GTG AAA TTC CTT AAA CAA ATG ACA GAA TGT TTA     1072
Tyr Ala Glu Tyr Ser Val Lys Phe Leu Lys Gln Met Thr Glu Cys Leu
    315                 320                 325

AGC CTT AAA GAC AAA CAA AAA ACC TTT GAA TTT CTT GCC CCC CTA CTC     1120
Ser Leu Lys Asp Lys Gln Lys Thr Phe Glu Phe Leu Ala Pro Leu Leu
330                 335                 340                 345

AAT AAA AAA ACC CTT TTA GAA TAC GTC TTT TTT AGA TTG AAT AGG ATT     1168
Asn Lys Lys Thr Leu Leu Glu Tyr Val Phe Phe Arg Leu Asn Arg Ile
                350                 355                 360

TTC AAA CGC TTA AAA GAA AAA TTT TTT AAC TCT TAGCGTTCTC GTTTGGGCAA   1221
Phe Lys Arg Leu Lys Glu Lys Phe Phe Asn Ser
            365                 370

CACGCTATAG GCGAATTTGA CATAAATCGC                                   1251
```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
Met Ser Ile Ile Ile Pro Ile Val Ile Ala Phe Asp Asn His Tyr Ala
 1               5                  10                  15
Met Pro Ala Gly Val Ser Leu Tyr Ser Met Leu Ala Cys Ala Lys Thr
            20                  25                  30
Glu His Pro Gln Ser Gln Asn Asp Ser Glu Lys Leu Phe Tyr Lys Ile
        35                  40                  45
His Cys Leu Val Asp Asn Leu Ser Leu Glu Asn Gln Ser Lys Leu Lys
    50                  55                  60
Glu Thr Leu Ala Pro Phe Ser Ala Phe Ser Ser Leu Glu Phe Leu Asp
65                  70                  75                  80
Ile Ser Thr Pro Asn Leu His Ala Thr Pro Ile Glu Pro Ser Ala Ile
                85                  90                  95
Asp Lys Ile Asn Glu Ala Phe Leu Gln Leu Asn Ile Tyr Ala Lys Thr
            100                 105                 110
Arg Phe Ser Lys Met Val Met Cys Arg Leu Phe Leu Ala Ser Leu Phe
        115                 120                 125
Pro Gln Tyr Asp Lys Ile Ile Met Phe Asp Ala Asp Thr Leu Phe Leu
    130                 135                 140
Asn Asp Val Ser Glu Ser Phe Phe Ile Pro Leu Asp Gly Tyr Tyr Phe
145                 150                 155                 160
Gly Ala Ala Lys Asp Phe Ala Ser Asp Lys Ser Pro Lys His Phe Gln
                165                 170                 175
Ile Val Arg Glu Lys Asp Pro Arg Gln Ala Phe Ser Leu Tyr Glu His
            180                 185                 190
Tyr Leu Asn Glu Ser Asp Met Gln Ile Ile Tyr Glu Ser Asn Tyr Asn
        195                 200                 205
Ala Gly Phe Leu Val Val Asn Leu Lys Leu Trp Arg Ala Asp His Leu
    210                 215                 220
Glu Glu Arg Leu Leu Asn Leu Thr His Gln Lys Gly Gln Cys Val Phe
225                 230                 235                 240
Tyr Pro Glu Gln Asp Leu Leu Thr Leu Ala Cys Tyr Gln Lys Val Leu
                245                 250                 255
Ile Leu Pro Tyr Ile Tyr Asn Thr His Pro Phe Met Ala Asn Gln Lys
            260                 265                 270
Arg Phe Ile Pro Asp Lys Lys Glu Ile Val Met Leu His Phe Tyr Phe
        275                 280                 285
Val Gly Lys Pro Trp Val Leu Pro Thr Phe Ser Tyr Ser Lys Glu Trp
    290                 295                 300
His Glu Thr Leu Leu Lys Thr Pro Phe Tyr Ala Glu Tyr Ser Val Lys
305                 310                 315                 320
Phe Leu Lys Gln Met Thr Glu Cys Leu Ser Leu Lys Asp Lys Gln Lys
                325                 330                 335
Thr Phe Glu Phe Leu Ala Pro Leu Leu Asn Lys Lys Thr Leu Leu Glu
            340                 345                 350
Tyr Val Phe Phe Arg Leu Asn Arg Ile Phe Lys Arg Leu Lys Glu Lys
        355                 360                 365
Phe Phe Asn Ser
```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...2193
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```
CAAGAAGCCA TAGAAGCTGA TGGGAAATTC CACAAAGAAT AAGGGTAGAA A ATG AAA      57
                                                           Met Lys
                                                            1

ATA ACA TAT TGT GAT GCG CTA ATT ATT GGA GGC GGA CTA GCT GGG TTA      105
Ile Thr Tyr Cys Asp Ala Leu Ile Ile Gly Gly Gly Leu Ala Gly Leu
          5                  10                  15

AGG GCT AGT ATC GCA TGC AAA CAA AAG GGT TTA AAC ACC ATC GTT TTA      153
Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile Val Leu
     20                  25                  30

AGC CTA GTG CCT GTC AGG CGT TCG CAC TCT GCA GCC GCT CAA GGG GGC      201
Ser Leu Val Pro Val Arg Arg Ser His Ser Ala Ala Ala Gln Gly Gly
35                   40                  45                  50

ATG CAA GCG AGC CTT GCG AAC GCT AAA AAA AGC GAG GGC GAT AAT GAA      249
Met Gln Ala Ser Leu Ala Asn Ala Lys Lys Ser Glu Gly Asp Asn Glu
                55                  60                  65

GAT TTA CAC TTT TTA GAC ACG GTT AAG GGG AGC GAT TGG GGG TGC GAT      297
Asp Leu His Phe Leu Asp Thr Val Lys Gly Ser Asp Trp Gly Cys Asp
            70                  75                  80

CAG CAA GTG GCT AGG ATG TTT GTA ACC ACT GCT CCT AAA GCC ATT AGG      345
Gln Gln Val Ala Arg Met Phe Val Thr Thr Ala Pro Lys Ala Ile Arg
        85                  90                  95

GAA TTG GCC AGT TGG GGG GTG CCT TGG ACT AGG ATT AAA AAG GGC GAT      393
Glu Leu Ala Ser Trp Gly Val Pro Trp Thr Arg Ile Lys Lys Gly Asp
    100                 105                 110

AGG CCT GCG GTC GTC AAT GGT GAG CAT GTA ACT ATC ACT GAA AGA GAC      441
Arg Pro Ala Val Val Asn Gly Glu His Val Thr Ile Thr Glu Arg Asp
115                 120                 125                 130

GAC AGG CAT GGT TAT ATC TTA AGC CGT GAT TTT GGC GGC ACT AAA AAA      489
```

```
Asp Arg His Gly Tyr Ile Leu Ser Arg Asp Phe Gly Gly Thr Lys Lys
                135                 140                 145

TGG CGC ACA TGC TTT ACG GCT GAT GCC ACA GGG CAT ACC ATG CTT TAT      537
Trp Arg Thr Cys Phe Thr Ala Asp Ala Thr Gly His Thr Met Leu Tyr
            150                 155                 160

GCG GTC GCT AAT GAA GCC TTA CAC CAC AAA GTG GAT ATT CAA GAC AGA      585
Ala Val Ala Asn Glu Ala Leu His His Lys Val Asp Ile Gln Asp Arg
        165                 170                 175

AAG GAC ATG CTC GCT TTC ATT CAT CAT GAT AAT AAA TGC TAT GGG GCG      633
Lys Asp Met Leu Ala Phe Ile His His Asp Asn Lys Cys Tyr Gly Ala
    180                 185                 190

GTG GTA AGG GAT TTG ATC ACA GGC GAA ATT TCA GCG TAT GTT TCT AAA      681
Val Val Arg Asp Leu Ile Thr Gly Glu Ile Ser Ala Tyr Val Ser Lys
195                 200                 205                 210

GGC ACG CTT TTA GCT ACC GGA GGT TAT GGG CGC GTG TAT AAA CAC ACC      729
Gly Thr Leu Leu Ala Thr Gly Gly Tyr Gly Arg Val Tyr Lys His Thr
                215                 220                 225

ACT AAC GCT GTG ATT TGC GAT GGA GCC GGG GCT GCA AGC GCC TTA GAA      777
Thr Asn Ala Val Ile Cys Asp Gly Ala Gly Ala Ala Ser Ala Leu Glu
            230                 235                 240

ACC GGC GTG GCT AAA TTG GGC AAC ATG GAA GCG GTG CAA TTC CAC CCT      825
Thr Gly Val Ala Lys Leu Gly Asn Met Glu Ala Val Gln Phe His Pro
        245                 250                 255

ACC GCT TTA GTG CCA AGC GGG ATT TTA ATG ACC GAA GGT TGC AGG GGC      873
Thr Ala Leu Val Pro Ser Gly Ile Leu Met Thr Glu Gly Cys Arg Gly
    260                 265                 270

GAT GGC GGT GTT TTA AGA GAC AAG TTT GGC AGA CGC TTC ATG CCC GCT      921
Asp Gly Gly Val Leu Arg Asp Lys Phe Gly Arg Arg Phe Met Pro Ala
275                 280                 285                 290

TAT GAG CCG GAG AAA AAA GAG CTT GCA AGC AGA GAT GTG GTC TCA AGG      969
Tyr Glu Pro Glu Lys Lys Glu Leu Ala Ser Arg Asp Val Val Ser Arg
                295                 300                 305

CGG ATT TTA GAG CAT ATC CAA AAA GGC TAT GGA GCC AAA TCG CCT TAT     1017
Arg Ile Leu Glu His Ile Gln Lys Gly Tyr Gly Ala Lys Ser Pro Tyr
            310                 315                 320

GGG GAT CAT GTG TGG CTG GAT ATT GCT ATT TTA GGG CGT AAC CAT GTG     1065
Gly Asp His Val Trp Leu Asp Ile Ala Ile Leu Gly Arg Asn His Val
        325                 330                 335

GAA AAA AAC TTA AGG GAT GTG CGC GAT ATA GCC ATG ACT TTT GCG GGC     1113
Glu Lys Asn Leu Arg Asp Val Arg Asp Ile Ala Met Thr Phe Ala Gly
    340                 345                 350

ATT GAT CCG GCT GAT AGC AAG GAA CAA ACC AAA GAC AAC ATG CAA GGA     1161
Ile Asp Pro Ala Asp Ser Lys Glu Gln Thr Lys Asp Asn Met Gln Gly
355                 360                 365                 370
```

```
GTG CCC GCA AAT GAG CCT GAA TAC GGG CAA GCG ATG GCC AAG CAA AAA    1209
Val Pro Ala Asn Glu Pro Glu Tyr Gly Gln Ala Met Ala Lys Gln Lys
                375                 380                 385

GGC TGG ATC CCC ATA AAA CCC ATG CAA CAC TAT TCT ATG GGT GGG GTT    1257
Gly Trp Ile Pro Ile Lys Pro Met Gln His Tyr Ser Met Gly Gly Val
            390                 395                 400

AGG ACA AAC CCT AAA GGC GAA ACC CAT TTA AAA GGC TTG TTT TGC GCG    1305
Arg Thr Asn Pro Lys Gly Glu Thr His Leu Lys Gly Leu Phe Cys Ala
        405                 410                 415

GGT GAA GCG GCA TGC TGG GAT TTG CAT GGG TTT AAC CGC TTG GGG GGT    1353
Gly Glu Ala Ala Cys Trp Asp Leu His Gly Phe Asn Arg Leu Gly Gly
    420                 425                 430

AAT TCT GTG AGT GAA GCG GTG GTC GCT GGC ATG ATC ATT GGG GAT TAT    1401
Asn Ser Val Ser Glu Ala Val Val Ala Gly Met Ile Ile Gly Asp Tyr
435                 440                 445                 450

TTT GCC TCG CAT TGT TTA GAA GCG CAA ATT GAA ATC AAC ACG CAA AAA    1449
Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr Gln Lys
                455                 460                 465

GTT GAA GCT TTC ATT AAA GAA AGC CAA GAC TAT ATG CAT TTT TTA TTG    1497
Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe Leu Leu
            470                 475                 480

CAT AAT GAA GGC AAA GAA GAT GTG TAT GAA ATT AGA GAG CGC ATG AAA    1545
His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg Met Lys
        485                 490                 495

GAA GTC ATG GAT GAA AAA GTG GGC GTT TTT AGA GAA GGC AAA AGG CTA    1593
Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys Arg Leu
    500                 505                 510

GAA GAA GCC CTT AAA GAA TTG CAA GAG CTT TAT GCA CGC TCC AAA AAC    1641
Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser Lys Asn
515                 520                 525                 530

ATT TGC GTG AAA AAC AAG GTT TTA CAC AAT AAC CCT GAA TTA GAA GAC    1689
Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu Glu Asp
                535                 540                 545

GCT TAC CGC ACC AAA AAA ATG CTC AAA CTC GCG CTT TGT ATC ACT CAA    1737
Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile Thr Gln
            550                 555                 560

GGA GCG TTA CTG CGC ACT GAA AGC AGA GGG GCT CAC ACA AGG ATT GAC    1785
Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg Ile Asp
        565                 570                 575

TAC CCT AAA AGA GAC GAT GAA AAA TGG CTT AAT CGG ACT CTA GCG AGC    1833
Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu Ala Ser
    580                 585                 590

TGG CCT AGC GCT GAG CAA GAC ATG CCC ACG ATT GAA TAC GAA GAA TTA    1881
Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu Glu Leu
```

```
595                 600                 605                 610

GAT GTG ATG AAA ATG GAA ATC AGC CCT GAT TTT AGG GGC TAT GGC AAA    1929
Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr Gly Lys
                615                 620                 625

AAG GGT AAT TTC ATC CCC CAC CCC AAA AAA GAA GAG CGC GAC GCT GAG    1977
Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp Ala Glu
            630                 635                 640

ATT TTG AAA ACG ATT TTA GAA CTA GAA AAG CTT GGA AAA GAC AGA ATA    2025
Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp Arg Ile
        645                 650                 655

GAA GTC CAA CAT GCG CTC ATG CCT TTT GAA TTG CAA GAA AAA TAC AAG    2073
Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys Tyr Lys
    660                 665                 670

GCT AGG AAT ATG CGT TTA GAA GAT GAG GAA GTC AGG GCT AGG GGG GAA    2121
Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg Gly Glu
675                 680                 685                 690

CAT TTG TAT TCT TTC AAT GTC CAT GAG TTA TTG GAC CAA CAC AAC GCT    2169
His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His Asn Ala
                695                 700                 705

AAC CTA AAA GGA GAA CAC CAT GAG TGATAATGAA CGAACGATTG TAGTTAGAGT   2223
Asn Leu Lys Gly Glu His His Glu
            710

GCTAAAATTT GACCCTCA                                                2241
```

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```
Met Lys Ile Thr Tyr Cys Asp Ala Leu Ile Ile Gly Gly Gly Leu Ala
 1               5                  10                  15
Gly Leu Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile
            20                  25                  30
Val Leu Ser Leu Val Pro Val Arg Arg Ser His Ser Ala Ala Ala Gln
        35                  40                  45
Gly Gly Met Gln Ala Ser Leu Ala Asn Ala Lys Lys Ser Glu Gly Asp
    50                  55                  60
Asn Glu Asp Leu His Phe Leu Asp Thr Val Lys Gly Ser Asp Trp Gly
65                  70                  75                  80
Cys Asp Gln Gln Val Ala Arg Met Phe Val Thr Thr Ala Pro Lys Ala
                85                  90                  95
Ile Arg Glu Leu Ala Ser Trp Gly Val Pro Trp Thr Arg Ile Lys Lys
```

```
                100                 105                 110
Gly Asp Arg Pro Ala Val Val Asn Gly Glu His Val Thr Ile Thr Glu
        115                 120                 125
Arg Asp Asp Arg His Gly Tyr Ile Leu Ser Arg Asp Phe Gly Gly Thr
    130                 135                 140
Lys Lys Trp Arg Thr Cys Phe Thr Ala Asp Ala Thr Gly His Thr Met
145                 150                 155                 160
Leu Tyr Ala Val Ala Asn Glu Ala Leu His His Lys Val Asp Ile Gln
                165                 170                 175
Asp Arg Lys Asp Met Leu Ala Phe Ile His His Asp Asn Lys Cys Tyr
            180                 185                 190
Gly Ala Val Val Arg Asp Leu Ile Thr Gly Glu Ile Ser Ala Tyr Val
        195                 200                 205
Ser Lys Gly Thr Leu Leu Ala Thr Gly Gly Tyr Gly Arg Val Tyr Lys
    210                 215                 220
His Thr Thr Asn Ala Val Ile Cys Asp Gly Ala Gly Ala Ala Ser Ala
225                 230                 235                 240
Leu Glu Thr Gly Val Ala Lys Leu Gly Asn Met Glu Ala Val Gln Phe
                245                 250                 255
His Pro Thr Ala Leu Val Pro Ser Gly Ile Leu Met Thr Glu Gly Cys
            260                 265                 270
Arg Gly Asp Gly Gly Val Leu Arg Asp Lys Phe Gly Arg Arg Phe Met
        275                 280                 285
Pro Ala Tyr Glu Pro Glu Lys Lys Glu Leu Ala Ser Arg Asp Val Val
    290                 295                 300
Ser Arg Arg Ile Leu Glu His Ile Gln Lys Gly Tyr Gly Ala Lys Ser
305                 310                 315                 320
Pro Tyr Gly Asp His Val Trp Leu Asp Ile Ala Ile Leu Gly Arg Asn
                325                 330                 335
His Val Glu Lys Asn Leu Arg Asp Val Arg Asp Ile Ala Met Thr Phe
            340                 345                 350
Ala Gly Ile Asp Pro Ala Asp Ser Lys Glu Gln Thr Lys Asp Asn Met
        355                 360                 365
Gln Gly Val Pro Ala Asn Glu Pro Glu Tyr Gly Gln Ala Met Ala Lys
    370                 375                 380
Gln Lys Gly Trp Ile Pro Ile Lys Pro Met Gln His Tyr Ser Met Gly
385                 390                 395                 400
Gly Val Arg Thr Asn Pro Lys Gly Glu Thr His Leu Lys Gly Leu Phe
                405                 410                 415
Cys Ala Gly Glu Ala Ala Cys Trp Asp Leu His Gly Phe Asn Arg Leu
            420                 425                 430
Gly Gly Asn Ser Val Ser Glu Ala Val Val Ala Gly Met Ile Ile Gly
        435                 440                 445
Asp Tyr Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr
    450                 455                 460
Gln Lys Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe
465                 470                 475                 480
Leu Leu His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg
                485                 490                 495
Met Lys Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys
            500                 505                 510
Arg Leu Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser
        515                 520                 525
Lys Asn Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu
    530                 535                 540
Glu Asp Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile
545                 550                 555                 560
Thr Gln Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg
```

```
                565                 570                 575
Ile Asp Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu
            580                 585                 590
Ala Ser Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu
        595                 600                 605
Glu Leu Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr
    610                 615                 620
Gly Lys Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp
625                 630                 635                 640
Ala Glu Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp
                645                 650                 655
Arg Ile Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys
            660                 665                 670
Tyr Lys Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg
        675                 680                 685
Gly Glu His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His
    690                 695                 700
Asn Ala Asn Leu Lys Gly Glu His His Glu
705                 710
```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 77...445
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```
ATTTAGTTCA AGAGCTTTTA GAAGAATTTT TGCAAAGCGG GGCTAAAGAG ATTTTAGAAA     60
AGGCGCAGTT GTTTTA ATG CGT TTG TTT ATC GCG CTA GTT TTG TTT TGG TGG    112
                  Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp
                   1               5                  10

TGG TTA AGC TTG AAC GCT AAA GAA GCG GAT TTT ATC TCT GAT TTA GAA      160
Trp Leu Ser Leu Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu
        15                  20                  25

TAC GGG ATG GCT CTT TAT AAA AAC CCT AGG GGT GTT GCG TGC GCG AAA      208
Tyr Gly Met Ala Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys
    30                  35                  40

TGC CAT GGC ATT AAA GGC GAA CAA CAA GAA ATC ACC TTT TAT TAT GAA      256
Cys His Gly Ile Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu
45                  50                  55                  60

AAA GGC GAG AAA AAA ATC CTC TAC GCC CCT AAA ATC AAC CAT TTG GAT      304
Lys Gly Glu Lys Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp
```

```
                65                  70                  75

TTT AAA ACC TTT AAA GAC GCC TTG AGT TTA GGC AAA GGC ATG ATG CCT      352
Phe Lys Thr Phe Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro
            80                  85                  90

AAA TAC AAT CTC AAT TTA GAA GAA ATC CAA GCG ATT TAT CTT TAT ATC      400
Lys Tyr Asn Leu Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile
        95                  100                 105

ATC TCT TTA GAG CAT AAA GAA GAG CGT AAG GAT TCT CCT AAG CCT TAATC    450
Ile Ser Leu Glu His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro
    110                 115                 120

AAAGCGCTTG ATTTATGCTA AAATGGAGCG TTGCATTTTT GTTTTG                   496
```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```
Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp Trp Leu Ser Leu
 1               5                  10                  15
Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala
            20                  25                  30
Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile
        35                  40                  45
Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys
    50                  55                  60
Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe
65                  70                  75                  80
Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu
                85                  90                  95
Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Ile Ser Leu Glu
            100                 105                 110
His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 72...464
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```
GTTGCAACAA AAAATAGAGA GCAGGAAAAC AGACATTGTG ATCCAATCCA TGGCGAATAT      60
TCTCAGCGGG A ATG AAT GAG CTT ATC CGC TAT GGC TTG ATA TTT CTC TTT     110
             Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe
              1               5                  10

TTT TTA AAG GCG TTT GGG CTT GAT TAT GGG ATA GAT AAA ACG CTA GAA      158
Phe Leu Lys Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu
    15                  20                  25

TTA AAA AAA GAT GAA GTG TTT AAA GCG ATC ATC AAA GAC ACT TCA AAT      206
Leu Lys Lys Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn
30                  35                  40                  45

GAA CAA ACC AAA GAA ATC ACG CTC TAT TGG ACG CTA TAT GCA AAT AAA      254
Glu Gln Thr Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys
                50                  55                  60

GGT TTA GTC ATC AAC ATG CGT TTT AAC CAT TTC CCT TAC CAG TTT ATT      302
Gly Leu Val Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile
            65                  70                  75

TTA TAC ACC GAT CAT GCG AGA AAC ACC TAT AAT CTC AAA GTT TTT GAA      350
Leu Tyr Thr Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu
        80                  85                  90

GAA AAA TTT TCT TCT AAC AGC ACT CTG TCG CTT GTG TTT AAA GAT TTT      398
Glu Lys Phe Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe
    95                  100                 105

AAA GAA GAT AAA GCC GCT TTA AGG CTT TTA GCC CTT ATG CCC CTT GTT      446
Lys Glu Asp Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val
110                 115                 120                 125

TTT TCT CCT AAA GAG CCT TAAGGAATTT GCATGCAAGA AAAACAACTT AAAACCAT    502
Phe Ser Pro Lys Glu Pro
                130

TCAAAATAAG ATCGCTTCC                                                521
```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```
Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe Phe Leu Lys
 1               5                  10                  15
Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu Leu Lys Lys
            20                  25                  30
Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn Glu Gln Thr
        35                  40                  45
Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys Gly Leu Val
    50                  55                  60
Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile Leu Tyr Thr
65                  70                  75                  80
Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu Glu Lys Phe
                85                  90                  95
Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe Lys Glu Asp
            100                 105                 110
Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val Phe Ser Pro
        115                 120                 125
Lys Glu Pro
    130
```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 55...222
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```
GCTCCCTCTA AAAGGGTTTT TAAACTATCT TGAGATTTAC CCAATTTATA GGTG ATG      57
                                                           Met
                                                            1

CTT TCA AAA CTC CCA TTT ACT GGT GTT TTA GCC TTA GTT TTA AAG GCT      105
Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys Ala
              5                  10                  15

GTC CAT GTT AGC TTA GCC GAA GAT AAA TCC AAA TTC ACC GCT TGC AAA      153
Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys Lys
        20                  25                  30

AAC CCT GCT AGT AAA ACC GAT ACC AAA ACC ATT TTT TTC ATT CAT TAT      201
Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His Tyr
    35                  40                  45

CCT TTA ATG TGG TCT TAT CAA TAACGCTTAT TATTTTAGTG TAAATAAGCA CGCT    256
Pro Leu Met Trp Ser Tyr Gln
50                  55
```

TACAACTAAA ACG 269

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```
Met Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys
 1               5                  10                  15
Ala Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys
            20                  25                  30
Lys Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His
        35                  40                  45
Tyr Pro Leu Met Trp Ser Tyr Gln
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 66...611
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```
AATGACTTTA GGGGATATTC TTAAAGAAAA ACTCTAAAGA GTGATTTTAA AAGCATGAGA     60
ATGGC ATG AGA TTT AAG GGT GTT GTT GCT TTT ATT TCC CTA GCT GTC GCT   110
      Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala
       1               5                  10                  15

CTT GGC GTT TTA GCC TAT TTG TTT TTA AGC GTT AAA AAA GAA ATG CCC     158
Leu Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro
                20                  25                  30

GCT ACT TCT CAT GCG ATC TCT CAA ACA CAT GCG ATC TCT CAA ACC AAT     206
Ala Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn
            35                  40                  45

GAA GGC CTC TCT CAA ACA GAT GCA AAA AGC CAT GAC ATC GAT CTA GAA     254
Glu Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu
```

```
        50                  55                  60

GAA AAT AGC CCC ACT GAA ACC TCT CAT AAT GAA AAA GCC TCC CAT AAC      302
Glu Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn
    65                  70                  75

GAA GAA GAT CAC AAT AAC GCC CTT TCT CAA AAT CTT GAT GCG CAA GAA      350
Glu Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu
80                  85                  90                  95

TCT ATC AAT TAC CCC GTT GTG GAA CAT TAT TCT GAA ATC CCT TTT GAA      398
Ser Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu
                100                 105                 110

GAA AAA AAA AGG GAA TAT TCA AAG CTT ATC ATT AAG GAT TTA AAG GAC      446
Glu Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp
            115                 120                 125

TAT CAA TGG TGG TGC TTA AAA GAA ATC CTC AAA AAA GAA CAG ATT GAT      494
Tyr Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp
        130                 135                 140

TAC GCT TAC GAT AAC ACC AAA AAC CAA CCT AAC CTC ATC ATC TAT TTA      542
Tyr Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu
    145                 150                 155

GAT GAA AAT AAA AAA GAA CGC TTG CTG GCT GAT TTA GAC TAT TAT AAA      590
Asp Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys
160                 165                 170                 175

ATA CGC TAT CAT GCT GTT TTT TAAATTCAAA GGATAAAAAT GTATCAAGTA GCCA    645
Ile Arg Tyr His Ala Val Phe
                180

TTTGCGACCC CATCCATGCT AAAGGC                                        671
```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```
Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala Leu
 1               5                  10                  15
Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro Ala
            20                  25                  30
Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn Glu
        35                  40                  45
Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu Glu
    50                  55                  60
Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn Glu
```

```
65                  70                  75                  80
Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu Ser
                85                  90                  95
Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu Glu
            100                 105                 110
Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp Tyr
        115                 120                 125
Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp Tyr
    130                 135                 140
Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu Asp
145                 150                 155                 160
Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys Ile
                165                 170                 175
Arg Tyr His Ala Val Phe
            180
```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 86...295
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```
ACCCACAAAA CTAAAACCCA CTAACACAAT TAACCCTAAC AACACATAAA GATTGCCCAA      60
AGACGCGCAC AACACGCTCG CAACA ATG GTT GCA AAA ACA AAC ACA ATC CCC      112
                            Met Val Ala Lys Thr Asn Thr Ile Pro
                             1               5

CCC ATC GTA GGG GTA TCT TTT TTA TTC TGG TGG CTT GGC ACG AAG CTA      160
Pro Ile Val Gly Val Ser Phe Leu Phe Trp Trp Leu Gly Thr Lys Leu
10                  15                  20                  25

GAA ATG GGC TGG TTA GCC TTT TTA GCC TTG GCC CAT AGA ATG AAT TTA      208
Glu Met Gly Trp Leu Ala Phe Leu Ala Leu Ala His Arg Met Asn Leu
                30                  35                  40

GGC ATT AAA AAA AGC GTG AGA AAA AAA GCT ATG AAA AAC CCT AAC CCT      256
Gly Ile Lys Lys Ser Val Arg Lys Lys Ala Met Lys Asn Pro Asn Pro
            45                  50                  55

GCT CTA AAA GTC AAA TAC TGG AAA AGA TTG ATA TTG AAA TAGCCATATA GT    307
Ala Leu Lys Val Lys Tyr Trp Lys Arg Leu Ile Leu Lys
        60                  65                  70

AAAGAATAGA GCATAAAATC CCCTAAAATC GCCA                                341
```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```
Met Val Ala Lys Thr Asn Thr Ile Pro Pro Ile Val Gly Val Ser Phe
 1               5                  10                  15
Leu Phe Trp Trp Leu Gly Thr Lys Leu Glu Met Gly Trp Leu Ala Phe
            20                  25                  30
Leu Ala Leu Ala His Arg Met Asn Leu Gly Ile Lys Lys Ser Val Arg
        35                  40                  45
Lys Lys Ala Met Lys Asn Pro Asn Pro Ala Leu Lys Val Lys Tyr Trp
    50                  55                  60
Lys Arg Leu Ile Leu Lys
65                  70
```

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 58...2430
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```
TTTTTTTTTT TTTTTGATTT TTATTTTTTA AATTTTTAGA TTAAGGAGAG TTGTTGG ATG     60
                                                                Met
                                                                 1

TTT TTA AGA GTA TAC CCA AAG CTT AGA TAC GCT TTA TGT TTC CCC CTA      108
Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro Leu
            5                  10                  15

CTC GCT GAG ACT TGC TAT AGC GAA GAG CGG ACT TTA AAT AAG GTT ACC      156
Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val Thr
        20                  25                  30

ACC CAA GCT AAA AGG ATT TTC ACT TAC AAC AAT GAG TTT AAA GTA ACT      204
Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val Thr
```

```
    35                  40                  45

TCT AAA GAA CTA GAT CAA CGC CAA AGC AAT GAA GTC AAG GAC TTG TTT      252
Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu Phe
50                  55                  60                  65

AGG ACT AAC CCT GAT GTG AAT GTG GGC GGA GGG AGC GTG ATG GGG CAG      300
Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly Gln
                70                  75                  80

AAA ATC TAT GTG AGA GGC GTT GAA GAC AGG CTT TTA AGG GTT ACA GTG      348
Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr Val
            85                  90                  95

GAT GGG GCT GCA CAA AAT GGC AAT ATC TAC CAC CAC CAA GGC AAC ACC      396
Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn Thr
        100                 105                 110

GTG ATT GAC CCT GGC ATG CTC AAA AGC GTG GAA GTT ACC AAA GGC GCG      444
Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly Ala
    115                 120                 125

GCG AAT GCG AGC GCG GGG CCA GGA GCG ATT GCG GGA GTG ATT AAA ATG      492
Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys Met
130                 135                 140                 145

GAG ACT AAA GGA GCG GCT GAT TTT ATC CCT AGG GGG AAA AAT TAT GCT      540
Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr Ala
                150                 155                 160

GCC AGT GGG GCG GTG AGT TTT TAT ACC AAT TTT GGC GAT CGA GAG ACT      588
Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu Thr
            165                 170                 175

TTC AGA TCG GCT TAT CAA AAC GCG CAT TTT GAT ATT ATC GCT TAC TAC      636
Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr Tyr
        180                 185                 190

ACG CAC CAA AAC ATC TTC TAT TAT AGA AGC GGC GCT ACA GCG ATG AAA      684
Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met Lys
    195                 200                 205

AAC CTT TTC AAT CCC ACA CAA GCC GAT AAA GAG CCA GGA ACT CCT AGC      732
Asn Leu Phe Asn Pro Thr Gln Ala Asp Lys Glu Pro Gly Thr Pro Ser
210                 215                 220                 225

GAG CAA AAC AAC GCT TTG ATT AAA ATG AAT GGT TAT TTG AGC GAC AGA      780
Glu Gln Asn Asn Ala Leu Ile Lys Met Asn Gly Tyr Leu Ser Asp Arg
                230                 235                 240

GAC ACG CTC ACT TTC AGC TGG AAC ATG ACA CGA GAT AAC GCT ACA CGC      828
Asp Thr Leu Thr Phe Ser Trp Asn Met Thr Arg Asp Asn Ala Thr Arg
            245                 250                 255

CCT TTA AGG AGT AAC GCT ATA GGG TTA GCC TAT CCT TGT GAA GCC CCC      876
Pro Leu Arg Ser Asn Ala Ile Gly Leu Ala Tyr Pro Cys Glu Ala Pro
        260                 265                 270
```

```
TTT AGT CCT GAT AGT TCT CAA GGG TGT CCT AAT GTG TTA GAT AGT TTC      924
Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser Phe
    275                 280                 285

ACA AGA TAC ATG TAT CAC TCT ATT AAT AGT GCC AAC AAT CTT TCC TTA      972
Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser Leu
290                 295                 300                 305

CAA TAC AAA AGG GAA GCG GGA AAT TCT TTT GGC GAC CCA CGA TTA GAT     1020
Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu Asp
                310                 315                 320

TTT ACC CTT TAT ACA AGC ATC AGG AAC GCT CAG TTT GAT CCC CTA TTT     1068
Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu Phe
            325                 330                 335

GAT CCT AAT GGC GTT TAT GCT AAA TTC CCC ACT TCT TTA GCG AGC GCA     1116
Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser Ala
        340                 345                 350

TGG GAA AAA GAA AAT TAC CCA TGC GTT GAA GGC GCT TAT TGC ACC CCA     1164
Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr Pro
    355                 360                 365

AGC TTT TCA GAT GTG GAT AAA CCA AGC TCA CAG CCT AGG AAT TTG TTT     1212
Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu Phe
370                 375                 380                 385

TTA AAC AAC ACC GGC TTA AAC CTT AAA GTC GCG CAT GTG ATT GAT GAA     1260
Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp Glu
                390                 395                 400

GCC ACA GAC AGC CTT TTT GAA TAC GGA TTC AAC TAC CAA AAT TTG AGC     1308
Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu Ser
            405                 410                 415

GTT TTT GAC GCT CGC ATC CCT AAA TCA GAA TTA TAC AGG CCT AAT CAA     1356
Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn Gln
        420                 425                 430

GTT TAT ACT GAT GAT AAA GGA CAA AAA CAA ATC GCT TGC TCT CTT GTG     1404
Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu Val
    435                 440                 445

AAT AAT AAC CCC AAT GAC CCC ACT CTG TGC CAA AGA GGG AAA GCG AAC     1452
Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala Asn
450                 455                 460                 465

GGG AAT ATT TAT GGA GGC TAC GTG CAA GCG AAT TAC TCG CCT CAT AAA     1500
Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His Lys
                470                 475                 480

ATC ATC ACT TTT GGA GCC GGG GTA AGG TGG GAC GCT TAC ACG CTT TAT     1548
Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu Tyr
            485                 490                 495

GAT AAA GAC TGG AAC CAC CGC TAC ACT CAA GGC TTT AGC CCT AGC GCG     1596
Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser Ala
```

```
          500                 505                 510

GCT CTT GTG CTA AGC CCC ATT GAG CCT TTA TCT TTA AAA ATC ACT TAT    1644
Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr Tyr
    515                 520                 525

TCT CAA GTT ACA AGA GGG GTG ATG CCA GGA GAT GGC GTG TAC ATG CGT    1692
Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met Arg
530                 535                 540                 545

CAA AAC GAT TTA CGA TAC GCC AAA AAC ATC AAG CCT GAA GTG GGC TCT    1740
Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly Ser
                550                 555                 560

AAC GCT GAA TTT AAT ATT GAT TAT TCA AGC CAG TAT TTT AGC GGG AGG    1788
Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly Arg
            565                 570                 575

GCT GCG GCG TTT TAT CAG GCT TTG GAT AAT TTC ATC TCA CAA TAC GCA    1836
Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr Ala
        580                 585                 590

CAA AAT TTG ATT GTA ACC AAT TTG AGT CAA GCG ATT CGT ATT TAT GGC    1884
Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr Gly
    595                 600                 605

TAT GAA GTG GGT GGG ACT TTC AGA TAC AAG GGC GTG AGT TTG AAT GTA    1932
Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn Val
610                 615                 620                 625

GGG GTC TCG CGC ACC TGG CCC ACC ACT AGG GGG TAT TTA ATG GCG GAT    1980
Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala Asp
                630                 635                 640

AGC TAT GAG CTT GCC GCA AGC ACC GGT AAT GTT TTT ATC ATC AAA TTG    2028
Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu
            645                 650                 655

GAT TAC ACC ATC CCC AAA ACA GGG ATC AAT CTT GCA TGG CTT AGC CGC    2076
Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser Arg
        660                 665                 670

TTT GTT ACC GGT TTA GAT TAT TGC GGG TTT GAT ATT TAC TTG CCT GAT    2124
Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro Asp
    675                 680                 685

TAT GGG ACG GCT GAG AAA CCC AAA ACC CCT ACC GAT TTA GCC AAA TGC    2172
Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys Cys
690                 695                 700                 705

GGA TCT CAA TTA GGG TTA GTG CAT ATG CAT AAA CCG GGC TAT GGC GTG    2220
Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly Val
                710                 715                 720

AGT AAT TTT TAT ATC AAT TGG AGT CCT AAA ACC AAA AGC CGC TGG AAG    2268
Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp Lys
            725                 730                 735
```

```
GGT TTG TTG CTT TCA GCC GTG TTT AAT AAT GTT TTC AAC AAA TTC TAT     2316
Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr
        740                 745                 750

GTG GAT CAA ACA AGC CCT TAT GTC ATG AGC CCG GAT ATG CCA GGC ACT     2364
Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr
    755                 760                 765

GAC GCT GTT AAA AGA GCG ATC GCT GAG CCT GGG TTT AAC GCG CGT TTT     2412
Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe
770                 775                 780                 785

GAA GTG GCT TAC AAA TGG TAGTTAATGG AGCTTTAAGC GTTGCGCATG CGTGATAG  2468
Glu Val Ala Tyr Lys Trp
                790

CAACGGCTAT CGC                                                     2481
```

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```
Met Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro
 1               5                  10                  15
Leu Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val
            20                  25                  30
Thr Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val
        35                  40                  45
Thr Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu
    50                  55                  60
Phe Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly
65                  70                  75                  80
Gln Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr
                85                  90                  95
Val Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn
            100                 105                 110
Thr Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly
        115                 120                 125
Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys
    130                 135                 140
Met Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr
145                 150                 155                 160
Ala Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu
                165                 170                 175
Thr Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr
            180                 185                 190
Tyr Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met
        195                 200                 205
Lys Asn Leu Phe Asn Pro Thr Gln Ala Asp Lys Glu Pro Gly Thr Pro
```

210 215 220
Ser Glu Gln Asn Asn Ala Leu Ile Lys Met Asn Gly Tyr Leu Ser Asp
225 230 235 240
Arg Asp Thr Leu Thr Phe Ser Trp Asn Met Thr Arg Asp Asn Ala Thr
245 250 255
Arg Pro Leu Arg Ser Asn Ala Ile Gly Leu Ala Tyr Pro Cys Glu Ala
260 265 270
Pro Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser
275 280 285
Phe Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser
290 295 300
Leu Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu
305 310 315 320
Asp Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu
325 330 335
Phe Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser
340 345 350
Ala Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr
355 360 365
Pro Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu
370 375 380
Phe Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp
385 390 395 400
Glu Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu
405 410 415
Ser Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn
420 425 430
Gln Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu
435 440 445
Val Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala
450 455 460
Asn Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His
465 470 475 480
Lys Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu
485 490 495
Tyr Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser
500 505 510
Ala Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr
515 520 525
Tyr Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met
530 535 540
Arg Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly
545 550 555 560
Ser Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly
565 570 575
Arg Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr
580 585 590
Ala Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr
595 600 605
Gly Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn
610 615 620
Val Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala
625 630 635 640
Asp Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys
645 650 655
Leu Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser
660 665 670
Arg Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro

```
        675                 680                 685
Asp Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys
    690                 695                 700
Cys Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly
705                 710                 715                 720
Val Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp
                725                 730                 735
Lys Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe
            740                 745                 750
Tyr Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly
        755                 760                 765
Thr Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg
    770                 775                 780
Phe Glu Val Ala Tyr Lys Trp
785                 790
```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 120...428
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```
GTCGGTCGGG TAATGTTCAA ATTCACAAAT GAGTCTGAAG ACAAAGAAGT CTTGATCTAG      60
AAGCCGAAAT TCTCATACCG CACTTAGAAT TGCGTCAAAA ACAAATTGAT GCGCTGTTG      119


GTG CAC GAT ATT ACC AAG CTA TGT TAC ACC AAA CCA CTA GGG TGT GTT       167
Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val
 1               5                  10                  15

GTG CTG TTC AGC AAG GAT ACT GAT CTT GTG CCT GTG TTA GAA TCC GCT       215
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala
            20                  25                  30

TGG GAG AAA GGC TTT GAA GTC TTC ATT GCT AAC ATT CAA GAA TGC CCC      263
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro
        35                  40                  45

AAT TCT GTC CCT TCA GAC TTG AAG AAG TCT TGC AAT GTG AGG GAA CGC      311
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg
    50                  55                  60

AGT GTC GCT GAA ATT GTA GAT AAC TTG CCC AAA AAT CAG CAC ACT CCC      359
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro
65                  70                  75                  80
```

```
AAG AAA AAG AAC TTT TCC ACC AAC GAG CCT TTT AAC AAC CCA TTT AAA      407
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys
                85                  90                  95

GAC CAA CTC TTT AAG AAG AAC TAACACGATC CCCACACCAA GGGGACAAAA AAGCA   463
Asp Gln Leu Phe Lys Lys Asn
            100

CCCATTTTAA AAGG                                                     477
```

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```
Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val
 1               5                  10                  15
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala
            20                  25                  30
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro
        35                  40                  45
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg
    50                  55                  60
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro
65                  70                  75                  80
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys
                85                  90                  95
Asp Gln Leu Phe Lys Lys Asn
            100
```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 220...624
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```
TCTTTTGAAA TTGCCTGATG TGGAAAAAGA AATGCCCAAA GAGACGACTC AAAAAAGCTT    60
```

```
GTTTTCGCAC AAACACTTTG TTTTTGGGGC TTGGGGATCT TTTTTTATGT GGGGGGAGAA    120
NTGGCGATTG GCTCATTCTT GGTGCTAAGC TTTGAAAAGC TTTTGAATTT AGACTCTCAA    180
TCAAGCGCGC ATTACTTGGT GTATTATTGG GGAGGCGCG ATG GTG GGC CGT TTC        234
                                          Met Val Gly Arg Phe
                                           1               5

TTA GGC AGT GTG TTG ATG AAT AAA ATT GCC CCT AAT AAA TAC TTG GCT      282
Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro Asn Lys Tyr Leu Ala
                10                  15                  20

TTC AAC GCC TTA AGC TCT ATT GTT CTC ATC GCT TTA GCC ATT ATC ATT      330
Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala Leu Ala Ile Ile Ile
            25                  30                  35

GGA GGC AAG ATC GCT TTA TTC GCT CTG ACT TTT GTG GGC TTT TTC AAC      378
Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe Val Gly Phe Phe Asn
        40                  45                  50

TCT ATC ATG TTC CCT ACC ATC TTT TCT TTG GCT ACG CTC AAT TTA GGG      426
Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala Thr Leu Asn Leu Gly
    55                  60                  65

CAT CTC ACT TCT AAA GCT TCT GGG GTG ATT AGC ATG GCG ATT GTG GGA      474
His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser Met Ala Ile Val Gly
70                  75                  80                  85

GGG GCG TTA ATC CCC CCC ATT CAA GGT GCG GTT ACA GAC ATG CTA ACA      522
Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val Thr Asp Met Leu Thr
                90                  95                  100

GCA ACC GAA TCA AAT TTG CTC TAC GCT TAT GGT GTG CCG TTG TTG TGC      570
Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly Val Pro Leu Leu Cys
            105                 110                 115

TAT TTT TAT ATT CTC TTC TTT GCG CTT AAA GGG TAT AAG CAA GAA GAA      618
Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly Tyr Lys Gln Glu Glu
        120                 125                 130

AAC TCC TAAAAAAAGG GGGGGTTTCT TTCTTCTTTC CTTTCTTTTA TCTTGTTTTA AA    676
Asn Ser
    135

AATCAGTAA                                                            685
```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 135 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met Val Gly Arg Phe Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro

```
 1               5                  10                  15
Asn Lys Tyr Leu Ala Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala
            20                  25                  30
Leu Ala Ile Ile Ile Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe
        35                  40                  45
Val Gly Phe Phe Asn Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala
    50                  55                  60
Thr Leu Asn Leu Gly His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser
65                  70                  75                  80
Met Ala Ile Val Gly Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val
                85                  90                  95
Thr Asp Met Leu Thr Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly
            100                 105                 110
Val Pro Leu Leu Cys Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly
        115                 120                 125
Tyr Lys Gln Glu Glu Asn Ser
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 58...765
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```
ACCGATCACT AAAACCAATG TAACTTACCG CTCTTTACAG CGTAAGTGAG AAAAGGA ATG     60
                                                                Met
                                                                 1

CAT TTG AAT ACG GAT TTT AGC CAT ATC ACC GAT ATA GAG GGC ATG CGT      108
His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met Arg
              5                  10                  15

TTT ATC AAT GAA GAA GAC GCT TTG AAC AAA TTG ATT AAT GAA ATC CAC      156
Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile His
         20                  25                  30

ACG CGC CAC ATT GAT TTA AAA GAT TCC ATC ATG CTC GCT TTG AGT TTT      204
Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser Phe
     35                  40                  45

AAC GCT CTG TAT TTA GCT CAC GCT TTA GCG CAA AAA TTT GGA GCG ACT      252
Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala Thr
 50                  55                  60                  65

TAT GAT ATA CTT TTT TTA GAA CCT ATC CTA GCC CCT TTA AAC TCA AAA      300
```

```
Tyr Asp Ile Leu Phe Leu Glu Pro Ile Leu Ala Pro Leu Asn Ser Lys
                70                  75                  80

TGC GAG ATC GCT TTA GTG AGT GAG AGC ATG GAT ATA GTG ATG AAT GAA      348
Cys Glu Ile Ala Leu Val Ser Glu Ser Met Asp Ile Val Met Asn Glu
            85                  90                  95

AGT TTG ATC AAT TCC TTT GAC ATC ACT TTA GAC TAT GTT TAT GGG GAA      396
Ser Leu Ile Asn Ser Phe Asp Ile Thr Leu Asp Tyr Val Tyr Gly Glu
        100                 105                 110

GCC AAG CGA GCT TAT GAA GAA GAC ATT TTG TCT CAC ATC TAT CAG TAT      444
Ala Lys Arg Ala Tyr Glu Glu Asp Ile Leu Ser His Ile Tyr Gln Tyr
    115                 120                 125

CGC AAA GGC AAT GCG ATC AAA AGC TTA AAA GAT AAA AAT ATT TTT ATC      492
Arg Lys Gly Asn Ala Ile Lys Ser Leu Lys Asp Lys Asn Ile Phe Ile
130                 135                 140                 145

GTA GAT AGG GGG ATT GAA ACC GGG TTT AGA GCA GGG TTA GGC GTG CAA      540
Val Asp Arg Gly Ile Glu Thr Gly Phe Arg Ala Gly Leu Gly Val Gln
                150                 155                 160

ACT TGC TTG AAA AAA GAA TGC CAA GAC ATT TAT ATT TTA ACC CCC ATT      588
Thr Cys Leu Lys Lys Glu Cys Gln Asp Ile Tyr Ile Leu Thr Pro Ile
            165                 170                 175

GTC GCG CAA AAT GTC GCT CAA GGC TTA GAA AGT TTG TGC GAT GGG GTG      636
Val Ala Gln Asn Val Ala Gln Gly Leu Glu Ser Leu Cys Asp Gly Val
        180                 185                 190

ATT AGT GTG TAT CGC CCT GAA TGT TTT GTC TCT GTG GAG CAT CAT TAT      684
Ile Ser Val Tyr Arg Pro Glu Cys Phe Val Ser Val Glu His His Tyr
    195                 200                 205

AAA GAA CTC AAG CGA TTA AGC AAT GAA GAA GTT GAA AAA TAC TTG GGC      732
Lys Glu Leu Lys Arg Leu Ser Asn Glu Glu Val Glu Lys Tyr Leu Gly
210                 215                 220                 225

GCT AAC AAC ATG CCT AAT TTA AAA AAG GAA CAT TAAATATGGA TTTTATCACC    785
Ala Asn Asn Met Pro Asn Leu Lys Lys Glu His
                230                 235

ATCAATTCTA GTAACAAAAC CGAA                                           809
```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```
Met His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met
 1               5                  10                  15
Arg Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile
            20                  25                  30
His Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser
        35                  40                  45
Phe Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala
    50                  55                  60
Thr Tyr Asp Ile Leu Phe Leu Glu Pro Ile Leu Ala Pro Leu Asn Ser
65                  70                  75                  80
Lys Cys Glu Ile Ala Leu Val Ser Glu Ser Met Asp Ile Val Met Asn
                85                  90                  95
Glu Ser Leu Ile Asn Ser Phe Asp Ile Thr Leu Asp Tyr Val Tyr Gly
            100                 105                 110
Glu Ala Lys Arg Ala Tyr Glu Glu Asp Ile Leu Ser His Ile Tyr Gln
        115                 120                 125
Tyr Arg Lys Gly Asn Ala Ile Lys Ser Leu Lys Asp Lys Asn Ile Phe
    130                 135                 140
Ile Val Asp Arg Gly Ile Glu Thr Gly Phe Arg Ala Gly Leu Gly Val
145                 150                 155                 160
Gln Thr Cys Leu Lys Lys Glu Cys Gln Asp Ile Tyr Ile Leu Thr Pro
                165                 170                 175
Ile Val Ala Gln Asn Val Ala Gln Gly Leu Glu Ser Leu Cys Asp Gly
            180                 185                 190
Val Ile Ser Val Tyr Arg Pro Glu Cys Phe Val Ser Val Glu His His
        195                 200                 205
Tyr Lys Glu Leu Lys Arg Leu Ser Asn Glu Glu Val Glu Lys Tyr Leu
    210                 215                 220
Gly Ala Asn Asn Met Pro Asn Leu Lys Lys Glu His
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 70...285
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```
TAACACAAGC CACCATGAGC ATACTATCGC CATAGTTGGC AATAAAGCAG TGATTCTTAC     60
GGAGCGTTA ATG GCA AGA GAT GAT GTT ATA GAA GTG GAT GGG AAA GTG ATT    111
          Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile
           1               5                  10

GAG GCG TTG CCT AAC GCT ACT TTT AAG GTG GAG TTA GAC AAT AAG CAT      159
Glu Ala Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His
15                  20                  25                  30
```

```
GTG GTG TTG TGC CGT ATT TCT GGA AAG ATG CGC ATG CAC TAT ATT AGG      207
Val Val Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg
                35                  40                  45

ATT GCT TTA GGC GAT AGG GTT AAG CTA GAG CTT ACG CCC TAT AGC TTA      255
Ile Ala Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu
            50                  55                  60

GAC AAA GGT CGG ATA ACT TTT AGA TAT AAA TGAATTTAAG GGTTATTTCA ATG    308
Asp Lys Gly Arg Ile Thr Phe Arg Tyr Lys
        65                  70

AAAATATGTT AATATAA                                                  325
```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```
Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile Glu Ala
 1               5                  10                  15
Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His Val Val
            20                  25                  30
Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg Ile Ala
        35                  40                  45
Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu Asp Lys
    50                  55                  60
Gly Arg Ile Thr Phe Arg Tyr Lys
65                  70
```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...309
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```
ATCGCTCAAA TTTCAACGAC CATGCTTGTT AAAAAAAACT AAAGGAATGT T ATG CAA     57
```

```
                                                                  Met Gln
                                                                   1

GAT GAA TTA TTT GAA ACC GAA AAA ATC CCC CCA AAA AAC ACT AAA AAT      105
Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr Lys Asn
          5                  10                  15

ACT AAA AAC GCC CCT AAA AAA AGT TTT GAA GAG CAT GTT CAT TCC CTA      153
Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His Ser Leu
     20                  25                  30

GAG CGA GCC ATA GAT CGC TTG AAT GAT CCC AAT TTA TCC TTA AAA GAC      201
Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu Lys Asp
35                   40                  45                  50

GGG ATG GAT TTG TAT AAA ACG GCC ATG CAA GAG TTG TTT TTG GCT CAA      249
Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu Ala Gln
                55                  60                  65

AAG CTT TTA GAA AAC GCT TAT TTA GAG CAT GAA AAA CTC CAA ACG CCA      297
Lys Leu Leu Glu Asn Ala Tyr Leu Glu His Glu Lys Leu Gln Thr Pro
           70                  75                  80

GAC CAA AAG GCT TAAAGCATGC GAGTGTTTGC TTTGCAATTA GAATCTTTTA AAGAA   354
Asp Gln Lys Ala
        85

AATCTC                                                              360
```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```
Met Gln Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr
 1               5                  10                  15
Lys Asn Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His
            20                  25                  30
Ser Leu Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu
        35                  40                  45
Lys Asp Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu
    50                  55                  60
Ala Gln Lys Leu Leu Glu Asn Ala Tyr Leu Glu His Glu Lys Leu Gln
65                  70                  75                  80
Thr Pro Asp Gln Lys Ala
                85
```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...795
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```
ATGACTAAAA AGATATAATT CATTCAAAAT TAAACAAGGA TTACA ATG AAA CTG ATT    57
                                                  Met Lys Leu Ile
                                                   1

TCA TGG AAT GTG AAC GGG TTA AGG GCT TGC ATG ACT AAG GGC TTT ATG     105
Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr Lys Gly Phe Met
 5                  10                  15                  20

GAT TTT TTC AAT AGC GTT GAT GCG GAT GTT TTT TGC ATT CAA GAA TCT     153
Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys Ile Gln Glu Ser
                25                  30                  35

AAA ATG CAG CAA GAA CAA AAC ACC TTT GAA TTT AAA GGG TAT TTT GAT     201
Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys Gly Tyr Phe Asp
            40                  45                  50

TTT TGG AAT TGC GCG ATT AAA AAG GGC TAT TCT GGG GTG GTA ACT TTC     249
Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly Val Val Thr Phe
        55                  60                  65

ACT AAA AAA GAG CCT TTA AGC GTG AGC TAT GGT ATT AAT ATG GAA GAG     297
Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile Asn Met Glu Glu
    70                  75                  80

CAT GAC AAA GAA GGG CGC GTA ATA ACT TGC GAA TTT GAG TCG TTT TAT     345
His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe Glu Ser Phe Tyr
85                  90                  95                  100

TTG GTG AAT GTT TAT ACC CCT AAT TCC CAA CAA GCC CTA TCC AGG CTT     393
Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala Leu Ser Arg Leu
                105                 110                 115

AGT TAT CGC ATG AGT TGG GAA GTG GAG TTT AAG AAA TTT TTA AAA GCT     441
Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys Phe Leu Lys Ala
            120                 125                 130

TTA GAG TTG AAA AAA CCG GTC ATT GTG TGT GGG GAT TTG AAT GTG GCT     489
Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp Leu Asn Val Ala
        135                 140                 145

CAC AAT GAA ATT GAT TTA GAA AAC CCC AAA ACC AAC CGA AAA AAT GCC     537
His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn Arg Lys Asn Ala
```

```
    150                 155                 160

GGC TTT AGC GAT GAA GAG AGA GAA AAA TTC AGC GAG CTT TTG AAC GCC      585
Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu Leu Leu Asn Ala
165                 170                 175                 180

GGT TTT ATT GAC ACT TTC CGT TAT TTT TAC CCT AAC AAA GAA AAG GCT      633
Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn Lys Glu Lys Ala
                185                 190                 195

TAC ACC TGG TGG AGT TAC ATG CAA CAA GCA AGG GAT AAA AAC ATT GGT      681
Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp Lys Asn Ile Gly
            200                 205                 210

TGG CGC ATT GAT TAT TTT TTA TGC TCT AAC CCT TTA AAA ACG CGC TTA      729
Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu Lys Thr Arg Leu
        215                 220                 225

AAA GAC GCT TTA ATC TAT AAA GAT ATT TTA GGG AGC GAT CAT TGC CCG      777
Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser Asp His Cys Pro
    230                 235                 240

GTA GGG TTG GAA TTA GTT TAAAGGTAGA AAGTGTGCGA AATAAAGACA GAAAAAAG    833
Val Gly Leu Glu Leu Val
245                 250

CCTTACAA                                                            841
```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```
Met Lys Leu Ile Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr
 1               5                  10                  15
Lys Gly Phe Met Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys
            20                  25                  30
Ile Gln Glu Ser Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys
        35                  40                  45
Gly Tyr Phe Asp Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly
    50                  55                  60
Val Val Thr Phe Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile
65                  70                  75                  80
Asn Met Glu Glu His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe
                85                  90                  95
Glu Ser Phe Tyr Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala
            100                 105                 110
Leu Ser Arg Leu Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys
        115                 120                 125
Phe Leu Lys Ala Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp
```

```
    130                 135                 140
Leu Asn Val Ala His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn
145                 150                 155                 160
Arg Lys Asn Ala Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu
                165                 170                 175
Leu Leu Asn Ala Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn
            180                 185                 190
Lys Glu Lys Ala Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp
        195                 200                 205
Lys Asn Ile Gly Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu
    210                 215                 220
Lys Thr Arg Leu Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser
225                 230                 235                 240
Asp His Cys Pro Val Gly Leu Glu Leu Val
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 62...571
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```
AGAATGCGAG CGTTAAAAAA GAAATTTATG TGCCTAATAA GCTTGTTAAT TTTGTTATCG     60
C ATG AGG GCT TTA CTT TTT TTT ATT TTG TTA CTT TGG TTC AAG GGT TGT    109
  Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys
   1               5                  10                  15

GGG TAT AAG CCT ATT GCA GCT TAC GCT CAA AAC GCT TTA GGC GAT AGC     157
Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser
            20                  25                  30

GTA TAC GTG AAA CTC ATT GTG AAT TTG CCT AAC CCT GAA AAC TCT GTA     205
Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val
        35                  40                  45

GAG TTT AAG GAT TTG ATG AAT CGT TTA GTC GTG CAA CGC TTC CAA AGC     253
Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser
    50                  55                  60

CGC TTA GCG AGT GAA AAG GAT GCG GAT TCT ATC ATT ATT ATA GAA ATC     301
Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile
65                  70                  75                  80

ACG AAT GTA ACC GAT ACG AGT ATC ACG CAA AAT AAA GAA GGC TTC ACG     349
Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr
```

```
                85                  90                  95

ACT TTC TAT CGC GCA ACC GTG TCT GTG AAT TAC ACC TAC GAT AAT AAA      397
Thr Phe Tyr Arg Ala Thr Val Ser Val Asn Tyr Thr Tyr Asp Asn Lys
            100                 105                 110

AGA GGC ACA CAA AAG ACT TTT CAA GAT AGC GGG TAT TAC AAT TAC GCT      445
Arg Gly Thr Gln Lys Thr Phe Gln Asp Ser Gly Tyr Tyr Asn Tyr Ala
        115                 120                 125

GTG AAT TTG CAA GAC CCC CTT AAT ACC TAC CAG AAC CGC TAT TAT GCT      493
Val Asn Leu Gln Asp Pro Leu Asn Thr Tyr Gln Asn Arg Tyr Tyr Ala
    130                 135                 140

ATC AAT CAG GCT GTG GAA CAG ACT TTG ACT AAA TTT GTG GCT CAA ATC      541
Ile Asn Gln Ala Val Glu Gln Thr Leu Thr Lys Phe Val Ala Gln Ile
145                 150                 155                 160

GCT TAT GAG GGG AAA TTC AAT AAT GAA AAA TAGCCCTTTG AATGGATTGA ATG    594
Ala Tyr Glu Gly Lys Phe Asn Asn Glu Lys
                165                 170

GACTAAAGGC GTTTTTAGAA ACAA                                           618
```

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```
Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys
 1               5                  10                  15
Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser
            20                  25                  30
Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val
        35                  40                  45
Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser
    50                  55                  60
Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile
65                  70                  75                  80
Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr
                85                  90                  95
Thr Phe Tyr Arg Ala Thr Val Ser Val Asn Tyr Thr Tyr Asp Asn Lys
            100                 105                 110
Arg Gly Thr Gln Lys Thr Phe Gln Asp Ser Gly Tyr Tyr Asn Tyr Ala
        115                 120                 125
Val Asn Leu Gln Asp Pro Leu Asn Thr Tyr Gln Asn Arg Tyr Tyr Ala
    130                 135                 140
Ile Asn Gln Ala Val Glu Gln Thr Leu Thr Lys Phe Val Ala Gln Ile
145                 150                 155                 160
Ala Tyr Glu Gly Lys Phe Asn Asn Glu Lys
```

165 170

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 61...1224
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```
AATACCCATA AAATACCTTA AGAGAACGCC TATTCAAAAA CCAAAAATAA GGAAATCCTA      60
 ATG ACT ACA GAC AGA AAT TTG TTT TTT TGC GCT TCG CTA TTG ATT TTT      108
 Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe
  1               5                  10                  15

TTG GGG GTA TTG ATG AGC TAT TCG CTC TCA ACT TAC ACC ACA GTG GTG      156
Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val
            20                  25                  30

CTG TAT CAT TAT GGG GAG TTC CAT TTT TTC ATA CGC CAG CTT GTG AGC      204
Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser
        35                  40                  45

GCG ATC ATA GGG ATT GTT ATC ATG TGG GGG TTG TCT AGG GTT GAT CCT      252
Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro
    50                  55                  60

AGC AAG TGG TTT AGC CGT TTG GGG TTT TTT CTT CTT TTT GTC CCA CCA      300
Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro
65                  70                  75                  80

TTA CTC ATT ATT GGC ATG TTT TTT TTG CCA GAA AGC CTT TCT AGC AGT      348
Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser
                85                  90                  95

GCT GGG GGG GCG AAG CGA TGG ATT CGT TTG GGG TTT TTT TCT CTA GCG      396
Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala
            100                 105                 110

CCT TTG GAG TTT TTG AAG ATT GGT TTC ACC TTT TTT CTT GCG TGG AGT      444
Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser
        115                 120                 125

TTG TCT CGC ACT TTT GTG GCA AAA GAA AAG GCT AAT GTT AAA GAA GAA      492
Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu
    130                 135                 140
```

```
CTC ATC ACT TTT GTG CCT TAT TCA GTG GTG TTT GTA GCC TTA GCG ATT      540
Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile
145                 150                 155                 160

GGG GTG GGG GTT TTG CAA AAC GAT TTG GGG CAG ATT GTT CTT TTG GGG      588
Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly
                165                 170                 175

GCG GTT TTA GCG GTG TTG TTG GTT TTT TCT GGG GGG AGC GTG CAT TTG      636
Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu
            180                 185                 190

TTT GGC TTG ATT ATT TCA GGG GCG TTT GCG ATC AGC GTT TTA GCG ATT      684
Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile
        195                 200                 205

GTT ACA AGC GAG CAT AGG ATT TTG CGC CTG AAA TTG TGG TGG TCT AAT      732
Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn
    210                 215                 220

TTG CAA AAT TCG CTT TTC ACG CTC TTG CCG GAT AGA TTA GCG AAC GCT      780
Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala
225                 230                 235                 240

CTT AGA ATA AGC GAC TTG CCC GAA TCC TAT CAG GTC TTT CAT GCA GGC      828
Leu Arg Ile Ser Asp Leu Pro Glu Ser Tyr Gln Val Phe His Ala Gly
                245                 250                 255

AAT GCC ATG CAT AAT GGG GGG TTG TTT GGG CAA GGG CTT GGG CTT GGG      876
Asn Ala Met His Asn Gly Gly Leu Phe Gly Gln Gly Leu Gly Leu Gly
            260                 265                 270

CAA ATC AAG CTT GGG TTT TTG AGC GAA GTG CAT ACG GAC ATG GTC TTA      924
Gln Ile Lys Leu Gly Phe Leu Ser Glu Val His Thr Asp Met Val Leu
        275                 280                 285

GCT GGG ATC GCC GAA GAA TGG GGG TTT TTG GGG CTA TGC GTT TGT TTT      972
Ala Gly Ile Ala Glu Glu Trp Gly Phe Leu Gly Leu Cys Val Cys Phe
    290                 295                 300

ATT TTG TTT TCT GTT TTG ATT GTT TTG ATT TTT AGG ATC GCT AAC CGC     1020
Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg
305                 310                 315                 320

TTG AAA GAG CCA AAA TAT TCG CTA TTT TGC GTG GGC GTG GTG CTG CTT     1068
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu
                325                 330                 335

ATT AGT TTT TCT TTG GTG ATC AAC GCC TTT GGG GTG GGC GGG ATT CTT     1116
Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu
            340                 345                 350

CCG GTT AAA GGT CTA GCG GTG CCG TTT TTG AGC TAT GGA GGG AGT TCG     1164
Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser
        355                 360                 365

CTT CTA GCG AAT TGT ATC GCT ATA GGG CTT GTT CTA AGC CTA GCG CGA     1212
Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg
```

370 375 380

TAC ACG AAA GGC TAAAAACATC AACCCCTTTT TAAAAATTAA TGCCATAAAA AGGGC 1269
Tyr Thr Lys Gly
385

TCAACCTC 1277

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe
1 5 10 15
Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val
20 25 30
Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser
35 40 45
Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro
50 55 60
Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro
65 70 75 80
Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser
85 90 95
Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala
100 105 110
Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser
115 120 125
Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu
130 135 140
Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile
145 150 155 160
Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly
165 170 175
Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu
180 185 190
Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile
195 200 205
Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn
210 215 220
Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala
225 230 235 240
Leu Arg Ile Ser Asp Leu Pro Glu Ser Tyr Gln Val Phe His Ala Gly
245 250 255
Asn Ala Met His Asn Gly Gly Leu Phe Gly Gln Gly Leu Gly Leu Gly
260 265 270
Gln Ile Lys Leu Gly Phe Leu Ser Glu Val His Thr Asp Met Val Leu
275 280 285
Ala Gly Ile Ala Glu Glu Trp Gly Phe Leu Gly Leu Cys Val Cys Phe

```
    290                 295                 300
Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg
305                 310                 315                 320
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu
                325                 330                 335
Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu
            340                 345                 350
Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser
        355                 360                 365
Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg
    370                 375                 380
Tyr Thr Lys Gly
385
```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...908
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```
AGAACAGTAT CTATTTTTGT TGCGGTTGTA TATTTAATTA GGAGTTTGGT GTG AAA      56
                                                        Val Lys
                                                          1

CGG ATT TTA TTT TTT TTA GTA GCT ACG ACT TTT TTG TTG AGA GCA GAA     104
Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg Ala Glu
          5                  10                  15

ACG GAT TCT GCC ACT ATT AAC ACT ACA GTT GAT CCC AAT GTT ATG TTT     152
Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val Met Phe
     20                  25                  30

TCT GAA AGC TCC ACA GGG AAT GTG AAA AAA GAC CGC AAG AGG GTT TTA     200
Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg Val Leu
35                  40                  45                  50

AAG AGC ATG GTT AAT TTG GAA AAA GAG CGC GTG AAG AAT TTT AAC CGG     248
Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe Asn Arg
                55                  60                  65

TAT TCT GAA ACC AAG ATG AGT AAG GGC GAC TTA TCC GCT TTT GGA GCT     296
Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe Gly Ala
            70                  75                  80

TTC TTT AAG GGG AGT TTG GAA AGT TGT GTG GAT CAA AAG ATT TGT TAT     344
```

```
Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile Cys Tyr
        85                  90                  95

TAT GAG CAT AAA GAT GGC AAG GTT TCT TTT GTG GTG AAT GAC AGG GAG      392
Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp Arg Glu
    100                 105                 110

AAG TTT TAT AAA CAT GTG CTT AAA GAC TTA GGG ACA GAG CTT TCG CTC      440
Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu Ser Leu
115                 120                 125                 130

CCT TTG TTT AAC TGG CTT TAC AAA GGC TCG GAT TTT GGG GCT TTG CAT      488
Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala Leu His
                135                 140                 145

GAG CAG TTT GGG GAT ATG TAT GAT GGG TAT ATC AAA TAC TTG ATC AGT      536
Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu Ile Ser
            150                 155                 160

ATG GTT AGA ATA AGC CAA AAA GAA AAG GCT AGA AAA GTG GAT GCA ATC      584
Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp Ala Ile
        165                 170                 175

GTT CTT AAG AAA ATG GAA GAA CAA GCT GAG AAA GAC ACT AAG GCA GCG      632
Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys Ala Ala
    180                 185                 190

TTT CAA AAG AGG AGC AGT GGG GAG CTT GAA AGC CAT ACT GAT AGC CCT      680
Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp Ser Pro
195                 200                 205                 210

GAA TTT ATA AGC TCT TCT AAG AGG ACA CAG AAC GCT TCT AAT TCG GAT      728
Glu Phe Ile Ser Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn Ser Asp
                215                 220                 225

CTC AAT TCT ATG ACC AAT GCT AAC GCG CTC AAA GAA ACA GCT TCA AAA      776
Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala Ser Lys
            230                 235                 240

GAG CCA GAG GCT TCT TCA AAA AAA GAG AAA AAG TCT AAG AAA AAA CGT      824
Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys Lys Arg
        245                 250                 255

CGC CTT TCA AAG AAA GAA AAA CAA CAA CAA GCC TTG CAA CAA GAG TTT      872
Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln Glu Phe
    260                 265                 270

GAA AAA CAA ATT AGC GAC TCT AGT AAG TCT GAA AAA TAGTAATAAT AGTTAA    924
Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys
275                 280                 285

GCTTACCTTT TTAGGGGGCT TTCAATAAAT CTCTTAA                             961
```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```
Val Lys Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg
 1               5                  10                  15
Ala Glu Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val
            20                  25                  30
Met Phe Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg
        35                  40                  45
Val Leu Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe
    50                  55                  60
Asn Arg Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe
65                  70                  75                  80
Gly Ala Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile
                85                  90                  95
Cys Tyr Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp
            100                 105                 110
Arg Glu Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu
        115                 120                 125
Ser Leu Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala
    130                 135                 140
Leu His Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu
145                 150                 155                 160
Ile Ser Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp
                165                 170                 175
Ala Ile Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys
            180                 185                 190
Ala Ala Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp
        195                 200                 205
Ser Pro Glu Phe Ile Ser Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn
    210                 215                 220
Ser Asp Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala
225                 230                 235                 240
Ser Lys Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys
                245                 250                 255
Lys Arg Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln
            260                 265                 270
Glu Phe Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1499

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```
CTTTTTAGCC TCAAGACTTG GGCTTTAACA TTAAAGAATT ATTTTAAGGA ATG ATC      56
                                                        Met Ile
                                                          1

ATG GAA AAA TAC CAT AGC GAC CAA GAA TAC GAA GAA ATC ATC ACC GAC     104
Met Glu Lys Tyr His Ser Asp Gln Glu Tyr Glu Glu Ile Ile Thr Asp
          5                  10                  15

CAA TTA GGC GAT ATG CAA TTA AGG GAA AAT TTG CGT TCT GCA ATG GAT     152
Gln Leu Gly Asp Met Gln Leu Arg Glu Asn Leu Arg Ser Ala Met Asp
     20                  25                  30

ACC TTA AGG GCT AAT CGT AAG AAT CTC CTT AAA AAT CGT TAC AGC GAA     200
Thr Leu Arg Ala Asn Arg Lys Asn Leu Leu Lys Asn Arg Tyr Ser Glu
35                  40                  45                  50

TGG GAA AAT TTA AGG GAA TTA GGC AAA GAA GTC AAG CTT AAA ATC TTA     248
Trp Glu Asn Leu Arg Glu Leu Gly Lys Glu Val Lys Leu Lys Ile Leu
                55                  60                  65

TCC AGG CTT GAT GAA TAT TTG GAA TTG TTT GAA AAA AAC GCC ACT CAA     296
Ser Arg Leu Asp Glu Tyr Leu Glu Leu Phe Glu Lys Asn Ala Thr Gln
           70                  75                  80

AAC GGC TTT AAA ATC CAT TAC GCT AAA GAC GGC GAT GAA GCT AAT GAA     344
Asn Gly Phe Lys Ile His Tyr Ala Lys Asp Gly Asp Glu Ala Asn Glu
      85                  90                  95

ATC ATT TAC AAC CTC GCT AAA GAA AAG AAT ATC AAG CGC ATT TTA AAG     392
Ile Ile Tyr Asn Leu Ala Lys Glu Lys Asn Ile Lys Arg Ile Leu Lys
 100                 105                 110

CAA AAA TCC ATG GCG AGC GAA GAA ATT GGC TTG AAC CAT TAC TTG AAA     440
Gln Lys Ser Met Ala Ser Glu Glu Ile Gly Leu Asn His Tyr Leu Lys
115                 120                 125                 130

GAA AAG GGC ATT CAA GCA CAA GAA ACG GAT TTG GGC GAA TTG ATT ATC     488
Glu Lys Gly Ile Gln Ala Gln Glu Thr Asp Leu Gly Glu Leu Ile Ile
                135                 140                 145

CAA CTC ATC AAT GAA CAC CCT GTG CAT ATT GTC GTG CCA GCT ATC CAT     536
Gln Leu Ile Asn Glu His Pro Val His Ile Val Val Pro Ala Ile His
           150                 155                 160

AAA AAC CGC AAG CAA ATC GGT AAG ATT TTT GAA GAA AAA CTC AAC GCC     584
Lys Asn Arg Lys Gln Ile Gly Lys Ile Phe Glu Glu Lys Leu Asn Ala
      165                 170                 175

GCT TAT GAA GAA GAG CCT GAA AAG CTT AAT GCG ATC GCC AGA AAA CAC     632
Ala Tyr Glu Glu Glu Pro Glu Lys Leu Asn Ala Ile Ala Arg Lys His
 180                 185                 190
```

```
ATG CGC AAA GAA TTT GAA AGC TTT AAA ATG GGG ATT AGT GGG GTT AAT      680
Met Arg Lys Glu Phe Glu Ser Phe Lys Met Gly Ile Ser Gly Val Asn
195                 200                 205                 210

TTT GCT ATC GCT AAC GAA GGA GCG ATC TGG TTA GTG GAA AAT GAA GGC      728
Phe Ala Ile Ala Asn Glu Gly Ala Ile Trp Leu Val Glu Asn Glu Gly
                215                 220                 225

AAT GGC AGA ATG AGC ACC ACT GCA TGC GAT GTG CAT GTC GCA ATT TGT      776
Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala Ile Cys
            230                 235                 240

GGG ATT GAA AAA TTA GTA GAA AGC TTT GAT GAT GCG GCG ATT TTA AAC      824
Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile Leu Asn
        245                 250                 255

AAT TTG CTC GCC CCA AGC GCT GTG GGT GTG CCT ATC ACT TGC TAT CAA      872
Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys Tyr Gln
    260                 265                 270

AAC ATT ATC ACA GGC CCT AGA AAA GAG GGC GAT TTA GAC GGC CCT AAA      920
Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly Pro Lys
275                 280                 285                 290

GAA GCC CAC ATC ATT TTA TTA GAC AAC AAC CGC TCT AAT ATT TTG GCT      968
Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile Leu Ala
                295                 300                 305

GAT GAA AAG TAT TAT CGC GCT CTT TCA TGC ATC CGT TGC GGG ACT TGT     1016
Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly Thr Cys
            310                 315                 320

TTG AAC CAC TGC CCT GTG TAT GAT AAA ATC GGT GGG CAT GCC TAT CTT     1064
Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala Tyr Leu
        325                 330                 335

TCT ACT TAT CCT GGC CCT ATA GGC GTG GTG GTA TCC CCC CAA CTC TTT     1112
Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln Leu Phe
    340                 345                 350

GGC TTG AAT AAT TAC GGG CAT ATC CCT AAT TTG TGC AGT CTT TGC GGG     1160
Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu Cys Gly
355                 360                 365                 370

CGT TGC ACT GAA GTA TGC CCC GTA GAA ATC CCT TTA GCC GAA CTC ATT     1208
Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu Leu Ile
                375                 380                 385

AGG GAT TTA CGA TCC GAT AAA GTG GGC GAG GGC AGG GGT GTA ATT AAG     1256
Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val Ile Lys
            390                 395                 400

GGG GCT AAA AGC ACC CAA CAC AGC GGG ATG GAA AAA TTC TCT ATG AAA     1304
Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser Met Lys
        405                 410                 415

ATG TTT GCC AAA ATG GCA AGC GAT GGG GCT AAG TGG CGT TTC CAA TTG     1352
Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe Gln Leu
```

```
    420                 425                 430

AAA ATG GCT CAA TTT TTC TCG CCT TTA GGC AAG CTT TTA GCT CCC ATA    1400
Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala Pro Ile
435                 440                 445                 450

CTG CCT TTA GTC AAA GAG TGG GCG AGC GTT AGG ACC TTA CCC AAT ATG    1448
Leu Pro Leu Val Lys Glu Trp Ala Ser Val Arg Thr Leu Pro Asn Met
                455                 460                 465

GAC ACG AGC TTG CAT GCA AAA GTC CAG CAC TTA GAA GGG GTG ATT TAT    1496
Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val Ile Tyr
            470                 475                 480

GAG TAAAGAGCTT ATTTTAAAGC GCATTAAAGA AGCCAGAGCC AAGCATGCCA TTCAGG  1555
Glu
```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```
Met Ile Met Glu Lys Tyr His Ser Asp Gln Glu Tyr Glu Glu Ile Ile
 1               5                  10                  15
Thr Asp Gln Leu Gly Asp Met Gln Leu Arg Glu Asn Leu Arg Ser Ala
            20                  25                  30
Met Asp Thr Leu Arg Ala Asn Arg Lys Asn Leu Leu Lys Asn Arg Tyr
        35                  40                  45
Ser Glu Trp Glu Asn Leu Arg Glu Leu Gly Lys Glu Val Lys Leu Lys
    50                  55                  60
Ile Leu Ser Arg Leu Asp Glu Tyr Leu Glu Leu Phe Glu Lys Asn Ala
65                  70                  75                  80
Thr Gln Asn Gly Phe Lys Ile His Tyr Ala Lys Asp Gly Asp Glu Ala
                85                  90                  95
Asn Glu Ile Ile Tyr Asn Leu Ala Lys Glu Lys Asn Ile Lys Arg Ile
            100                 105                 110
Leu Lys Gln Lys Ser Met Ala Ser Glu Glu Ile Gly Leu Asn His Tyr
        115                 120                 125
Leu Lys Glu Lys Gly Ile Gln Ala Gln Glu Thr Asp Leu Gly Glu Leu
    130                 135                 140
Ile Ile Gln Leu Ile Asn Glu His Pro Val His Ile Val Val Pro Ala
145                 150                 155                 160
Ile His Lys Asn Arg Lys Gln Ile Gly Lys Ile Phe Glu Glu Lys Leu
                165                 170                 175
Asn Ala Ala Tyr Glu Glu Glu Pro Glu Lys Leu Asn Ala Ile Ala Arg
            180                 185                 190
Lys His Met Arg Lys Glu Phe Glu Ser Phe Lys Met Gly Ile Ser Gly
        195                 200                 205
Val Asn Phe Ala Ile Ala Asn Glu Gly Ala Ile Trp Leu Val Glu Asn
```

```
    210                 215                 220
Glu Gly Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala
225                 230                 235                 240
Ile Cys Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile
                245                 250                 255
Leu Asn Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys
            260                 265                 270
Tyr Gln Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly
        275                 280                 285
Pro Lys Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile
    290                 295                 300
Leu Ala Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly
305                 310                 315                 320
Thr Cys Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala
                325                 330                 335
Tyr Leu Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln
            340                 345                 350
Leu Phe Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu
        355                 360                 365
Cys Gly Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu
    370                 375                 380
Leu Ile Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val
385                 390                 395                 400
Ile Lys Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser
                405                 410                 415
Met Lys Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe
            420                 425                 430
Gln Leu Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala
        435                 440                 445
Pro Ile Leu Pro Leu Val Lys Glu Trp Ala Ser Val Arg Thr Leu Pro
    450                 455                 460
Asn Met Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val
465                 470                 475                 480
Ile Tyr Glu
```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 294...1577
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```
GTATCGCCAC TTTGCGTAAC AGGATGTTGA AAGTGGGTAA AAGCCGCTAA TTTCTTTTTA    60
GTGGGTCGTT TTTGAAAATC TTTTTAGTCT TTTTAAGCGT CTTTTTTTTT AATGGGTGTT   120
TTGGGTTAGT CTATAAGACT CCCATTTCAA GCTCTCCTAT CTCTTATGAT CCCTACACTA   180
```

```
CCCCCATTGG GAGCTTGTAT GCTGAAAAAT TAAAAGAAAA CCCTAACCAT AGCGCGGCCA   240
TTCTTTTAGA AGATGGCTTT GACGCTCTGT TGCATAGAGT GGGACTTATT AGA ATG      296
                                                              Met
                                                               1

AGC CAA AAA AGC ATT GAC ATG CAA ACT TAT ATC TAT AAA AAC GAC CTT      344
Ser Gln Lys Ser Ile Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp Leu
            5                  10                  15

TCT TCT CAA GTG ATT GCT AAA GAA CTT TTA AAT GCG GCC AAT CGT GGG      392
Ser Ser Gln Val Ile Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg Gly
        20                  25                  30

GTA AAA GTG CGC ATC CTT TTA GAC GAT AAC GGA TTG GAT TCG GAT TTT      440
Val Lys Val Arg Ile Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp Phe
    35                  40                  45

TCA GAT ATT ATG CTC TTA AAT TTC CAT AAA AAC ATT GAG GTG AAA ATT      488
Ser Asp Ile Met Leu Leu Asn Phe His Lys Asn Ile Glu Val Lys Ile
50                  55                  60                  65

TTT AAC CCC TAC TAT ATC CGC AAT AAA GGC TTG CGT TAT TTT GAA ATG      536
Phe Asn Pro Tyr Tyr Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu Met
                70                  75                  80

CTT GCG GAT TAT GAG CGC ATT AAA AAA CGC ATG CAC AAC AAG CTT TTC      584
Leu Ala Asp Tyr Glu Arg Ile Lys Lys Arg Met His Asn Lys Leu Phe
            85                  90                  95

ATC GTG GAT AAT TTC GCT GTC ATT ATA GGG GGG CGC AAT ATT GGG GAC      632
Ile Val Asp Asn Phe Ala Val Ile Ile Gly Gly Arg Asn Ile Gly Asp
        100                 105                 110

AAT TAT TTT GAT AAC GAT TTA GAC ACG AAT TTT TTA GAT TTA GAC GCT      680
Asn Tyr Phe Asp Asn Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp Ala
    115                 120                 125

TTG TTT TTT GGG GGG GTT GCT TCA AAA GCC AAA GAA AGC TTT GAA CGC      728
Leu Phe Phe Gly Gly Val Ala Ser Lys Ala Lys Glu Ser Phe Glu Arg
130                 135                 140                 145

TAT TGG AGA TTC CAC CGC TCT ATC CCT GTT TCA TTA CTA AGA ACC CAT      776
Tyr Trp Arg Phe His Arg Ser Ile Pro Val Ser Leu Leu Arg Thr His
                150                 155                 160

AAA AGA CTC AAA AAC AAC GCT AAA GAA ATC GCT AAA CTC CAT GAA AAA      824
Lys Arg Leu Lys Asn Asn Ala Lys Glu Ile Ala Lys Leu His Glu Lys
            165                 170                 175

ATC CCT ATC AGC GCT GAA GAC AAA AAC CAG TTT GAA AAA AAA GTC AAT      872
Ile Pro Ile Ser Ala Glu Asp Lys Asn Gln Phe Glu Lys Lys Val Asn
        180                 185                 190

GAT TTT ATA GAT CGT TTC CAA AAA TAC CAA TAC CCC ATT TAT TAT GGG      920
Asp Phe Ile Asp Arg Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr Gly
    195                 200                 205

AAT GCC ATT TTT TTA GCC GAT TCA CCC AAA AAA ATT GAC ACG CCC TTG      968
```

```
Asn Ala Ile Phe Leu Ala Asp Ser Pro Lys Lys Ile Asp Thr Pro Leu
210                 215                 220                 225

TAT TCG CCT ATC AAA ATC GCT TTT GAG AAA GCC CTT AAA AAC GCT AAG    1016
Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala Lys
                230                 235                 240

GAC TCC GTT TTT ATC GCT TCA TCG TAT TTT ATT CCA GGC AAA AAG ATG    1064
Asp Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys Met
            245                 250                 255

ATG AAA ATC TTT AAA AAT CAA ATT TCT AAG GGG ATT GAA TTG AAC ATC    1112
Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn Ile
        260                 265                 270

CTT ACC AAT TCC CTT TCA TCT ACT GAT GCG ATA GTG GTC TAT GGG GCA    1160
Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val Tyr Gly Ala
    275                 280                 285

TGG GAA AGG TAT CGC AAC CAA TTA GTG CGA ATG GGC GCG AAT GTC TAT    1208
Trp Glu Arg Tyr Arg Asn Gln Leu Val Arg Met Gly Ala Asn Val Tyr
290                 295                 300                 305

GAA ATA CGA AAC GAT TTT TTC AAC CGC CAG ATT AAA GGG CGC TTT AGC    1256
Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe Ser
                310                 315                 320

ACC AAA CAT TCC TTG CAT GGC AAG ACG ATT GTT TTT GAT GAC AAT TTA    1304
Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp Asp Asn Leu
            325                 330                 335

ACG CTT CTA GGG AGT TTC AAT ATT GAT CCG CGC TCT GCA TAC ATC AAC    1352
Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile Asn
        340                 345                 350

ACT GAA AGC GCG GTT TTG TTT GAC AAC CCG TCT TTT GCT AAA AGG GTG    1400
Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg Val
    355                 360                 365

CGT TTG TCG CTT AAA GAT CAT GCC CAA CAA TCA TGG CAT TTG GTG GTG    1448
Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His Leu Val Val
370                 375                 380                 385

TAT CGG CAT AGA GTG ATT TGG GAA GCG GTG GAA GAA GGC ATT TTA ATC    1496
Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu Ile
                390                 395                 400

CAT GAA AAA ACT TCG CCT GAC ACT TCC TTC TTT TTG CGC TTG ATT AAA    1544
His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile Lys
            405                 410                 415

GAA TGG TCT AAA GTC CTT CCT GAA AGA GAG CTT TAAAACTTTT AATGCGCTTT  1597
Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu
        420                 425

ATTTTGCGAA AAAGCGATGT TATTGGTAAC GGC                               1630
```

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 428 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```
Met Ser Gln Lys Ser Ile Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp
 1               5                  10                  15
Leu Ser Ser Gln Val Ile Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg
            20                  25                  30
Gly Val Lys Val Arg Ile Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp
        35                  40                  45
Phe Ser Asp Ile Met Leu Leu Asn Phe His Lys Asn Ile Glu Val Lys
    50                  55                  60
Ile Phe Asn Pro Tyr Tyr Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu
65                  70                  75                  80
Met Leu Ala Asp Tyr Glu Arg Ile Lys Lys Arg Met His Asn Lys Leu
                85                  90                  95
Phe Ile Val Asp Asn Phe Ala Val Ile Ile Gly Gly Arg Asn Ile Gly
            100                 105                 110
Asp Asn Tyr Phe Asp Asn Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp
        115                 120                 125
Ala Leu Phe Phe Gly Gly Val Ala Ser Lys Ala Lys Glu Ser Phe Glu
    130                 135                 140
Arg Tyr Trp Arg Phe His Arg Ser Ile Pro Val Ser Leu Leu Arg Thr
145                 150                 155                 160
His Lys Arg Leu Lys Asn Asn Ala Lys Glu Ile Ala Lys Leu His Glu
                165                 170                 175
Lys Ile Pro Ile Ser Ala Glu Asp Lys Asn Gln Phe Glu Lys Lys Val
            180                 185                 190
Asn Asp Phe Ile Asp Arg Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr
        195                 200                 205
Gly Asn Ala Ile Phe Leu Ala Asp Ser Pro Lys Lys Ile Asp Thr Pro
    210                 215                 220
Leu Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala
225                 230                 235                 240
Lys Asp Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys
                245                 250                 255
Met Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn
            260                 265                 270
Ile Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val Tyr Gly
        275                 280                 285
Ala Trp Glu Arg Tyr Arg Asn Gln Leu Val Arg Met Gly Ala Asn Val
    290                 295                 300
Tyr Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe
305                 310                 315                 320
Ser Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp Asp Asn
                325                 330                 335
Leu Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile
            340                 345                 350
Asn Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg
        355                 360                 365
Val Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His Leu Val
```

```
    370                 375                 380
Val Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu
385                 390                 395                 400
Ile His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile
                405                 410                 415
Lys Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 79...510
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```
AACTCTTTTG GTGTAGGATA GCGATCAAGG TTTTTATGAA AATAAAAGCC TAAAACAATT     60
TTAAAAAAAG GACTTTTG ATG AAA ACA TTT GAA ATT CTA AAA CAT TTG CAA      111
                    Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln
                     1               5                  10

GCG GAT GCG ATC GTG TTA TTT ATG AAA GTG CAT AAC TTC CAT TGG AAT      159
Ala Asp Ala Ile Val Leu Phe Met Lys Val His Asn Phe His Trp Asn
            15                  20                  25

GTG AAA GGC ACC GAT TTT TTC AAT GTG CAT AAA GCC ACT GAA GAA ATT      207
Val Lys Gly Thr Asp Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile
        30                  35                  40

TAT GAA GAG TTT GCG GAC ATG TTT GAC GAT CTC GCT GAA AGG ATC GTT      255
Tyr Glu Glu Phe Ala Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val
    45                  50                  55

CAA TTA GGG CAT CAC CCC TTA GTC ACT TTA TCC GAA GCG ATC AAA CTC      303
Gln Leu Gly His His Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu
60                  65                  70                  75

ACT CGT GTT AAA GAA GAA ACT AAA ACG AGC TTC CAC TCT AAA GAC ATC      351
Thr Arg Val Lys Glu Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile
                80                  85                  90

TTT AAA GAA ATT CTA GAG GAC TAC AAA TAT CTA GAA AAA GAA TTT AAA      399
Phe Lys Glu Ile Leu Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys
            95                  100                 105

GAG CTC TCT AAC ACC GCT GAA AAA GAA GGC GAT AAA GTT ACC GTA ACT      447
Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr
```

```
        110                 115                 120

TAT GCG GAT GAT CAA TTA GCC AAG TTG CAA AAA TCC ATT TGG ATG CTG     495
Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu
    125                 130                 135

CAA GCC CAT TTG GCT TAAGCGACCA AAAAGAAGCC AGCATGAGAG ATTACAGCGA     550
Gln Ala His Leu Ala
140
```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val
 1               5                  10                  15
Leu Phe Met Lys Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp
            20                  25                  30
Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile Tyr Glu Glu Phe Ala
        35                  40                  45
Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His
    50                  55                  60
Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu
65                  70                  75                  80
Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu
                85                  90                  95
Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr
            100                 105                 110
Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln
        115                 120                 125
Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu Gln Ala His Leu Ala
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...323
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
CTTTTTTCTC TTCCACTTTT TCCACTTTTT TAAGAGCCTT GTGTTTATGA  TTG GGC      56
                                                        Leu Gly
                                                         1

TTT TTG GGT TCA GGT TTG GGT TTT GGT TTA GGC TCA GGC TTA GGC TTT      104
Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu Gly Phe
          5                  10                  15

TCT ATA GGT TTT GGC GGG GTT GGC GGG GTT GGC GGA GTT GGG GGT GTG      152
Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly Gly Val
     20                  25                  30

GGA GGC GTT GGA GGT TTT TGG GGG CCA GCC AGC GTG GGT TTA GGA GCG      200
Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu Gly Ala
35                  40                  45                  50

CCC TGG GTG TTT TTA CTG GGA TCT TGC GAA TGG CCT CTT TTT AAA ACC      248
Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe Lys Thr
                55                  60                  65

AAT AAA TTT TCA GGA TTT AAT TTA ACA AGC TTG GGT TTT GAA GGA AAA      296
Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu Gly Lys
           70                  75                  80

AAA TCT TCT CTG TGT TCA AAT AAA AAA TAAATCAACC AGTGTAACAA TACAGAC    350
Lys Ser Ser Leu Cys Ser Asn Lys Lys
        85                  90

AGAATGAGAG AAAAGAAAAA ATTCCT                                        376
```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```
Leu Gly Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu
 1               5                  10                  15
Gly Phe Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly
            20                  25                  30
Gly Val Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu
        35                  40                  45
Gly Ala Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe
    50                  55                  60
Lys Thr Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu
65                  70                  75                  80
Gly Lys Lys Ser Ser Leu Cys Ser Asn Lys Lys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2890 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 458...2836
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```
TCAAAATTTA AGTTAATTTT AATAATTATT TTTATAGTAT GCATCGGTTT GAATTAAATG     60
AGAAAGGTTA TCACAATGAA TGGTTATTTG AGAGTAAAAA CCTCTTATTT TTTAGCGTTG    120
AACGCTTTGA CTTTTTTGTC TTTTAACTCT TTGGTGGGCG CGAAAGAACA GCATCACACT    180
TTGCAAAAAG TGACAACCAC TGAGCAAAAA TTCAATCCAA GCGCGCCGCT TTCATGGCAA    240
AGCGAAGAGA TGCGTAATTC CACAAGCTCT CGCACGGTGA TTTCCAACAA GGAACTCAAA    300
AAAACGGGGA ATTTGAATAT TGAAAACGCC TTGCAAAACG TGCCAGGGAT TCAAATCAGA    360
GACGCTACAG GCACAGGCGT GCTGCCTAAA ATTTCGGTGC TCAAAATTTA AGTTAATTTT    420
AATAATTATT TTTATAGTAT GCATCGGTTT GAATTAA ATG AGA AAG GTT ATC ACA     475
                                          Met Arg Lys Val Ile Thr
                                           1               5

ATG AAT GGT TAT TTG AGA GTA AAA ACC TCT TAT TTT TTA GCG TTG AAC      523
Met Asn Gly Tyr Leu Arg Val Lys Thr Ser Tyr Phe Leu Ala Leu Asn
            10                  15                  20

GCT TTG ACT TTT TTG TCT TTT AAC TCT TTG GTG GGC GCG AAA GAA CAG      571
Ala Leu Thr Phe Leu Ser Phe Asn Ser Leu Val Gly Ala Lys Glu Gln
        25                  30                  35

CAT CAC ACT TTG CAA AAA GTG ACA ACC ACT GAG CAA AAA TTC AAT CCA      619
His His Thr Leu Gln Lys Val Thr Thr Thr Glu Gln Lys Phe Asn Pro
    40                  45                  50

AGC GCG CCG CTT TCA TGG CAA AGC GAA GAG ATG CGT AAT TCC ACA AGC      667
Ser Ala Pro Leu Ser Trp Gln Ser Glu Glu Met Arg Asn Ser Thr Ser
55                  60                  65                  70

TCT CGC ACG GTG ATT TCC AAC AAG GAA CTC AAA AAA ACG GGG AAT TTG      715
Ser Arg Thr Val Ile Ser Asn Lys Glu Leu Lys Lys Thr Gly Asn Leu
                75                  80                  85

AAT ATT GAA AAC GCC TTG CAA AAC GTG CCA GGG ATT CAA ATC AGA GAC      763
Asn Ile Glu Asn Ala Leu Gln Asn Val Pro Gly Ile Gln Ile Arg Asp
            90                  95                  100

GCT ACA GGC ACA GGC GTG CTG CCT AAA ATT TCG GTG CGC GGT TTT GGT      811
Ala Thr Gly Thr Gly Val Leu Pro Lys Ile Ser Val Arg Gly Phe Gly
        105                 110                 115

GGG GGC GGT AAC GGG CAT AGC AAT ACC AAC ATG ATT TTA GTC AAT GGT      859
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Gly Gly Gly Asn Gly His Ser Asn Thr Asn Met Ile Leu Val Asn Gly
    120                 125                 130

ATC CCC ATT TAT GGC GCG CCG TAT TCC AAT ATT GAA CTG GCG ATT TTC      907
Ile Pro Ile Tyr Gly Ala Pro Tyr Ser Asn Ile Glu Leu Ala Ile Phe
135                 140                 145                 150

CCT GTA ACT TTC CAG TCA GTG GAT AGG ATT GAT GTG ATT AAA GGG GGC      955
Pro Val Thr Phe Gln Ser Val Asp Arg Ile Asp Val Ile Lys Gly Gly
                155                 160                 165

ACG AGC GTG CAA TAC GGC CCT AAT ACT TTT GGA GGC GTG GTG AAT ATC     1003
Thr Ser Val Gln Tyr Gly Pro Asn Thr Phe Gly Gly Val Val Asn Ile
            170                 175                 180

ATC ACT AAA GAA ATC CCT AAA GAG TGG GAA AAT CAA GCG GCT GAA AGG     1051
Ile Thr Lys Glu Ile Pro Lys Glu Trp Glu Asn Gln Ala Ala Glu Arg
        185                 190                 195

ATC ACT TTT TGG GGG CGA TCC TCT AAT GGG AAT TTT GTA GAT CCC AAA     1099
Ile Thr Phe Trp Gly Arg Ser Ser Asn Gly Asn Phe Val Asp Pro Lys
    200                 205                 210

GAA AAA GGC AAG CCT TTA GCC CAA ACT TTA GGA AAC CAA ATG CTG TTT     1147
Glu Lys Gly Lys Pro Leu Ala Gln Thr Leu Gly Asn Gln Met Leu Phe
215                 220                 225                 230

AAC ACT TAC GGG CGA ACG GCT GGA ATG TTG GGT AAG CAT GTA GGA ATT     1195
Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu Gly Lys His Val Gly Ile
                235                 240                 245

AGC GCT CAA GGC AAT TGG ATT AAC GGG CAA GGT TTC AGG CAA AAC AGC     1243
Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln Gly Phe Arg Gln Asn Ser
            250                 255                 260

CCC ACA AAG GTG CAA AAC TAC TTG CTT GAT GCG GTT TAT AAG ATT AAT     1291
Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp Ala Val Tyr Lys Ile Asn
        265                 270                 275

GCG ACC AAT ACT TTT AAA GCT TAT TAC CAA TAT TAT CAA TAC AAC TCT     1339
Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln Tyr Tyr Gln Tyr Asn Ser
    280                 285                 290

TAC CAT CCA GGC ACT TTG AGT GCA CAA GAT TAT GCT TAT AAC CGC TTC     1387
Tyr His Pro Gly Thr Leu Ser Ala Gln Asp Tyr Ala Tyr Asn Arg Phe
295                 300                 305                 310

ATT AAT GAG CGC CCT GAC AAT CAA GAT GGA GGG CGA GCC AAG CGC TTT     1435
Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly Gly Arg Ala Lys Arg Phe
                315                 320                 325

GGG ATC GTG TAT CAA AAT TAT TTT GGC GAT CCG GAT AGG AAA GTG GGG     1483
Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp Pro Asp Arg Lys Val Gly
            330                 335                 340

GGA GAT TTT AAA TTC ACT TAT TTC ACG CAT GAC ATG AGT AGG GAT TTT     1531
Gly Asp Phe Lys Phe Thr Tyr Phe Thr His Asp Met Ser Arg Asp Phe
        345                 350                 355
```

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GGG TTT TCC AAC CAA TAC CAA AGC GTG TAT ATG AGC AGT CAA AAC AAG     1579
Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr Met Ser Ser Gln Asn Lys
    360                 365                 370

ATT TTA CCT TTT AAA GGC AAG GGA AAA ATT AGC GCG ACT AAC CCT AAT     1627
Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile Ser Ala Thr Asn Pro Asn
375                 380                 385                 390

TGC GGT TTG TAT TCT TAT AGC GAC ACG AAC AGC CCT TGT TGG CAA TTT     1675
Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn Ser Pro Cys Trp Gln Phe
                395                 400                 405

TTT GAC AAT ATC CGC CGA TCC GTG GTG AAT GCC TTT GAG CCA AAA CTC     1723
Phe Asp Asn Ile Arg Arg Ser Val Val Asn Ala Phe Glu Pro Lys Leu
            410                 415                 420

AAT CTT ATC GTC AAT ACC GGT AAA GTC AAA CAA ACT TTT AAT ATG GGA     1771
Asn Leu Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Asn Met Gly
        425                 430                 435

ATG CGC TTT TTA ACT GAA GAT TTA TAC CGC CGA TCC ACC ACC AGG AAA     1819
Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg Arg Ser Thr Thr Arg Lys
    440                 445                 450

AAC CCT AGC ATG CCT AAT AAT GGG AGT GGT TTT GAT GCA GGA ACT TCA     1867
Asn Pro Ser Met Pro Asn Asn Gly Ser Gly Phe Asp Ala Gly Thr Ser
455                 460                 465                 470

CTC AAT AAT TTC AAC AAT TAT ACC GCT GTG TAT GCC AGC GAT GAG ATC     1915
Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val Tyr Ala Ser Asp Glu Ile
                475                 480                 485

AAT TTC AAT AAC GGC ATG CTA ACG ATC ACG CCG GGC TTG AGA TAC ACT     1963
Asn Phe Asn Asn Gly Met Leu Thr Ile Thr Pro Gly Leu Arg Tyr Thr
            490                 495                 500

TTT TTA AAT TAC GAA AAA AAA GAC GCT CCT CCT TTT AAA GCA GGC CAA     2011
Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro Pro Phe Lys Ala Gly Gln
        505                 510                 515

ACA GGA AAA ACC ATT AAA GAT CGT TAT AAC CAA TGG AAT CCA GCA GTG     2059
Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn Gln Trp Asn Pro Ala Val
    520                 525                 530

AAT GTC GGC TAT AAA CCC ATT AAA GAA TTG TTG TTT TAT TTC AAT TAC     2107
Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu Leu Phe Tyr Phe Asn Tyr
535                 540                 545                 550

CAA AGA AGC TAC ATT CCG CCT CAA TTC AGC AAT ATC GGT AGT TTT GTA     2155
Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser Asn Ile Gly Ser Phe Val
                555                 560                 565

GGC ACA AGC ACG GAT TAT TTT CAA ATC TTT AAT GTC ATG GAA GGC GGC     2203
Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe Asn Val Met Glu Gly Gly
            570                 575                 580

TCA AGA TAT TAT TTT AAC AAC CAA GTG AGT TTT AAC GCG AAT TAT TTT     2251
Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser Phe Asn Ala Asn Tyr Phe
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          585                 590                 595

GTG ATT TTT GCG AAT AAC TAT TTT ACC GGG CGC TAT GGG GAT AAT AAA    2299
Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly Arg Tyr Gly Asp Asn Lys
    600                 605                 610

GAG CCG GTC AAT GCG AGA TCG CAA GGC GTG GAG CTA GAG TTG TAT TAC    2347
Glu Pro Val Asn Ala Arg Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr
615                 620                 625                 630

ACG CCG ATT AGA GGG CTT AAT TTC CAT GCG GCT TAC ACT TTC ATA GAT    2395
Thr Pro Ile Arg Gly Leu Asn Phe His Ala Ala Tyr Thr Phe Ile Asp
                635                 640                 645

GCC AAT ATC ACA AGC CAC ACG ATG GTT ACT AAC CCC GCT AAT CCT AAA    2443
Ala Asn Ile Thr Ser His Thr Met Val Thr Asn Pro Ala Asn Pro Lys
            650                 655                 660

GGG CCT AAA AAA GAT ATT TTT GGC AAA AAG CTC CCT TTT GTA AGC CCG    2491
Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys Leu Pro Phe Val Ser Pro
        665                 670                 675

CAC CAA TTC ATT TTA GAC GCG AGC TAC ACT TAC GCT AAA ACC ACG ATT    2539
His Gln Phe Ile Leu Asp Ala Ser Tyr Thr Tyr Ala Lys Thr Thr Ile
    680                 685                 690

GGG TTG AGT TCT TTC TTT TAT AGC CGA ACT TAT AGC GAT GTG TTA AAC    2587
Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr Tyr Ser Asp Val Leu Asn
695                 700                 705                 710

ACC GTG CCT TTT ATT CAA TAC GCG CCC ACG ATC AAA AAT GGT GCT ATC    2635
Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr Ile Lys Asn Gly Ala Ile
                715                 720                 725

ACT ACC AAA ACA GCG GGC ATG ACG CCA TGG TAT TGG GTG TGG AAT TTG    2683
Thr Thr Lys Thr Ala Gly Met Thr Pro Trp Tyr Trp Val Trp Asn Leu
            730                 735                 740

CAA ATT TCT ACC ACT TTT TGG GAA CGC AAA AAG CAA AGC GTT AAT GCG    2731
Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys Lys Gln Ser Val Asn Ala
        745                 750                 755

AGC TTG CAA ATC AAT AAC ATT TTT AAC ATG AAA TAT TGG TTT AGC GGG    2779
Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Trp Phe Ser Gly
    760                 765                 770

ATA GGC ACT AGC CTA ACG GGA AAG AAG CCG CGC CTC CTA GGA GCA TCA    2827
Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro Arg Leu Leu Gly Ala Ser
775                 780                 785                 790

CAG CGT ATG TGAGCTATCA TTTTTAATTT TAGGGTTGTA ATGTTTTGAG AAGTTGGGC  2885
Gln Arg Met

GTAAA                                                              2890
```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 793 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```
Met Arg Lys Val Ile Thr Met Asn Gly Tyr Leu Arg Val Lys Thr Ser
 1               5                  10                  15
Tyr Phe Leu Ala Leu Asn Ala Leu Thr Phe Leu Ser Phe Asn Ser Leu
            20                  25                  30
Val Gly Ala Lys Glu Gln His His Thr Leu Gln Lys Val Thr Thr Thr
        35                  40                  45
Glu Gln Lys Phe Asn Pro Ser Ala Pro Leu Ser Trp Gln Ser Glu Glu
    50                  55                  60
Met Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu
65                  70                  75                  80
Lys Lys Thr Gly Asn Leu Asn Ile Glu Asn Ala Leu Gln Asn Val Pro
                85                  90                  95
Gly Ile Gln Ile Arg Asp Ala Thr Gly Thr Gly Val Leu Pro Lys Ile
            100                 105                 110
Ser Val Arg Gly Phe Gly Gly Gly Gly Asn Gly His Ser Asn Thr Asn
        115                 120                 125
Met Ile Leu Val Asn Gly Ile Pro Ile Tyr Gly Ala Pro Tyr Ser Asn
    130                 135                 140
Ile Glu Leu Ala Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile
145                 150                 155                 160
Asp Val Ile Lys Gly Gly Thr Ser Val Gln Tyr Gly Pro Asn Thr Phe
                165                 170                 175
Gly Gly Val Val Asn Ile Ile Thr Lys Glu Ile Pro Lys Glu Trp Glu
            180                 185                 190
Asn Gln Ala Ala Glu Arg Ile Thr Phe Trp Gly Arg Ser Ser Asn Gly
        195                 200                 205
Asn Phe Val Asp Pro Lys Glu Lys Gly Lys Pro Leu Ala Gln Thr Leu
    210                 215                 220
Gly Asn Gln Met Leu Phe Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu
225                 230                 235                 240
Gly Lys His Val Gly Ile Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln
                245                 250                 255
Gly Phe Arg Gln Asn Ser Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp
            260                 265                 270
Ala Val Tyr Lys Ile Asn Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln
        275                 280                 285
Tyr Tyr Gln Tyr Asn Ser Tyr His Pro Gly Thr Leu Ser Ala Gln Asp
    290                 295                 300
Tyr Ala Tyr Asn Arg Phe Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly
305                 310                 315                 320
Gly Arg Ala Lys Arg Phe Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp
                325                 330                 335
Pro Asp Arg Lys Val Gly Gly Asp Phe Lys Phe Thr Tyr Phe Thr His
            340                 345                 350
Asp Met Ser Arg Asp Phe Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr
        355                 360                 365
Met Ser Ser Gln Asn Lys Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile
```

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    370                 375                 380
Ser Ala Thr Asn Pro Asn Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn
385                 390                 395                 400
Ser Pro Cys Trp Gln Phe Phe Asp Asn Ile Arg Arg Ser Val Val Asn
                405                 410                 415
Ala Phe Glu Pro Lys Leu Asn Leu Ile Val Asn Thr Gly Lys Val Lys
            420                 425                 430
Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg
        435                 440                 445
Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly
    450                 455                 460
Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val
465                 470                 475                 480
Tyr Ala Ser Asp Glu Ile Asn Phe Asn Asn Gly Met Leu Thr Ile Thr
                485                 490                 495
Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro
            500                 505                 510
Pro Phe Lys Ala Gly Gln Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn
        515                 520                 525
Gln Trp Asn Pro Ala Val Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu
    530                 535                 540
Leu Phe Tyr Phe Asn Tyr Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser
545                 550                 555                 560
Asn Ile Gly Ser Phe Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe
                565                 570                 575
Asn Val Met Glu Gly Gly Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser
            580                 585                 590
Phe Asn Ala Asn Tyr Phe Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly
        595                 600                 605
Arg Tyr Gly Asp Asn Lys Glu Pro Val Asn Ala Arg Ser Gln Gly Val
    610                 615                 620
Glu Leu Glu Leu Tyr Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala
625                 630                 635                 640
Ala Tyr Thr Phe Ile Asp Ala Asn Ile Thr Ser His Thr Met Val Thr
                645                 650                 655
Asn Pro Ala Asn Pro Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys
            660                 665                 670
Leu Pro Phe Val Ser Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr
        675                 680                 685
Tyr Ala Lys Thr Thr Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr
    690                 695                 700
Tyr Ser Asp Val Leu Asn Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr
705                 710                 715                 720
Ile Lys Asn Gly Ala Ile Thr Thr Lys Thr Ala Gly Met Thr Pro Trp
                725                 730                 735
Tyr Trp Val Trp Asn Leu Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys
            740                 745                 750
Lys Gln Ser Val Asn Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met
        755                 760                 765
Lys Tyr Trp Phe Ser Gly Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro
    770                 775                 780
Arg Leu Leu Gly Ala Ser Gln Arg Met
785                 790
```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...353
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```
TCGTCTTTTG TCGGTTCAAA AAAATCTCTC GACTTAAAAA AACCTATTAA  ATC AAG      56
                                                        Ile Lys
                                                         1

ATA ATC TAT CAA ATC ATC AAG TTT TTT CGT TCT AAG AAT TTT ATT TTG      104
Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe Ile Leu
         5                  10                  15

TTT TTT AGA ATA GCA ACG ATA AAG TTC TTC TTT TAT CTC ATT TGG GAA      152
Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile Trp Glu
    20                  25                  30

TTT TTG AAT GTT ATA GAC AAT TTC ACT ATC TCT TTG ATT TTG TTT ATA      200
Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu Phe Ile
35                  40                  45                  50

TTT TTT AGC CCC ATA CCA AAG AAA TAT TTG ATA AAA AAT AAG AAA AAT      248
Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys Lys Asn
                55                  60                  65

AGC GTA AAA GAA AAA GAA AAT AAA GAA AAA AGA AAG AGA AAA AGA AAG      296
Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys Arg Lys
            70                  75                  80

GAT TTT GTT TTG GGT GTA TTG GAA AAT AGA CTC AAA AAT CAA TTG AAA      344
Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln Leu Lys
        85                  90                  95

AAC CCC TTT TAGATTAAAA ATAAAAACAA TAAGCGAAAC GACAAAAGCA AGCAGAAAA   402
Asn Pro Phe
    100

GAAG                                                                406
```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```
Ile Lys Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe
 1               5                  10                  15
Ile Leu Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile
            20                  25                  30
Trp Glu Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu
        35                  40                  45
Phe Ile Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys
    50                  55                  60
Lys Asn Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys
65                  70                  75                  80
Arg Lys Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln
                85                  90                  95
Leu Lys Asn Pro Phe
            100
```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 89...1087
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```
GATTTTGTGA AAAATAGTTT CATTTTTACT GCTTGTATTT CCTTAATGGT GTTATAATCG      60
CTCCATAAAT CATACAAAAA GGATCGTT ATG TTA GTT ACT CGC TTT AAA AAA          112
                               Met Leu Val Thr Arg Phe Lys Lys
                                1               5

GCT TTA ATC TCT TAT TCT TTA GGC GCG CTT CTT GTT TCA TCG TTA TTG         160
Ala Leu Ile Ser Tyr Ser Leu Gly Ala Leu Leu Val Ser Ser Leu Leu
    10                  15                  20

GGC GTG GCT AGT GCT TCC AAT CAA GAA ATC CAA GTC AAA GAT TAT TTT         208
Gly Val Ala Ser Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe
25                  30                  35                  40

GGG GAT CAA GCC ATC AAG CTT CCT GTT TCT AAA ATA ATC TAC TTG GGT         256
Gly Asp Gln Ala Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly
                45                  50                  55

AGC TTT GCA GAA GTG CCT GCT ATG TTC CAT ACT TGG GAT AGG GTC GTG         304
Ser Phe Ala Glu Val Pro Ala Met Phe His Thr Trp Asp Arg Val Val
            60                  65                  70

GGA ATT TCG GAT TAC GCT TTT AAA TCT GAT ATT GTT AAA GCT ACT CTC         352
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu
```

```
        75                  80                  85

AAA GAT CCT AAA CGC ATT AAA TCC ATG AGC AGT GAT CAT GTG GCG GCG      400
Lys Asp Pro Lys Arg Ile Lys Ser Met Ser Ser Asp His Val Ala Ala
    90                  95                  100

TTG AAT GTG GAG CTT TTA AAA AAG CTT GGC CCC GAT CTT GTG GTA ACC      448
Leu Asn Val Glu Leu Leu Lys Lys Leu Gly Pro Asp Leu Val Val Thr
105                 110                 115                 120

TTT GTG GGC AAC CCT AAA GCG GTA GAG CAT GCG AAA AAA TTT GGT ATA      496
Phe Val Gly Asn Pro Lys Ala Val Glu His Ala Lys Lys Phe Gly Ile
                125                 130                 135

TTA TTT CTT TCT TTC CAA GAA AAA ACC ATT GCA GAA GTC ATG GAA GAT      544
Leu Phe Leu Ser Phe Gln Glu Lys Thr Ile Ala Glu Val Met Glu Asp
            140                 145                 150

ATT GAC GCT CAA GCT AAA GCC TTA GAA ATT GAT GCT TCT AAA AAA CTG      592
Ile Asp Ala Gln Ala Lys Ala Leu Glu Ile Asp Ala Ser Lys Lys Leu
        155                 160                 165

GCC AAA ATG CAA GAA ACT TTG GAT TTT ATT GCT GAG CGT TTG AAA GGT      640
Ala Lys Met Gln Glu Thr Leu Asp Phe Ile Ala Glu Arg Leu Lys Gly
    170                 175                 180

GTC AAA AAG AAA AAA GGG GTG GAG CTT TTC CAT AAG GCC AAT AAG ATC      688
Val Lys Lys Lys Lys Gly Val Glu Leu Phe His Lys Ala Asn Lys Ile
185                 190                 195                 200

AGC GGC CAT CAA GCC CTT GAT TCA GAC ATT TTA GAA AAA GGA GGC ATA      736
Ser Gly His Gln Ala Leu Asp Ser Asp Ile Leu Glu Lys Gly Gly Ile
                205                 210                 215

GAC AAT TTT GGC TTG AAA TAT GTC AAA TTT GGG CGT GCT GAC ATT AGC      784
Asp Asn Phe Gly Leu Lys Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser
            220                 225                 230

GTG GAA AAA ATC GTT AAA GAA AAC CCT GAG ATT ATC TTT ATT TGG TGG      832
Val Glu Lys Ile Val Lys Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp
        235                 240                 245

ATA AGC CCA CTC ACG CCT GAA GAT GTG TTA AAC AAC CCC AAA TTT GCT      880
Ile Ser Pro Leu Thr Pro Glu Asp Val Leu Asn Asn Pro Lys Phe Ala
    250                 255                 260

ACC ATC AAA GCC ATT AAA AAC AAG CAG GTT TAT AAA CTC CCC ACA ATG      928
Thr Ile Lys Ala Ile Lys Asn Lys Gln Val Tyr Lys Leu Pro Thr Met
265                 270                 275                 280

GAT ATT GGC GGG CCT AGA GCC CCA CTC ATA AGT CTT TTT ATC GCT CTA      976
Asp Ile Gly Gly Pro Arg Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu
                285                 290                 295

AAA GCC CAC CCT GAA GCC TTT AAG GGC GTG GAT ATT AAT GCG ATT GTT     1024
Lys Ala His Pro Glu Ala Phe Lys Gly Val Asp Ile Asn Ala Ile Val
            300                 305                 310
```

```
AAA GAC TAC TAT AAA GTG GTT TTT GAT TTG AAT GAT GCA GAG GTT GAA    1072
Lys Asp Tyr Tyr Lys Val Val Phe Asp Leu Asn Asp Ala Glu Val Glu
        315                 320                 325

CCC TTT TTA TGG CAT TAATTTTTAA AAAAGGGCTG ATATTTTTAG CCCTTTGTGT A  1128
Pro Phe Leu Trp His
    330

TCGCGCTAGG ATTAG                                                   1143
```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```
Met Leu Val Thr Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly
 1               5                  10                  15
Ala Leu Leu Val Ser Ser Leu Leu Gly Val Ala Ser Ala Ser Asn Gln
            20                  25                  30
Glu Ile Gln Val Lys Asp Tyr Phe Gly Asp Gln Ala Ile Lys Leu Pro
        35                  40                  45
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met
    50                  55                  60
Phe His Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys
65                  70                  75                  80
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Lys Arg Ile Lys Ser
                85                  90                  95
Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu Leu Lys Lys
            100                 105                 110
Leu Gly Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val
        115                 120                 125
Glu His Ala Lys Lys Phe Gly Ile Leu Phe Leu Ser Phe Gln Glu Lys
    130                 135                 140
Thr Ile Ala Glu Val Met Glu Asp Ile Asp Ala Gln Ala Lys Ala Leu
145                 150                 155                 160
Glu Ile Asp Ala Ser Lys Lys Leu Ala Lys Met Gln Glu Thr Leu Asp
                165                 170                 175
Phe Ile Ala Glu Arg Leu Lys Gly Val Lys Lys Lys Lys Gly Val Glu
            180                 185                 190
Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Leu Asp Ser
        195                 200                 205
Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val
    210                 215                 220
Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn
225                 230                 235                 240
Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro Glu Asp
                245                 250                 255
Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys Asn Lys
            260                 265                 270
Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro
```

```
        275                 280                 285
Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys
    290                 295                 300
Gly Val Asp Ile Asn Ala Ile Val Lys Asp Tyr Tyr Lys Val Val Phe
305                 310                 315                 320
Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 898 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...845
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```
GGGGGGTTAT AGTAAAAACA TGCAAGTAAT TTAAAGTTAA TTTAAGATAA  TTA GGC      56
                                                        Leu Gly
                                                         1

ACA ATA GCC ACA AAA AGT TTA AGG CTG TAT TTG AAA ACT CTA TTT AGT      104
Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu Phe Ser
          5                  10                  15

ATT TAT CTC TTT TTA TCG TTG AAC CCA CTC TTT TTA GAA GCT AAT GAA      152
Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala Asn Glu
     20                  25                  30

ATC ACT TGG TCT AAA TTC TTG GAA AAT TTT AAA AAC AAG AAT GAT GAT      200
Ile Thr Trp Ser Lys Phe Leu Glu Asn Phe Lys Asn Lys Asn Asp Asp
35                  40                  45                  50

GAC AAA CCT AAA CCC CTA ACT ATT GAT AAA AAC AAT GAA AAA CAG CAA      248
Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys Gln Gln
                55                  60                  65

ATC TTA GAC AAA AAC CAG CAA ATC TTA AAA AGG GCT TTG GAA AAA AGC      296
Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu Lys Ser
          70                  75                  80

CTT AAA TTC TTT TTC ATT TTT GGA TAC AAC TAT TCG CAA GCC ACT TTT      344
Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala Thr Phe
          85                  90                  95

TCA ACT TCT AAC CAA ACC TTG ACT TTT GTA GCC AAT AGC ATA GGG TTT      392
Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile Gly Phe
    100                 105                 110
```

```
AAC ACC GCT ACC GGT TTA GAG CAT TTT TTA AGA AAC CAC CCT AAA GTC      440
Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro Lys Val
115                 120                 125                 130

GGT TTT AGA ATC TTT AGC GTC TAT AAC TAT TTC CAT TCT GTT TCC CTC      488
Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val Ser Leu
                135                 140                 145

TCC CAG CCT CAA ACC TTA ATG GTG CAA AAT TAT GGG GGC GCG TTA GAT      536
Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala Leu Asp
            150                 155                 160

TTT TCT TGG ATT TTT GTA GAT AAA AAT ATT TAT CGC TTT AGG AGT TAT      584
Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg Ser Tyr
        165                 170                 175

TTA GGG ATC GCT TTA GAA CAA GGG GTG TTG TTA GTG GAT ACG ATT AAA      632
Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr Ile Lys
    180                 185                 190

CCA GGT GCT ATC ACA ACG ATT ATC CCA AGA ACC AAA AAA ACC TTT TTT      680
Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr Phe Phe
195                 200                 205                 210

CAA GCC CCT TTG CGT TTT GGT TTT ATC GTG GAT TTT ATC GGC TAT TTG      728
Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly Tyr Leu
                215                 220                 225

TCT TTG CAA TTA GGG ATT GAA ATG CCT TTA GTG AGG AAT GTT TTT TAC      776
Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val Phe Tyr
            230                 235                 240

ACC TAC AAC AAC CAT CAA GAA AGA TTC AAA CCA CGA TTT AAC GCT AAT      824
Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn Ala Asn
        245                 250                 255

CTT TCT TTA ATC GTT TCG TTT TAGCCCCCCT TTTCCCCTTT TAAATAAGCC CATG    879
Leu Ser Leu Ile Val Ser Phe
    260                 265

ATTTTCCTAG GGTATTTTA                                                898
```

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```
Leu Gly Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu
 1               5                  10                  15
Phe Ser Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala
```

```
                20                  25                  30
Asn Glu Ile Thr Trp Ser Lys Phe Leu Glu Asn Phe Lys Asn Lys Asn
        35                  40                  45
Asp Asp Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys
    50                  55                  60
Gln Gln Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu
65                  70                  75                  80
Lys Ser Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala
                85                  90                  95
Thr Phe Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile
            100                 105                 110
Gly Phe Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro
        115                 120                 125
Lys Val Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val
    130                 135                 140
Ser Leu Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala
145                 150                 155                 160
Leu Asp Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg
                165                 170                 175
Ser Tyr Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr
            180                 185                 190
Ile Lys Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr
        195                 200                 205
Phe Phe Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly
    210                 215                 220
Tyr Leu Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val
225                 230                 235                 240
Phe Tyr Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn
                245                 250                 255
Ala Asn Leu Ser Leu Ile Val Ser Phe
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 742 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...689
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```
GCACTTCACG CATTCCATAA ACGATATTGA TTATTTGCTA GACAGCTTGA  AAA AAG      56
                                                        Lys Lys
                                                         1

CAG TTA AAA AAT TGC GTT AAG CTA AAA CTA TTT TTA AGG AAA AAT TTG      104
Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys Asn Leu
 5                  10                  15
```

```
GAT ATT TTA GAT TTG AAC AAA GCG CAA GCG GTG CAA CAA AAT GAA CAA      152
Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu Gln
    20                  25                  30

GAG GTA GAG GAT AAA GAG CGA GAG TCT AAA GAG CCG GTG GTT TTA GAA      200
Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu Glu
35                  40                  45                  50

GAT TTG AGC GCT TTA GCG TGG CTT GAA TTA GAA GAG TTT AGC CGC CTT      248
Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg Leu
                55                  60                  65

TCA GGG CTT CCT AAA GAA AGG ATT TTG GAA TTA GTG AAT CTT GGT AAA      296
Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly Lys
            70                  75                  80

ATC AAG AGC AAA ATA AGC AGC AAC AAG CTT TTA ATT GAT GCG AGC AGC      344
Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser Ser
        85                  90                  95

GGG ACA AAC GCT TTA ATC AAA AAG GTA GAA AAT AGT TTG ATT TCT ATG      392
Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser Met
    100                 105                 110

GAT ATG AAC GGG CGT TCT TTA GAA CCT GTG TTT GTG GAA AAG ACC ATT      440
Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr Ile
115                 120                 125                 130

AAC ACG ATT TTA AAC TTG CAT GAT AAG GTC ATT GGC GCT AAA GAT GAA      488
Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp Glu
                135                 140                 145

ACG ATT TCA GCC TTT AAA AAT GAA AAC ATG TTT TTA AAA GAC GCT TTA      536
Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala Leu
            150                 155                 160

ATC TCT ATG CAA GAA GTC TAT GAA GAA GAT AAA AAA ACC ATT GAT CTT      584
Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp Leu
        165                 170                 175

TTG CGC GAT GAA CTC AAT CAA GCG AGA GAA GAA ATT GAA TTT ATG AAG      632
Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met Lys
    180                 185                 190

AGG AAA TAC CGC TTG ATG TGG GGG AAA GTC GCT GAC ATG AGC AGC GTG      680
Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser Val
195                 200                 205                 210

AAT AAA AAG TAGTTTTAAA TTAACGCCCA TGCTGAGGGC TTATTAGCGG TAATTTTAG   738
Asn Lys Lys

GTGA                                                                742
```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```
Lys Lys Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys
 1               5                  10                  15
Asn Leu Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn
            20                  25                  30
Glu Gln Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val
        35                  40                  45
Leu Glu Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser
    50                  55                  60
Arg Leu Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu
65                  70                  75                  80
Gly Lys Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala
                85                  90                  95
Ser Ser Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile
            100                 105                 110
Ser Met Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys
        115                 120                 125
Thr Ile Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys
    130                 135                 140
Asp Glu Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp
145                 150                 155                 160
Ala Leu Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile
                165                 170                 175
Asp Leu Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe
            180                 185                 190
Met Lys Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser
        195                 200                 205
Ser Val Asn Lys Lys
    210
```